Curriculum Vitae

Chaochun Wei ScD

Professor
Department of Bioinformatics and Biostatistics
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Research interests

- Finding functional elements in genomes
  - Gene prediction, alternative splicing prediction
  - Regulatory element finding
  - Identification and evolutionary analysis of repeat regions in genomes
- Metagenomics, pan-genomics
- High performance computing for bioinformatics

Education

2000-2006	D.Sc. in Computer Science Washington University in St. Louis, USA
1996-1999	M.E. in Signal and Information Processing Beijing University, China
1991-1996	B.S. in Mathematics Beijing University, China

Experience

2015-Present	Professor
2014-2019	Associate Chair of Department
2008-2015	Associate Professor Department of Bioinformatics and Biostatistics Shanghai Jiao Tong University, Shanghai, China
2008-Present	Group Leader, joint appointment in Shanghai Center for Bioinformation Technology
2006-2007	Software Engineer Microsoft Company, Seattle, WA, USA
2000-2006	Research Assistant in Computational Biology CSE Department, Washington University in St. Louis, USA
1996-1999	Research Assistant in Signal Processing Center for Information Science, Beijing University, China

Funding

As PI

1. Computational Biology Program of Science and Technology Commission of Shanghai Municipality (STCSM) ((24JS2840300, PI, ￥3M)， 2024.12-2027.11

   “Cancer pan-genomics-based mutation identification and application in precision diagnosis and therapy”

2. National Key Research and Development Program (2023YFF1001600, PI, ￥25M), 2023.12-2027.11

   “Validation and evaluation of genome editing in agricultural plants and animals”

3. Science and Technology Commission of Shanghai Municipality (22ZR1433600, ￥200K) 2022.4-2025.3

   “Identification and characterization of horizontal gene transfer in bat genomes”

4. NSFC Project (32170643, PI, ￥580K), 2022.1-2025.12

   "A third-generation-sequencing-based pan-genome construction method and its application in rice genome analysis"

5. Science and Technology Commission of Shanghai Municipality (20ZR1428200, ￥200K) 2020.7-2023.6

   “Construction of rice pan-genome browser 2.0”

6. Medicine and Engineering joint project (YG2017ZD01, co-PI, ￥750K) 2018.1-2020.12

   “Data analysis platform for big omics data from gastric cancer considering complex cancer phenotypes and microbiome diversity”

7. NSFC Project (61472246, PI, ￥800K), 2015.1-2018.12

   " Finding and characterizing complex structure sequence modules in metagenomes"

8. NSFC Project (61272250, PI, ￥800K), (2013.1-2016.12)

   “Finding and characterization of genes containing repeat regions”

9. NSFC Project (60970050, PI, ￥300K), (2010.1-2012.12)

   “An index measuring gene structure variation and its application on the study of disease susceptibility of genes”

10. National High-Tech R&D Program (863) (2009AA02Z310, PI, ￥1.6 1million), (2009.1-2011.12)

    “Metagenomics data collection and analysis system based on the next-generation sequencing technologies”

11. The Shanghai Magnolia Science and Technology Talent Fund (2010B084, PI, ￥30K), (2010.6-2011.5)

    “Conditional random filed theory and its application in regulatory element identification”

12. Shanghai Pujiang Program (09PJ1407900, PI, ￥200K), (2009.8-2011.7)

    “Conditional random field theory and its applications in Bioinformatics”

13. Science and Technology Innovation Program of Basic Science Foundation of Shanghai (08JC1416700, PI,￥250K), 2008.10-2010.9

    “Algorithms and system for complex sequence module finding”

As Co-PI:

1. Computational Biology Program of Science and Technology Commission of Shanghai Municipality (STCSM) ((23JS1400800, co-PI, ￥2M)，（2023.12-2026.11）

    “Common technologies for multi-level data integration for tumor cohorts”

2. National Basic Research Program of China (973) (2013CB956103, Co-PI, ￥1.04M, total budget ￥26M), (2013.1 – 2017.12)

    “The degeneration mechanism and recovery potential of coral reefs in South China sea”

3. National High-Tech R&D Program (863) (2014AA02502, Co-PI, ￥650K，total￥7.2M), (2014.1-2017.12)

    “Key technologies for microbial genomic data integration and analysis”

4. Shanghai Industry-Academia-Research Collaboration Project (CXY-2013-58, Co-PI, ￥1.20M), (2013.1-2015.12)

    “Development and Application of Broad-Spectrum and High-Efficiency Detection Systems for Foodborne Pathogens”

Publications

1. “Widespread of horizontal gene transfer regions in eukaryotes”, Li, K., Yan, F., Duan, Z., Adelson, D., **Wei, C.***, ***bioRxiv***, 2022, **doi:** https://doi.org/10.1101/2022.07.26.501571.

Publications in peer reviewed journals (*: corresponding author, citations >6,000)

1. “Pangenome reveals genomic variations associated with seed size/weight traits in peanut”, Zhao, K., Xue, H., Li, G., Chiitkineni, A., Fan, Y., Cao, Z., Dong, X., Lu, H., Zhao, K., Zhang, L., Qiu, D., Ren, R., Gong, F., Li, Z., Ma, X., Wan, S., Varshney, R.*, Wei, C.*, Yin, D.*, ***Nature Genetics***, 2025, accepted in principle

2. “Gastric cancer genomics study using reference human pangenomes”, Jiao, D., Dong, X., Fan, S., Liu, X., Yu, Y.*, Wei, C.*, ***Life Science Alliance***, 2025, 8:4, e202402977

3. “Identification of diversity-generating retroelements in host-associated and

environmental genomes: prevalence, diversity, and roles”, Carrasco-Villanueva, M.#, Wang, C.#, Wei, C.*, ***BMC Genomics***, 2024, 25:1227.

4. “A near complete genome of *Arachis monticola*, an allotetraploid wild peanut”, Xue，H.#, Zhao, K.#, Zhao, K., Han, S., Chitikineni, A., Zhang, L., Qiu, D., Ren, R., Gong, F., Li, Z., Ma, X., Zhang, X., Varshney, R., Zhang, X., Wei, C.*, Yin, D.*, ***Plant Biotechnology Journal***, 2024, https://doi.org/10.1111/pbi.14331.

5. “PPanG: a precision pangenome browser enabling nucleotide-level analysis of genomic variations in individual genomes and their graph-based pangenome”, Liu, M., Zhang, F., Lu, H., Xue, H., Li, Z., Xu, J., Wang, W.*, Wei, C.*, ***BMC Genomics***, 2024, 25:405

6. “A pangenome reference of 36 Chinese populations”, Gao, Y*, Yang, X.*, Chen, H.*, Tan, X., Yang, Z., Deng, L., Wang, B., Kong, S., Li, S., Cui, Y., Lei, C., Wangle， Y., Pan, Y., Ma, S., Sun, H., Zhao, X., Shi, Y., Yang, Z., Wu, D., Wu, S., Zhao, X., Shi, B., Jin, L., Hu, Z., Chinese Pangenome Consortium (CPC), Yan, L.#, Chu, J.#, Ye, K.#, Xu, S.#, ***Nature***, 2023, 619:112-121.

