

Curriculum Vitae

Chaochun Wei ScD

Professor
Department of Bioinformatics and Biostatistics
School of Life Sciences and Biotechnology
Shanghai Jiao Tong University

Room 422, Ye Jiequan Building, 800 Dongchuan Rd, Minhang District
Shanghai, China 200240
Phone:0086-21-34204083
Email: ccwei@sjtu.edu.cn
Homepage: <http://cgm.sjtu.edu.cn/>

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

2016-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

1. 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"
2. Science and Technology Commission of Shanghai Municipality (22ZR1433600, ¥ 200K) 2022.4-2025.3
"Identification and characterization of horizontal gene transfer in bat genomes"
3. Science and Technology Commission of Shanghai Municipality (20ZR1428200, ¥ 200K) 2020.7-2023.6
"Construction of rice pan-genome browser 2.0"
4. 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"
5. NSFC Project (61472246, PI, ¥ 800K), 2015.1-2018.12
" Finding and characterizing complex structure sequence modules in metagenomes"
6. National High-Tech R&D Program (863) (2014AA02502, Co-PI, budget ¥ 650K, total budget ¥ 7.2M), 2014.1-2017.12
"Key technologies for microbial genomic data integration and analysis"
7. National Basic Research Program of China (973) (2013CB956103, Co-PI, budget ¥ 1.04M, total budget ¥ 26M), 2013.1 – 2017.12
"The degeneration mechanism and recovery potential of coral reefs in South China sea"
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. Shanghai Pujiang Program (09PJ1407900, PI, ¥ 200K), (2009.8-2011.7)
"Conditional random field theory and its applications in Bioinformatics"

12.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”

Patents

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 nucleic acid sequence amplification primer design system and its application”, patent number: 20150559179.9.
7. “A fast isothermal identification system for *Cronobacter sakazakii*”, application number: 201510556917.4.
8. “A fast isothermal identification system for *Salmonella*”, patent number: ZL201610767608.6.
9. “A kit for fast isothermal identification of *Listeria monocytogenes*”, patent number: ZL201610767426.9.
10. “A fast isothermal identification method for *Cronobacter sakazakii*, primers and their applications”, patent number: ZL201610767354.8.
11. “A fast isothermal identification system for *Bacillus cereus*”, application number: 201610767579.3.
12. “A fast isothermal identification system for *Virbrio cholera o1*”, patent number: ZL201610767491.1.
13. “A fast isothermal identification system for *Virbrio vulnificus*”, patent number: ZL201610767402.3.
14. “A fast isothermal identification method for *Cronobacter sakazakii*, primers and their applications”, patent number: ZL201610767389.1.
15. “A fast isothermal identification method for *Staphylococcus aureus Rosenbach*, primers and their applications”, patent number: ZL201610767576.X
16. “A fast isothermal identification method for *Vibrio Parahaemolyticus*, primers and their applications”, patent number: ZL201610780447.4
17. “A fast isothermal identification method for *Yersinia pseudotuberculosis*, primers and their applications”, patent number: ZL201610767506.4
18. “A fast isothermal identification method for *Listeria monocytogenes*, primers and their applications”, patent number: ZL201610767436.2

19. “A fast isothermal identification method for *Bacillus cereus*, primers and reagent kit”, patent number: ZL201610780460.X
20. “A fast isothermal identification method for *Vibrio cholera* 01, primers and reagent kit”, patent number: ZL201610780456.3
21. “A fast isothermal identification method for *Staphylococcus aureus*, primers and reagent kit”, patent number: ZL201610767557.7
22. “A fast isothermal identification method for *Vibrio vulnificus*, primers and their applications”, patent number: ZL201610780421.X
23. “A fast isothermal method for simultaneously identification of *Vibrio cholerae* and *Vibrio vulnificus*, primers and reagent kit”, patent number: ZL201610780489.8
24. “A fast isothermal identification method for *Yersinia enterocolitica*, primers and reagent kit”, patent number: ZL201610767671.X
25. “A fast isothermal identification method for *Shigella*, primers and reagent kit”, patent number: ZL201610767703.6
26. “A fast isothermal identification method for *Vibrio vulnificus*, primers and reagent kit”, patent number: ZL201610780407.X
27. “A fast isothermal identification method for *Vibrio parahemolyticus*, primers and reagent kit”, patent number: ZL201610780425.8
28. “A fast isothermal identification method for *Yersinia pseudotuberculosis*, primers and reagent kit”, patent number: ZL201610780457.8
29. “A fast isothermal identification method for *Slomonella*, primers and reagent kit”, patent number: ZL201610780485.X

Software copyright

1. “Metagenome NGS simulation system (NeSSM)”, registration number: 2010SR029333
2. “A visualization system for complex subsequence module identification (FlexSA)”, registration number: 2010SR057696
3. “A transcription factor binding site prediction system based on conditional random field theory(CTF)”, registration number: 2011SR086086
4. “Shigella genome db”, registration number: 2011R11L179894
5. “A gene function analysis system for metagenomes”, registration number:2011R11L181725
6. “Logistic regression based protein lysine acetylation sites prediction system”, registration number: 2015SR171889
7. “An integrated gene and protein annotation system for biological feature exploring”, registration number: 2015SR171886

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

2. “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.
3. “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.
4. “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.
5. “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.
6. “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
7. “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
8. “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.
9. “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
10. “CDKAM: a taxonomic classification tool using discriminative k-mers and approximate matching strategies”, Bui, V. and Wei, C., *BMC Bioinformatics*, 2020, 21:468
11. “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.
12. “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.