7. “Pangenomic analysis of Chinese gastric cancer”, Yu, Y.* #, Zhang, Z. #, Dong, X. #, Yang, R. #, Duan, Z. #, Xiang, Z., Li, J., Li, G., Yan, F., Xue, H., Jiao, D., Lu, J., Lu, H., Zhang, W., Wei, Y., Fan, S., Li, J., Jia, J., Zhang, J., Ji, J., Liu, P., Lu, H., Zhao, H., Chen, S., **Wei, C.***, Chen, H.*, Zhu, Z.*, ***Nature Communications***, 2022, 13:5412.

8. “Long-read sequencing of 111 rice genomes reveals significantly larger pan-genomes”, Zhang, F., Xue, H., Dong, X., Li, M., Zheng, X., Li, Z., Xu, J., Wang, W., and **Wei, C.***, ***Genome Research***, 2022,32:853-863.

9. “mbDenoise: microbiome data denoising using zero-inflated probabilistic principal components analysis”, Zeng, Y., Li, J., **Wei, C**, Zhao, H., Wang, T., ***Genome Biology***, 2022, 23**:** 94.

10. “Open pangenome of Lactococcus lactis generated by a combination of metagenome-assembled genomes and isolate genomes”, Zhai, Y. and Wei.C, **Frontiers in Microbiology**, 2022, 10.3389.

11. “Gene Presence/Absence Variation analysis of coronavirus family displays its pan-genomic diversity***”,*** Jiao, D., Dong, X., Yu, Y.*, **Wei, C.***, ***International Journal of Biological Sciences***, 2021, 17(14):3717-3727.

12. “Genetic Profiles Affect the Biological Effects of Serine on Gastric Cancer Cells”, Li, J., Xue, H., Xiang, Z., Song, S., Yan, R., Ji, J, Zhu, Z., **Wei, C.**, Yu, Y., ***Frontiers in Pharmacology***, 2021, 11:1183.

13. “GESLM algorithm for detecting causal SNPs in GWAS with multiple phenotypes”, Lyu, R., Sun, J., Jiang, Q., **Wei, C.***, Zhang, Y.*, ***Briefings in Bioinformatics***, 2021, 22(6), 1–12

14. “ivTerm—An R package for interactive visualization of functional analysis results of meta-omics data”, Dong, X., Xue, H., **Wei, C.***, ***Journal of Cellular Biochemistry***, 2021, 122:1428-1434

15. “UHRF1 regulates alternative splicing by binding to splicing factors and U snRNAs”， Xu, P., Zhang, L., Xiao, Y., Li, W., Hu, Z., Zhang, R., Li, J., Wu, F., Xi, Y., Zou, Q., Wang, Z., Guo, R., Ma, H., Dong, S., Xiao, M., Yang, Z., Ren, X., **Wei, C.*,** , Yu, W.*, , ***Human Molecular Genetics***, 2021, 30(22)2110-2122.

16. “A powerful HUPAN on a pan-genome study: significance and perspectives”, Yu, Y. and Wei, C., ***Cancer Biology & Medicine***, 2020, doi:10.20892/j.issn.2095-3941.2019.0317

17. “CDKAM: a taxonomic classification tool using discriminative k-mers and approximate matching strategies”, Bui, V. and Wei, C., ***BMC Bioinformatics,*** 2020, 21:468

18. “HUPAN: a pan-genome analysis pipeline for human genomes”, Duan, Z., Qiao, Y., Lu, J., Lu, H., Zhang, W., Yan, F., Sun, C., Hu, Z., Zhang, Z., Li, G., Chen, H., Xiang, Z., Zhu, Z., Zhao, H., Yu, Y.*, Wei, C.*, ***Genome Biology***, 2019, 20:149.

19. “Discovery and characterization of the evolution, variation and functions of Diversity-Generating Retroelements using thousands of genomes and metagenomes”, Yan, F., Yu, X., Duan, Z., Lu, J., Jia, B., Qiao, Y., Sun, C., **Wei, C.***., ***BMC Genomics***, 2019, 20:595.

20. “PaSS: A sequencing simulator for PacBio sequencing”, Zhang, W., Ben, J., **Wei, C.***, ***BMC Bioinformatics***, 2019, 20:352.

21. “GLAPD: whole genome based LAMP primer design for a set of target genomes”, Jia, B.#, Li, X.#, Liu, W., Lu, C., Lu, X., Ma, L., Li, Y.*, **Wei, C.***, ***Frontiers in Microbiology***, 2019， 10:2860

22. “Towards a deeper haplotype mining of complex traits in rice with RFGB v2.0”, Wang, C., Yu, H., Huang, J., Wang, W., Faruquee, M., Zhang, F., Zhao, X., Fu, B., Chen, K., Zhang, H., Tai, S., **Wei, C.**, Li, J., McNally, K., Alexandrov, N., Gao, X., Li, Z., Xu, J., Zheng, T., ***Plant Biotechnology Journal***, 2019, pp. 1-3.

23. “Comparative genomics analysis and Characterization of two Salmonella enterica Serova Enteritidis isolates from poultry with notably different survival abilities in egg whites”, Wang, Y., Jia, B., Xu, X., Zhang, L., **Wei, C.**, Ou, H., Cui, Y., Shi, C., Shi, X., ***Frontiers in Microbiology***, 2018, 9:2111

24. “MetaBinG2: a fast and accurate metagenomic sequence classification system for samples with many unknown organisms”, Qiao, Y., Jia, B., Hu, Z., Sun, C., Xiang, Y., **Wei, C.***, ***Biology Direct***, 2018, 13(1):15.

25. “Genomic variation in 3,010 diverse accessions of Asian cultivated rice”, Wang, W. *, Mauleon, R.*, Hu, Z. *, Chebotarov, D. *, Tai, S. *, Wu, Z.*, Li, M. *, Zheng, T. *, Fuentes, R. *, Zhang, F. *, Mansueto, L. *, Copetti, D. *, Sanciangco, M., Palis, K., Xu, J., Sun, C., Fu, B., Zhang, H., Gao, Y., Zhao, X., Shen, F., Cui, X., Yu, H., Li, Z., Chen, M., Detras, J., Zhou, Y., Zhang, X., Zhao, Y., Kudrna, D., Wang, C., Li, R., Jia, B., Lu, J., He, X., Dong, Z., Xu, J., Li, Y., Wang, M., Shi, J., Li, J., Zhang, D., Lee, S., Hu, W., Poliakov, A., Dubchak, I., Ulat, V., Borja, F., Mendoza, J., Ali, J., Li, J., Gao, Q., Niu, Y., Yue, Z., Naredo, M., Talag, J., Wang, X., Li, J., Fang, X., Yin, Y., Glaszmann, J., Zhang, J., Li, J., Hamilton, R.2, Wing, R.*, Ruan, J.*, Zhang, G.*, **Wei,**

C.*, Alexandrov, N.*, McNally*, K., Li, Z.*, Leung, H., ***Nature***, 2018, 553:43-49 (co-corresponding author)

26. "In silico analysis of endogenous siRNAs associated transposable elements and NATs in Schistosoma japonicum reveals their putative roles during reproductive development", Giri, B.*, Ye, J.*, Chen, Y., **Wei, C.***, Cheng, G.*, ***Parasitology Research***, 2018, 117(5):1549-1558.

27. "Genome-wide analysis of the association of transposable elements with gene regulation suggests that Alu elements have the largest overall regulatory impact", Zeng, L., Pederson, S., Cao, D., Qu, Z., Hu, Z., Adelson, D., **Wei, C.***, ***Journal of Computational Biology***, 2018, Jun;25(6):551-562.

28. "Novel sequences, structural variations and gene presence variations of Asian cultivated rice", Hu, Z., Wang, W., Wu, Z., Sun, C., Li, M., Lu, J., Fu, B., Shi, J., Xu, J., **Wei, C.***, Li, Z.*, ***Scientific Data***, 2018, 5:180079

29. "Dosage compensation in the process of inactivation/reactivation during both germ cell development and early embryogenesis in mouse", Li, X., Hu, Z., Yu, X., Ma, B., Zhang, C., **Wei, C.***, and Wu, J.*, ***Scientific Reports***, 2017, 7:3729.

30. "EUPAN enables pan-genome studies of a large number of eukaryotic genomes", Hu, Z., Sun, C., Lu, K., Chu, X., Zhao, Y., Lu, J., Shi, J., **Wei, C.***, ***Bioinformatics***, 2017, 23(15);2408-2409

31. "Widespread of Horizontal Gene Transfer in the Human Genome", Huang, W., Tsai L., Li, Y., Hua, N., Sun, C., **Wei, C.***, ***BMC Genomics***, 2017, 18:274

32. "RNA virus receptor Rig-I monitors gut microbiota and inhibits colitis-associated colorectal cancer", Zhu, H., Xu, W., Hu, Z., Zhang, H., Shen, Y., Lu, S., **Wei, C.***, Wang, Z.*, ***J. of Experimental & Clinical Cancer Research***, 2017, 36:2.

33. "RPAN: Rice Pan-genome Browser for ~3,000 rice genomes", Sun, C., Hu, Z., Lu, K., Zhao, Y., Lu, J., Zheng, T., Wang, W., Shi, J., Zhang, D., Li, Z., **Wei, C.***, ***Nucleic Acids Research***, 2017, 45(2): 597-605.

34. "Revealing missing human protein isoforms based on *ab initio* prediction, RNA-sesq and proteomics", Hu, Z., Scott, H., Qin, G., Zheng, G, Chu, X., Xie, L., Adelson, D., Oftedal, B., Venugopal, P., Babic, M., Hahn, C., Zhang, B., Wang, X., Li, N., **Wei, C.***, ***Scientific Reports***, 2015, 5:10940

35. "MOST+: a *de novo* motif finder combining genomic sequence and heterogeneous genome-wide signatures", Zhang, Y., He, Y., Zheng, G., **Wei, C.***, ***BMC Genomics***, 2015, 16(Suppl 7):S13

36. "Whole genome sequencing of six dog breeds from continuous altitudes reveals adaption to high-altitude hypoxia", Xiao, G. et al., ***Genome Research***, 2014, 24(8)1308-15.

37. "LAceP: lysine acetylation sites prediction using logistic regression classifier", Hou, T., Zheng, G., Zhang P., Jia, J., Li, J., Xie, L., **Wei, C.***, Li, Y., 2014, ***PLoS ONE***, 9(2): e89575.

38. "NeSSM: a Next-generation Sequencing Simulator for Metagenomics", Jia, B., Cai, K., Xuan, L., **Wei, C.***, 2013, ***PLoS ONE***, 8(10):e75448.

39. “cGRNB: a web server for building combinatorial gene regulatory networks through integrated engineering of seed-matching sequence information and gene expression datasets”, Xu, H., Yu, H., Tu, K., Shi, Q., **Wei, C.**, Li, Y., Li, Y., (2013) ***BMC Systems Biology***, 7(Suppl 2):S7

40. “PMRD: a curated database for genes and mutants involved in plant male reproduction”, Cui, X., Wang, Q., Yin, W., Xu, H., Wilson, Z., Pan, S., **Wei, C.** and Zhang, D., (2012) ***BMC Plant Biology***, 12:215

41. “Towards biological characters of interactions between transcription factors and their DNA targets in Mammals”, Zheng, G., Liu, Q., Ding, G., **Wei, C.***, Li, Y., (2012) ***BMC Genomics*** ,13:388

42. “CTF: A transcription factor binding site prediction system using conditional random fields”, He, Y., Zheng, G., **Wei, C.***, (2012) ***BMC Genomics,*** 13(Suppl 8):S18

43. “iGepros: An integrated gene and protein annotation server for biological nature exploration”, Zheng, G., Wang, H., **Wei, C.***, Li, Y., (2011) ***BMC Bioinformatics***, 12(Suppl 14):S6

44. “MetaBinG: Using GPUs to accelerate metagenomic sequence classification”, Jia, P., Liu, L., **Wei, C.***, (2011) ***PloS ONE***, 6(11): e25353

45. “Analysis of oral microbiota in children with dental caries by PCR-DGGE and Barcoded Pyrosequencing”, Ling, Z., Kong, J., Jia, P., **Wei, C.**, Wang, Y., Pan, Z., Huang, W., Chen, H., Xiang, C., (2010) ***Microbial Ecology***, 60(3):677-90

46. “The Completion of the Mammalian Gene Collection (MGC), The MGC Project Team. (2009) ***Genome Research***, 19:2324-2333

47. “Interactions between gut microbiota, host genetics, and diet relevant to development of metabolic syndromes in mice”, Zhang, C., Zhang, M., Wang, S., Han R., Cao, Y., Hua, W., Mao, Y., Zhang X., Pang X., Wei, C., Zhao, G., Chen, Y., Zhao, L., (2010) ***ISME J***, 4,232-241

48. “More Than 9,000,000 unique Genes in Human Gut Bacterial Community: Estimating Gene Numbers inside a Human Body”, Yang, X., Xie, L. LI, Y. and **Wei, C***. (2009) ***PLoS ONE***, 4(6): e6074.

49. “The prediction of interferon treatment effects based on time series microarray gene expression profiles”, Huang, T., Tu, K., Shyr, Y, **Wei, C.**, Xie, L. and Li, Y.（2008）, ***Journal of Transcriptional Medicine***, 6:44.

50. “ITFP: an integrated platform of mammalian transcription factors”, Zheng, G., Tu, K., Yang, Q., Xiong, Y., **Wei, C.**, Xie, L., Zhu, Y. and Li, Y. （2008）***Bioinformatics***, 24(20):2416-2417

51. “The Combination Approach of SVM and ECOC for Powerful Identification and Classification of Transcription Factor”, Zheng, G., Qian, Z., Yang, Q., **Wei, C.**, Xie, L.,

Zhu, Y. and Li, Y.（2008）***BMC Bioinformatics***, 9(1):282.