13. “PaSS: A sequencing simulator for PacBio sequencing”, Zhang, W., Ben, J., **Wei, C.***, *BMC Bioinformatics*, 2019, 20:352.
14. “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
15. “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.
16. “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
17. “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.
18. “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. *, Sanciango, 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)
19. “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.
20. “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.
21. “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
22. “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.

23. "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
24. "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
25. "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.
26. "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.
27. "Revealing missing human protein isoforms based on *ab initio* prediction, RNA-seq 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
28. "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
29. "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.
30. "LAcP: 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.
31. "NeSSM: a Next-generation Sequencing Simulator for Metagenomics", Jia, B., Cai, K., Xuan, L., **Wei, C.***, 2013, *PLoS ONE*, 8(10):e75448.
32. "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
33. "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
34. "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
35. "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
36. "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

37. “MetaBinG: Using GPUs to accelerate metagenomic sequence classification”, Jia, P., Liu, L., **Wei, C.***, (2011) *PloS ONE*, 6(11): e25353
38. “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
39. “The Completion of the Mammalian Gene Collection (MGC), The MGC Project Team. (2009) *Genome Research*, 19:2324-2333
40. “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
41. “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.
42. “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.
43. “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
44. “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.
45. “Using ESTs to Improve the Accuracy of de novo Gene Prediction”, **Wei, C.** and Brent, M. R. (2006) *BMC Bioinformatics*, 7:327. **Highly accessed**
46. “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.
47. “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**”.)
48. "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. “Evolution of the Human Genome I” , Springer, 2017, 978-4-431-56603-8

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

Presentations

1. “EUPAN for eukaryote pan-genome analysis”, Invited talk, the 7th National Conference on Computational Biology and Bioinformatics, Yantai, Shandong, China, 7/16/202
2. “HUPAN: a human pan-genome analysis pipeline”, Invited talk, the 17th Asian Bioinformatics Consortium, Gui'an, Guizhou, China, 8/22/2019
3. “The rice pan-genome derived from 3,010 diverse accessions”, Invited talk, Network for Food Security (Net4FS), Shanghai, China, 7/19/2019
4. “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
5. “Widespread of Horizontal Gene Transfer in the Human Genome”, Invited talk, The 1st AsiaEvo Conference, Shengzhen, China, April 19, 2018
6. “The rice pan-genome: gene presence/absence variation derived from >3000 rice genomes”, Invited talk, Net4FS, Montpellier, France, October 16, 2017
7. “RPAN: the rice pan-genome browser”, Breakthrough Highlight Oral Presentation, ISMB 2017, Prague, Czech Republic, 7/24/2017
8. “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
9. "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
10. “The rice pan-genome: gene presence/absence variation derived from >3000 rice genomes”, Net4FS, Shanghai, China, 11/08/2016
11. “How many protein isoforms are encoded in the human genome?”, EBI, Cambridge, UK, 7/16/2015
12. “EUPAN: a large-scale pan-genome analysis pipeline for eukaryotic large genomes”, Poster, Dublin, Ireland, 7/12/2015-7/14/2015
13. “MOST+: A motif finding approach combining genomic sequence and heterogeneous genome-wide signatures”, Poster, ISMB2013, Berlin, German, 2013/7/23
14. “Finding functional elements in genomes with statistical models”, Lecture, the 11th Japan-Korea-China Bioinformatics Training Course, 6/18/2013
15. “NeSSM: Next-generation sequencing simulator for metagenomics”, Poster, GIW 2012, Tainan, Taiwan, 2012/12/13
16. “MetaBinG: Using GPUs to accelerate metagenomic sequence classification”, Invited talk, ANRRC, Jeju Island, Korea, 2012/10/19