52. “Using ESTs to Improve the Accuracy of de novo Gene Prediction”, **Wei, C.** and Brent, M. R. (2006) ***BMC Bioinformatics,*** 7:327. Highly accessed

53. “PAIRAGON + N-SCAN: A Model-Based Gene Annotation Pipeline”, Arumugam, M., **Wei, C.**, Brown, R. H. and Brent, M. R. (2006) ***Genome Biology***, 7(Suppl 1): S5.

54. “Closing in on the *C. elegans* ORFeome by Cloning TWINSCAN predictions”, **Wei, C.**, Lamesch, P., Arumugam M., Rosenberg, J., Hu, P., Vidal, M., and Brent, M. R. (2005) ***Genome Research*** 15:577-582. (Reported by ***Nature Reviews Genetics*** Vol.6 No.5 as “***Research highlight***”.)

55. "The Genome Sequence of *Caenorhabditis briggsae*: A Platform for Comparative Genomics", Stein, L. D., Bao, Z., et al. (2003) ***PLoS Biol*** 1(2): E45.

Book Chapters

1. “Epigenomics” (in Chinese), Chapter 55 “Bioinformatics for RNA splicing”, Science Press, 2023

2. “Evolution of the Human Genome I” , Springer, 2017, 978-4-431-56603-8

3. “The Pangenome --Diversity, Dynamics and Evolution of Genomes”, Springer, 2020

Presentations

1. “Gastric cancer genomics study using reference human pangenomes”，Poster，Cold Spring Harbor Asia, Computational biology of the Genome, Suzhou, China, 2024.10.23

2. “Pangenome-based disease genomics”，invited talk，the annual meeting of Shanghai Society for Bioinformatics, special seminar for Life Omics，Tsung-Dao Lee Library, Shanghai Jiao Tong University, 2024.10.19

3. “Pangenome-based disease genomics”, Oral talk，The 13th National Conference of Bioinformatics and Systems Biology, Haikou, 2024.10.10

4. “How many proteins can the human genome encode”, invited talk, The 18th China Annual Meeting for Artificial Intelligence Foundation”, Xi’an, 2023.11.26

5. “Long read sequencing data reveals a much larger rice pangenome”, invited talk, the 9th National Conference on Computational Biology and Bioinformatics & Conference on Artificial Intelligence and Biomedical Informatics”, Xuzhou, 2023.5.14

6. “Pangenomic analysis of Chinese gastric center”，ABC-symposium（China-Japan-Korea Bioinformatics Symposium），online，12/9/2022

7. “Pangenomic analysis of Chinese gastric center”, Invited talk, “GWAS in the era of Big Data: the training course of omics new technologies from genomes to phenomes”, Shanghai Society for Bioinformatics and Shanghai Institute of Nutrition and Health, CAS, 2022.12.2

8. “The number of human genes and their evolution origin”, “The software and hardware in Bioinformatics”, Invited talk, The summer training course for biology teachers of Shanghai Municipality, by Shanghai Municipal Education Commission and Shanghai Association for Science and Technology, 2021.7.11

9. “EUPAN for eukaryote pan-genome analysis”, Invited talk, the 7th National Conference on Computational Biology and Bioinformatics, Yantai, Shandong, China, 7/16/2021

10. “HUPAN: a human pan-genome analysis pipeline”, Invited talk, the 17th Asian Bioinformatics Consortium, Guian, Guizhou, China, 8/22/2019

11. “The rice pan-genome derived from 3,010 diverse accessions”, Invited talk, Network for Food Security (Net4FS), Shanghai, China, 7/19/2019

12. “The rice pan-genome derived from 3,010 diverse accessions”, Invited talk, the 13th Annual Meeting of the International Conference on Genomics, Shenzhen, China, 10/27/2018

13. “Widespread of Horizontal Gene Transfer in the Human Genome”, Invited talk, The 1st AsiaEvo Conference, Shengzhen, China, April 19, 2018

14. “The rice pan-genome: gene presence/absence variation derived from >3000 rice genomes”, Invited talk, Net4FS, Montpellier, France, October 16, 2017

15. “RPAN: the rice pan-genome browser”, Breakthrough Highlight Oral Presentation, ISMB 2017, Prague, Czech Republic, 7/24/2017

16. “MetaBinG2: a fast and accurate metagenomics sequence classification method for samples with many unknown organisms”, Oral Presentation, CAMDA, ISMB, 2017, Prague, Czech Republic, 7/23/2017

17. "The rice pan-genome: gene presence/absence variation derived from >3000 rice genomes", Oral Presentation, the 15th Japan-Korea-China Bioinformatics Symposium, Seoul, Korea, 6/21/2017

18. “The rice pan-genome: gene presence/absence variation derived from >3000 rice genomes”, Net4FS, Shanghai, China, 11/08/2016

19. “How many protein isoforms are encoded in the human genome?”, EBI, Cambridge, UK, 7/16/2015

20. “EUPAN: a large-scale pan-genome analysis pipeline for eukaryotic large genomes”, Poster, Dublin, Ireland, 7/12/2015-7/14/2015

21. “MOST+: A motif finding approach combining genomic sequence and heterogeneous genome-wide signatures”, Poster, ISMB2013, Berlin, German, 2013/7/23

22. “Finding functional elements in genomes with statistical models”, Lecture, the 11th Japan-Korea-China Bioinformatics Training Course, 6/18/2013

23. “NeSSM: Next-generation sequencing simulator for metagenomics”, Poster, GIW 2012, Tainan, Taiwan, 2012/12/13

24. “MetaBinG: Using GPUs to accelerate metagenomic sequence classification”, Invited talk, ANRRC, Jeju Island, Korea, 2012/10/19

25. “Regulatory element finding by integrating the genomic sequence and epigenetic information”, Invited talk, International IRSES meeting, Shanghai, China, 9/10/2012

26. “Using GPUs to accelerate metagenomic sequence classification”, Invited talk, ICB, Xi’an, China, 8/19/2012

27. “MetaBinG: a GPU-based fast metagenomic sequence classification system using high-order Markov models”, Poster, ISMB, Vienna, Austria, 7/18/2011.

28. “Gene Prediction Methods and Algorithms”, Lecture, the 10th Japan-Korea-China Bioinformatics Training Course, Jeju Island, Korea, 5/12/2011.

29. “Bioinformatics for Microbial biology”, Lecture, Fudan University, Shanghai, China, 1/13/2011.

30. “Gene Prediction algorithms and systems, and their application for algal genome analysis”, Lecture, Top China and Brazil course, Shanghai, China, 7/16/2010.

31. “Gene Prediction and Annotations”, Lecture, Next Generation Sequencing Data Analysis Training Course, Fudan University, Shanghai, China, 7/30/2010.

32. “Methods and Algorithms for Gene Prediction”, Lecture, the 9th Japan-Korea-China Bioinformatics Training Course, CAS, Shanghai, China, 4/20/2010.

33. “Finding diversity of a microbe community: 16S rRNA or metagenome shotgun sequencing method?”, Invited talk, Japan-Korea-China Symposium on Bioinformatics, JST, Tokyo, Japan, 3/1/2010.

34. “Estimation of gene numbers in a human bogy”, talk, Symposium “Analysis of complex biological systems”, Shanghai Jiao Tong University, Shanghai, China, 8/19/2009.

35. “More than 9,000,000 genes in the human gut bacterial community: Estimation of gene numbers in human”, Invited talk, Spring School on Multiscale Methods and Modeling in Biophysics and Systems Biology, Chinese Academy of Science, Shanghai, 5/22/2009.

36. “Estimation of gene numbers in human”, Invited talk, the 8th Japan-Korea-China Bioinformatics Symposium, Kyoto University, Kyoto, Japan, 2/28/2009.

37. “Methods and Algorithms for Gene Prediction”, Invited talk, the 8th Japan-Korea-China Bioinformatics Training Course, Kyoto University, Kyoto, Japan, 2/27/2009.

38. “Measuring the Impact of Genomic Sequence Variations on Gene Structure Variations”, Invited talk, Theory and Applications of Computational Chemistry, Shanghai, China, 9/27/2008.

39. “Using EST to Improve Gene Structure Prediction”, Invited talk, Summer Course for Plant Molecular Biology, Shanghai Jiao Tong University, Shanghai, 7/17/2008.

40. “Using EST to Improve Gene Structure Prediction”, Invited talk, The Institute of Systems Biology, Seattle, Washington, 7/6/2006.

41. “Integrating EST alignments into TWINSCAN”, Poster, Biology of Genomes, CSHL, NY, 5/12/2004.

42. “Experimental Verification of Twinscan Predictions on *C. elegans*”, Talk, the 3rd Annual ORFeome Meeting, Boston, MA, 12/3/2003.

43. “Using Gene Prediction to Guide Experiments by Summing Over Consistent Gene Models”, Talk, Genome Informatics, CSHL, NY, 5/11/2003.

Patents

58 pattern applications (56 authorized)

1. "A kit for large scale HPV typing", patent number: ZL200910049555.4.

2. "A GPU-based fast metagenomic sequence classification algorithm", patent number: ZL201110125025.0.

3. "A metagenomics-based unknown pathogen identification system", patent number: ZL2011045266.7.

4. "A fluorescence imaging system and image analysis method", application number: 201510186113.X.

5. "A fluorescence image analysis system", application number: 201520237179.2.

6. "A fast isothermal identification system for *Cronobacter sakazakii*", application number: 201510556917.4.

7. "A nucleic acid sequence amplification primer design system and its application", patent number: 20150559179.9.

8. "A fast isothermal method for simultaneously identification of *Vibrio cholerae* and *Vibrio vulnificus*, primers and reagent kit", patent number: ZL201610780489.8

9. "A fast isothermal identification method for *Salmonella*, primers and reagent kit", patent number: ZL201610767608.6.

10. "A fast isothermal identification method for *Yersinia enterocolitica*, primers and reagent kit", patent number: ZL201610767671.X

11. "A fast isothermal identification method for *Vibrio parahemolyticus*, primers and reagent kit", patent number: ZL201610780425.8

12. "A fast isothermal identification method for *Yersinia pseudotuberculosis*, primers and reagent kit", patent number: ZL201610780457.8

13. "A fast isothermal identification method for *Vibrio vulnificus*, primers and their applications", patent number: ZL201610780421.X

14. "A fast isothermal identification method for *Staphyloccocus aureus Rosenbach*, primers and their applications", patent number: ZL201610767576.X

15. "A fast isothermal identification method for *Shigella*, primers and reagent kit", patent number: ZL201610767703.6

16. “A fast isothermal identification method for *Vibrio parahaemolyticus* and its applications”, patent number: ZL202010036130.6
17. “A fast isothermal identification method for *Vibrio parahaemolyticus, p*rimers and reagent kit”, patent number: ZL202010036146.7
18. “A fast isothermal identification method for *Vibrio parahaemolyticus, p*rimers and reagent kit”, patent number: ZL202010035808.9
19. “A fast isothermal identification method for *Vibrio vulnificus,* primers and reagent kit”, patent number: ZL201610780407.X
20. “A fast isothermal identification method for *Vibrio vulnificus, p*rimers and reagent kit”, patent number: ZL202010018176.5
21. “A fast isothermal identification method for *Salmonella*, *p*rimers and applications”, patent number: ZL202010017854.6
22. “A fast isothermal identification method for *Vibrio vulnificus, p*rimers and applications”, patent number: ZL202010035775.8
23. “A fast isothermal identification method for *Vibrio vulnificus* and reagent kit”, patent number: ZL202010035791.7
24. “A fast isothermal identification method for *Vibrio vulnificus* and applications”, patent number: ZL202010042444.7
25. “A fast isothermal identification method for *Vibrio parahaemolyticus, p*rimers and applications”, patent number: ZL202010042450.2
26. “A fast isothermal identification method for *Yersinia pseudotuberculosis, p*rimers and reagent kit”, patent number: ZL201911281105.8
27. “A fast isothermal identification method for *Vibrio vulnificus* and applications”, patent number: ZL202010042443.2
28. “A fast isothermal identification method for *Vibrio parahaemolyticus* and reagent kit”, patent number: ZL 202010042446.6
29. “A fast isothermal identification method for *Yersinia pseudotuberculosis* and applications”, patent number: ZL201911281772.6
30. “A fast isothermal identification method for *vibrio vulnificus* and reagent kit”, patent number: ZL202010043524.4
31. “A fast isothermal identification system for *Virbrio vulnificus*”, patent number: ZL201610767402.3
32. “A fast isothermal identification method for *Bacillus cereus,* primers and reagent kit”, patent number: ZL201610780460.X
33. “A fast isothermal identification method for *Vibrio Parahaemolyticus*, primers and their applications”, patent number: ZL201610780447.4
34. “A fast isothermal identification method for *Yersinia pseudoberculosis*, primers and their applications”, patent number: ZL201610767506.4
35. “A fast isothermal identification method for *Cronobacter sakazakii*, primers and their applications”, patent number: ZL201610767354.8
36. “A fast isothermal identification method for *Vibrio cholerae O1* and reagent kit”, patent number: ZL202010036105.8
37. “A fast isothermal identification method for *Bacillus cereus, p*rimers and reagent kit”, patent number: ZL202010035788.5

38. “A fast isothermal identification method for *Bacillus cereus* and applications”, patent number: ZL202010036127.4

39. “A fast isothermal identification method for *Vibrio cholerae O1, p*rimers and applications”, patent number: ZL202010035787.0

40. “A fast isothermal identification method for *Vibrio cholerae O1* and applications”, patent number: ZL202010035771.X

41. “A fast isothermal identification method for *Salmonella, p*rimers and reagent kit”, patent number: ZL202010017846.1

42. “A fast isothermal identification method for *Cronobacter sakazakii, p*rimers and applications”, patent number: ZL202010004056.X

43. “A fast isothermal identification method for *Cronobacter sakazakii* and reagent kit”, patent number: ZL202010004055.5

44. “A fast isothermal identification method for *Cronobacter sakazakii, p*rimers and reagent kit”, patent number: ZL202010004054.0

45. “A fast isothermal identification method for *Bacillus cereus, p*rimers and reagent kit”, patent number: ZL202010286793.3

46. “A fast isothermal identification system for *Bacillus cereus*”, application number: 201610767579.3.