17. “Regulatory element finding by integrating the genomic sequence and epigenetic information”, Invited talk, International IRSES meeting, Shanghai, China, 9/10/2012
18. “Using GPUs to accelerate metagenomic sequence classification”, Invited talk, ICB, Xi’an, China, 8/19/2012
19. “MetaBinG: a GPU-based fast metagenomic sequence classification system using high-order Markov models”, Poster, ISMB, Vienna, Austria, 7/18/2011.
20. “Gene Prediction Methods and Algorithms”, Lecture, the 10th Japan-Korea-China Bioinformatics Training Course, Jeju Island, Korea, 5/12/2011.
21. “Bioinformatics for Microbial biology”, Lecture, Fudan University, Shanghai, China, 1/13/2011.
22. “Gene Prediction algorithms and systems, and their application for algal genome analysis”, Lecture, Top China and Brazil course, Shanghai, China, 7/16/2010.
23. “Gene Prediction and Annotations”, Lecture, Next Generation Sequencing Data Analysis Training Course, Fudan University, Shanghai, China, 7/30/2010.
24. “Methods and Algorithms for Gene Prediction”, Lecture, the 9th Japan-Korea-China Bioinformatics Training Course, CAS, Shanghai, China, 4/20/2010.
25. “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.
26. “Estimation of gene numbers in a human body”, talk, Symposium “Analysis of complex biological systems”, Shanghai Jiao Tong University, Shanghai, China, 8/19/2009.
27. “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.
28. “Estimation of gene numbers in human”, Invited talk, the 8th Japan-Korea-China Bioinformatics Symposium, Kyoto University, Kyoto, Japan, 2/28/2009.
29. “Methods and Algorithms for Gene Prediction”, Invited talk, the 8th Japan-Korea-China Bioinformatics Training Course, Kyoto University, Kyoto, Japan, 2/27/2009.
30. “Measuring the Impact of Genomic Sequence Variations on Gene Structure Variations”, Invited talk, Theory and Applications of Computational Chemistry, Shanghai, China, 9/27/2008.
31. “Using EST to Improve Gene Structure Prediction”, Invited talk, Summer Course for Plant Molecular Biology, Shanghai Jiao Tong University, Shanghai, 7/17/2008.
32. “Using EST to Improve Gene Structure Prediction”, Invited talk, The Institute of Systems Biology, Seattle, Washington, 7/6/2006.
33. “Integrating EST alignments into TWINSKAN”, Poster, Biology of Genomes, CSHL, NY, 5/12/2004.
34. “Experimental Verification of Twinscan Predictions on *C. elegans*”, Talk, the 3rd Annual ORFeome Meeting, Boston, MA, 12/3/2003.

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

Teaching

1. “Omics big data”, Credit 3, Spring 2017, 2018, 2019, Fall 2020, Spring 2021, 2022
2. "Advanced Bioinformatics", Credit 3, Spring 2012-2015
3. “Programming languages for Bioinformatics”, Credit 3, Spring 2013-2016, Credit 2, Spring 2017, 2018, 2019, 2020
4. “Matlab programming”, Credit 2, Spring 2012
5. “Computational Biology”, Bioinformatics session, Credit 3, Fall 2011- 2016
6. “Algorithms in Bioinformatics”, Credit 3, Fall 2011 – 2016, Spring 2018, 2021, 2022
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

Mentoring

11PhD students, 22 Master students, 37 undergraduate thesis students, 28 intern students

11 PhD students (5 graduated)

- Xiaorui Dong, 2021-, Advisor, SJTU
- Kun Li, 2020-, Advisor, SJTU
- Du Jiao, 2019-, Advisor, SJTU
- Hongzhang Xue, 2018 -, Advisor, SJTU
- Huimin Lu, 2017-, Advisor, SJTU
- 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

22 Master students (19 graduated)

- Mingwei Liu, 2022 - , Master student, Advisor, SJTU
- Ziyao Feng, 2021 - , Master student, Advisor, SJTU
- 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, now a PhD student 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)

37 undergraduate independent study students (37 graduated)

- Mingwei Liu, 2021 -2022, School of Life Sciences and Biotechnology, SJTU

- Xinyi Liu, 2021 -2022, School of Life Sciences and Biotechnology, SJTU
- Chen Zhu, 2020-, School of Life Sciences and Biotechnology, SJTU
- Zhiyao Feng, 2020-, School of Life Sciences and Biotechnology, SJTU
- Yunzhe Jiang, 2020-, School of Life Sciences and Biotechnology, SJTU
- 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, 2016-2017, 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 Illumina
- 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 Instructor

- 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
- 2020, Gold Medal, team leader: Ruiqi Lyu
- 2021, Gold Medal, team leader: Yuanjie Hu

Academic Service

1. *Scientific Reports* (IF 4.26), Editorial Board Member, 2016/8 -
2. *Genome Biology, ISME J., BMC Bioinformatics, Bioinformatics*: Invited reviewer
3. *ICIBM* 2018, Conference committee panel, Los Angeles, CA, USA, 6/10-12/2018
4. *ICIBM* 2016, Conference committee panel, Huston, Texas, USA, 12/8-10/2016
5. *ICIBM* 2015, Conference committee panel, Indianapolis, IN, USA, 11/13-15,2015
6. *ICIBM* 2014, Conference committee panel, San Antonio, Texas, USA, 12/4-6/2014
7. *BioMed Research International* (IF 2.88), Editorial Board Member, 2013/5 - 2014.12
8. *RECOMB-seq* 2013, Conference committee panel and session chair, Beijing China, 4/11-12/2013
9. Shanghai Association of Bioinformatics, Committee member, 2013/10 -.
10. Asia Bioinformatics Institute (ABI, under construction), member of the working group, 2010 - 2012
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. Major selection advisor committee for undergraduates, School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, member, 2009-
2. Graduate student recruiting committee, the School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, member, 2009-

Awards

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| 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, 2020)
Excellent Graduate of Beijing University	(1996)