47. “A fast isothermal identification method for *Vibrio cholera* 01, primers and reagent kit”, patent number: ZL201610780456.3

48. “A fast isothermal identification method for *Cronobacter sakazakii*, primers and their applications”, patent number: ZL201610767389.1.

49. “A kit for fast isothermal identification of *Listeria monocytogenes*”, patent number: ZL201610767426.9.

50. “A fast isothermal identification method for *Slomonella*, primers and reagent kit”, patent number: ZL201610780485.X

51. “A fast isothermal identification method for *Staphylococcus aureus*, primers and reagent kit”, patent number: ZL201610767557.7

52. “A fast isothermal identification method for *Yersinia enterocolitica, p*rimers and reagent kit”, patent number: ZL202010017857.X

53. “A fast isothermal identification method for *Listeria Monocytogenes, p*rimers and reagent kit”, patent number: ZL201911337898.0

54. “A fast isothermal identification method for *Listeria Monocytogenes* and applications”, patent number: ZL201911337926.9

55. “A fast isothermal identification method for *Staphylococcus aureus, p*rimers and reagent kit”, patent number: ZL202010042445.1

56. “A fast isothermal identification method for *Staphylococcus aureus* and applications”, patent number: ZL202010043523.X

57. “A fast isothermal identification system for *Virbrio cholera o1*”, patent number: ZL201610767491.1.

58. “A fast isothermal identification method for *Listeria monocytogenes*, primers and applications”, patent number: ZL201610767436.2

Software copyright

59. "Metagenome NGS simulation system (NeSSM)", registration number: 2010SR029333

60. "A visualization system for complex subsequence module identification (FlexSA)", registration number: 2010SR057696

61. "A transcription factor binding site prediction system based on conditional random field theory(CTF)", registration number: 2011SR086086

62. "Shigella genome db", registration number: 2011R11L179894

63. "A gene function analysis system for metagenomes", registration number:2011R11L181725

64. "Logistic regression based protein lysine acetylation sites prediction system", registration number: 2015SR171889

65. "An integrated gene and protein annotation system for biological feature exploring", registration number: 2015SR171886

Teaching

1. "Omics big data", Credit 3, Spring 2017, 2018, 2019, Fall 2020, Spring 2021-2025, "The Inaugural Graduate-level High-quality Courses of Shanghai Jiao Tong University" Award (2024)

2. "Programming languages for Bioinformatics", Credit 3, Spring 2013-2016, Credit 2, Spring 2017-2020

3. "Algorithms in Bioinformatics", Credit 3, Fall 2011 – 2016, Spring 2018, 2021-2025

4. "Matlab programming", Credit 2, Spring 2012

5. "Computational Biology", Bioinformatics session, Credit 3, Fall 2011- 2018

6. "Advanced Bioinformatics", Credit 3, Spring 2012-2015

7. "Genomics and Proteomics", Credit 3, Fall 2010

8. "Digital Signal Processing", Credit 3, Fall 2009

9. "Frontier topics in Bioinformatics", Biological Sequence Analysis session, Spring 2009

10. "Introduction to Bioinformatics", Course introduction and biological sequence analysis part, Spring 2013, Fall 2014-2016

Mentoring

15 PhD students (3 assistant mentoring, 2 graduated; 10 independent mentoring, 3 graduated; 2 co-mentoring, 1 graduated)

29 Master students (19 graduated, 3 transferred to doctoral programs)

45 undergraduate thesis students (18 went abroad to world famous universities for graduate programs, 18 went to graduate programs in China)

28 intern students (2 from Harvard University, 1 from UCLA)

iGEM team (SJTU 2009, SJTU-software 2014- now)

15 PhD students (6 graduated)

- Chunlu Wang, 2023-, Advisor, SJTU
- Zijie Jiang, 2024-, Advisor, SJTU
- Ye Zhang, 2023, Co-Advisor, first advisor Zhangsheng Yu, School of Mathematical Sciences, SJTU
- Ziyao Feng, 2022-, Advisor, SJTU
- Xiaorui Dong, 2021-, Advisor, SJTU
- Kun Li, 2020-, Advisor, SJTU
- Du Jiao, 2019-, Advisor, SJTU
- Huimin Lu, 2017-, Advisor, SJTU
- Hongzhang Xue, 2018 - 2023, Advisor, SJTU. Now work in our lab as a research scientist.
- Zhongqu Duan, 2015-2019, Co-advisor, first advisor Hongyu Zhao, SJTU-Yale Joint Center for Biostatistics; now a bioinformatics scientist in West Lake University
- Ben Jia, 2014 - 2020, Advisor, SJTU; now work in a bioinformatics startup company
- Zhiqiang Hu, 2010 - 2016, Advisor, SJTU; Postdoc in University of California, Berkeley; now a research scientist in Illumina.
- Zhaohui Gu, 2009 -2015, PhD Committee Member, SJTU. Now a PI in National Medical Center at City of Hope, USA
- Huayong Xu, 2010 -， Co-advisor with Prof. Yixue Li, SJTU, an entrepreneur in Suzhou
- Guangyong Zheng, 2008 - 2009, PhD Committee Member, Fudan University, now a Research Scientist, CAS

29 Master students (20 graduated)

- Peitong Wu， 2024-，Master student, Advisor, SJTU
- Shengnian Liu, 2024-, Master student, Advisor, SJTU
- Siyu Ye, 2023 - , Master student, Advisor, SJTU
- Chunlu Wang, 2023 - , Master student, Advisor, SJTU (transferred to doctoral program)

- Anfisa Rudakova, 2023 - , Master student, Advisor, SJTU (International student from Russia)
- Guanran Fu, 2022 - , Master student, Advisor, SJTU
- Mingwei Liu, 2022 - 2025, Master student, Advisor, SJTU, PhD in CS department of SJTU
- Ziyao Feng, 2021 - , Master student, Advisor, SJTU (transferred to doctoral program in)
- Yiting Zhai, 2020 - 2022, Master student, Advisor, SJTU
- Yangzhen Wei, 2019 - 2022, Master student, Advisor, SJTU
- Shiyu Fan, 2019 - 2022, Master student, Advisor, SJTU
- Mariela Carrasco Villanueva, 2019 - 2022, Master student, Advisor, SJTU (international student from Peru)
- Van Kien Bui, 2018 - 2021, Master student, Advisor, SJTU (international student from Vietnam)
- Xiaorui Dong, 2018 – 2021, Master student, Advisor, SJTU
- Fazhe Yan, 2017 - 2020, Master student, Advisor, SJTU
- Wenmin Zhang, 2016 - 2019, Master student, Advisor, SJTU
- Yuyang Qiao, 2015 - 2018, Master student, Advisor, SJTU
- Chen Sun, 2014 - 2017, Master student, Advisor, SJTU, PhD in University of Michigan, USA
- Jingyuan Lu, 2014 -, Master student, Advisor, SJTU, an entrepreneur in Shanghai
- Xuling Yu, 2013 - 2016, Master student, Advisor, SJTU, last seen as a graduate student in New York University
- Ben Jia, 2011 - 2014, Master student, Advisor, SJTU, PhD student in SJTU
- Lu Zeng, 2011 - 2014, Master student, co-advisor with David Adelson, Adelaide University, SJTU, PhD student in Adelaide University, Australia
- Ting Hou, 2011 - 2014, Master student, co-advisor with Prof. Yixue Li, ECUST, PhD student in ECUST.
- Danfeng Cao, 2012 - 2015, Master student, Advisor, SJTU
- Jun Xie, 2012 - 2015, Master student, Advisor, SJTU
- Liming Xuan, 2010 - 2012, Master student, co-advisor with Prof. Yixue Li, ECUST, now work for a bioinformatics company in Wuxi, Jiangsu
- Peng Jia, 2009 - 2011, Master student, co-advisor with Prof. Lei Liu, CAS, now work for an advertisement company, Shanghai,
- Linlin Song (2008 - 2010, Master student, co-advisor with Prof. Saijuan Chen, SJTU, now work for ICBC, Beijing)

45 undergraduate independent study students (41 graduated)

- Zhexuan Tao, 2024-2025, School of Life Sciences and Biotechnology, SJTU, admitted by graduate school of Tokyo University, Japan
- Yang Su, 2024-2025, School of Life Sciences and Biotechnology, SJTU, admitted by Peking University graduate school
- Kunyue Wang, 2024-2025, School of Life Sciences and Biotechnology, SJTU, admitted by Fudan University graduate school
- Junchen Luo, 2024-2025, School of Life Sciences and Biotechnology, SJTU, admitted by Peking University graduate school
- Xiangyu Zhu, 2023-2024, School of Life Sciences and Biotechnology, SJTU, graduate student in Xi’an Jiao Tong University
- Chaoxian Wang, 2023-2024, School of Life Sciences and Biotechnology, SJTU, graduate student in Fudan University
- Boyi Fei, 2023-2024, Zhiyuan College, SJTU, graduate student in Tsinghua University
- Chunlu Wang, 2022-2023, School of Agriculture and Biological Sciences, SJTU, graduate student in SJTU
- Mingwei Liu, 2021-2022, School of Life Sciences and Biotechnology, SJTU, graduate student in SJTU
- Xinyi Liu, 2021-2022, School of Life Sciences and Biotechnology, SJTU, graduate student in Tokyo University, Japan
- Longwei Zhang， 2021-2022， Zhiyuan College, SJTU, Master student in Georgetown University, USA
- Chen Zhu, 2020-2021, School of Life Sciences and Biotechnology, SJTU, last seen as a graduate student in Tsinghua University
- Zhiyao Feng, 2020-2021, School of Life Sciences and Biotechnology, SJTU, graduate student in SJTU
- Yunzhe Jiang, 2020-2021, School of Life Sciences and Biotechnology, SJTU, Phd student in Yale University, USA
- Jiawei Tong, 2019-2020, School of Life Sciences and Biotechnology, SJTU
- Ding Sun, 2019-2020, School of Life Sciences and Biotechnology, SJTU
- Yiting Zhai, 2018-2019, School of Medicine, SJTU, graduate student in SJTU
- Du Jiao, 2018-2019, School of Life Sciences, Tong Ji University, PhD student in SJTU
- Yangzhen Wei, 2018-2019, School of Life Sciences and Biotechnology, SJTU, graduate student in SJTU
- Juncheng Yang, 2018-2019, School of Life Sciences and Biotechnology, SJTU, PhD student in Yale University, USA
- Han Wu, 2017-2018, School of Life Sciences and Biotechnology, SJTU, graduate student in SJTU
- Kuangchen Lu， 2015-2018, School of Life Sciences and Biotechnology, SJTU, graduate student in Indiana University, USA

- Fazhe Yan, 2016-2017, School of Life Sciences and Biotechnology, SJTU, graduate student in SJTU
- Yuanyuan Xi, 2016-2017, School of Life Sciences and Biotechnology, SJTU, admitted to a Swiss graduate school
- Jiannan Ye, 216-2017, Zhiyuan College, SJTU, graduate student in SJTU
- Humin Lu, 2016-2017, School of Life Sciences, NJAU, graduate student in SJTU
- Yichen Si, 2015-2016, Zhiyuan College, SJTU, now a graduate student in University of Michigan, USA.
- Wenze Huang, 2014-2016, School of Life Sciences and Biotechnology, SJTU, now a graduate student in Tsinghua University, China
- Liangjie Liu, 2013-2016, School of Life Sciences and Biotechnology, SJTU, now a graduate student in SJTU
- Jiayao Wang, 2013 - 2015, School of Electronic Engineering, SJTU, last seen as a graduate student in Indiana University, USA
- Jinyuan Lu, 2013 - 2014, Zhiyuan College, SJTU, a graduate student in SJTU, last seen as an entrepreneur in Shanghai
- Mai Shi, 2013 - 2014, Zhiyuan College, SJTU, last seen as a graduate student in Chinese University of Hong Kong
- Cheng Sun, 2013 - 2014, School of Life Sciences and Biotechnology, SJTU, a master student in SJTU and now as a PhD student in University of Michigan, USA
- Hailing Wang, 2013 - 2014, School of Life Sciences and Biotechnology, SJTU, last seen as a graduate student in Hong Kong University
- Zixu Ding, 2013 - 2014, School of Life Sciences and Biotechnology, SJTU, now a graduate student in Carnegie Mellon University, USA
- Nan Hua, 2012 - 2013, School of Life Sciences and Biotechnology, SJTU, last seen as a PhD student in the University of Southern California, USA
- Xueling Yu, 2012 - 2013, School of Life Sciences and Biotechnology, SJTU, last seen as a graduate student in New York University
- Jia Hou, 2011 - 2012, School of Life Sciences and Biotechnology, SJTU, last seen as a graduate student in Australia
- Chang Huang, 2011 - 2012, School of Life Sciences and Biotechnology, SJTU, now work in Shanghai
- Yupeng He, 2009 - 2011, last seen as PhD graduate student at University of California, San Diego, USA
- Zhiqiang Hu, 2008 -2010, a PhD student in SJTU, postdoc at UC Berkeley, USA, now Scientist in Iluumina
- Yunfan Cui, 2010, SJTU, last seen as a graduate student at the School of Software, SJTU
- Bing He, 2008 - 2010, SJTU, last seen as a PhD student at the University of Iowa, USA

- Wenjia Wang, 2008 - 2009, SJTU, last seen as a graduate student at the University Paris Sud (Paris XI), France
- Xing Yang, 2008 - 2009, Tong Ji University, last seen as a graduate student at Florida International University, USA
- Jie Du, 2008 – 2009, SJTU

28 PRP or other intern program students

- Chen Zhu, 2019, National undergraduate innovation contest, School of Life Sciences and Biotechnology, SJTU
- Wangjie Zheng, 2018, PRP, School of Life Sciences and Biotechnology, SJTU
- Zhengxin Li, 2018, PRP, School of Life Sciences and Biotechnology, SJTU
- Yijin Xiang, 2017, Summer intern, School of Medicine, SJTU
- Xiaojing Zhu, 2017, Summer intern, University of California, Los Angeles, USA
- Kuangchen Lu, 2014 -, PRP, School of Life Sciences and Biotechnology, SJTU
- Siyuan Ma, 2015-2017, School of Life Sciences and Biotechnology, SJTU, exchange to Yale University
- Yulong Li, 2014 summer, Zhiyuan College, SJTU
- Lillian Tsai, 2014 Summer, Harvard University, USA
- Nicholas Lee, 2012 Summer, Harvard University, USA
- Zixu Ding, 2012, RPR student, School of Life Sciences and Biotechnology, SJTU
- Bo Yang, 2012 Summer, School of Life Sciences and Biotechnology, SJTU, then a graduate student in Hong Kong University
- Mai Shi, 2012 Summer, Zhiyuan College, SJTU
- Shiyi Liu, 2012 Summer, School of Life Sciences and Biotechnology, SJTU
- Cheng Sun, 2012 Summer, School of Life Sciences and Biotechnology, SJTU
- Bingqing Shen, 2012 Summer, School of Life Sciences and Biotechnology, SJTU
- Xin Yi, 2012 Summer, School of Life Sciences and Biotechnology, SJTU
- Yiwei Zhou, 2012 Summer, School of Life Sciences and Biotechnology, SJTU, then a graduate student in Chinese Academy of Science
- Ming Lin, 2012 Summer, School of Electric Engineering, SJTU
- Yuanfang Xia, 2012 Summer, School of Electric Engineering, SJTU
- Cong Xu, 2012 Summer, Zhiyuan College, SJTU
- Danjin Shen, 2012 Summer, Medical School, SJTU

- Jie Bi, 2012 Summer, School of Life Sciences and Biotechnology, SJTU, now a graduate student at Shanghai Tech
- Tao Hu, 2011 - 2012, Intern, now a graduate student at the North Carolina State University, USA
- Linchang Tan, 2011 Summer, Mathematics Department, SJTU, now a graduate student at the University of Michigan, USA
- Mengdi Lu, 2011, PRP student, Undergraduate student, School of Biomedical Engineering, SJTU
- Yujie He, 2010 - 2011, now graduate student at the department of Computer Science and Engineering, Washington University in St. Louis, USA
- Yuanchun Zhao, 2009 - 2010, intern, now a graduate student at Michigan State University, USA
- Xufei Wu, 2009, PRP student, Undergraduate student, Physics Department, SJTU

iGEM teams

- 2009, Created SJTU iGEM team, Gold Medal
- 2014, Created SJTU-software iGEM team, team leader: Jiabei Yang, master program in Harvard University
- 2015, Gold Medal, team leader: Liangjie liu, now a PhD student in SJTU
- 2016, Gold Medal, team leader: Shiyu Fan (Freshman), SJTU Paris Elite Institute of Technology, master program in SJTU
- 2017, Bronze Medal, team leader: Chenchao Ding
- 2018, Silver Medal, team leader: Yangzhen Wei, master program in SJTU
- 2019, Gold Medal, team leader: Haoyu Meng, PhD in History, Tsinghua University
- 2020, Gold Medal, team leader: Ruiqi Lyu, Master program in CMU
- 2021, Gold Medal, team leader: Yuanjie Hu, Master program in NSU
- 2022, Gold Medal, team leader: Jialu Wei, Master program in SJTU
- 2023, Silver Medal, Best Software and AI Project, team leader: Junjie Zhu, PhD program in SJTU
- 2024, Gold Medal, team leader: Xinyu Qian

Academic Service

1. Shanghai Association of Bioinformatics, Committee member, 2013/10 -.
2. ***Scientific Reports*** (IF 4.26), Editorial Board Member, 2016.8 -
3. ***Scientific data***(IF 5.8), Editorial Board Member, 2024.1 -

4. ***BMC Genomics*** (IF 3.5), Editorial Board Member, 2023.12 -
5. ***Science*****、*****Genome Biology*****、 *****ISME J.*****、*****PLoS Genetics*****、*****BMC Biology*****、*****Bioinformatics*****、*****BMC Bioinformatics*****、*****GigaSciences*****、*****Genomics, Proteomics & Bioinformatics:*** Invited reviewer
6. ***RECOMB-seq*** 2013, Conference committee panel and session chair, Beijing China, 4/11-12/2013
7. ***ICIBM,*** International conference committee panel, 2014-2016, 2018-2020,2022-2023
8. Asia Bioinformatics Institute (ABI, under construction), member of the working group, 2010 - 2012
9. The 9th Bioinformatics training course of China, Japan and Korea, Shanghai, China, 4/20-23/2010, （Co-organizer）
10. Lecture in Bioinformatics training course of China, Japan and Korea, 2009, 2010, 2011, 2013
11. EMBO World Practical Course: Computational Biology: from (meta)genomes to phenotype and environment, Shanghai, China, local organizer, 8/16-22/2009
12. Symposium "Analysis of complex Biological Systems", Shanghai Jiao Tong University, organizer, 8/19/2009
13. Multiscale Methods and Modeling in Biophysics and Systems Biology, Chinese Academy of Science, Shanghai, Symposium session chair, 5/22/2009

Committees

1. Teaching Committee of School of Life Sciences and Biotechnologies, 2016-2019
2. Drafting Committee Member, Undergraduate Bioinformatics Program Standards, Ministry of Education, China, 2015.9
3. Associate Chair, Department of Bioinformatics and Biostatistics, 2014.1 – 2019.3
4. Core Member, Curriculum Design Committee for Undergraduate, Master and Doctoral Programs, Department of Bioinformatics and Biostatistics, 2010, 2011, 2015
5. Admissions Committee, Department of Bioinformatics and Biostatistics, 2010–Present
6. Lecturer, Bioinformatics Outreach Program for Shanghai High School, 2010, 2011
7. Founder and Lead Instructor(SJTU-Software 2014-); Gold Medal (2009, 2014, 2015, 2016, 2019–2022, 2024)
8. Co-Founder and Instructor, SJTU iGEM Team (2009); Gold Medal
9. Major selection advisor committee for undergraduates, School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, member, 2009-
10. Graduate student recruiting committee, the School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, member, 2009- 2015

11. Key Member of Preparatory Committee, International Joint Master Program between Shanghai Jiao Tong University and the University of Adelaide, Australia, 2010–2011; Served as a Supervisor after Program Establishment

12. Key Member of Preparatory Committee, Shanghai Jiao Tong University-Yale University Joint Center for Biostatistics, 2015; Act as Supervisor upon Center Establishment

13. Expert Interviewer, Independent Undergraduate Admissions Program, Shanghai Jiao Tong University, 2013–2016

Awards

2019 Annual Award of Top 10 Bioinformatics Algorithms and Tools	(2020)
Chancellor’s Award (校长奖), SJTU	(2019)
Distinguished Teaching and Mentoring Award （教书育人奖）, SJTU	(2018)
Excellence in Teaching, SJTU	(2015)
Chenxing Scholar, SJTU	(2013)
New Century Excellent Talents, Minister of Education, China	(2013)
Shanghai Pujiang Talent Award	(2009)
Gold Award in iGEM competition	(2009, 2014 - 2016, 2019-2022, 2024)
Excellent Graduate of Beijing University	(1996)