CURRICULUM VITAE

Brief Information

Name: Yiyong Zhao, Ph.D

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Education

2016.09-2021.06: Fudan University, China - Ph.D. in Bioinformatics (Integrated Master's and Ph.D. Program) (2024 QS/US News Global Rankings = 50th/116th); Supervisor by Prof. Hong Ma (https://science.psu.edu/bio/people/hxm16, the President of American Society of Plant biologists)

2019.09-2020.10: Pennsylvania State University, USA (Major in Bioinformatics, Joint Ph.D. Program); Supervisor by Prof. Hong Ma (the President of American Society of Plant biologists)

2012.09-2016.06: Northeast Forestry University, China; Bachelor of Agriculture (*summa cum laude*)

2013.06-2014.01: Kangwon National University, South Korea. (Joint Bachelor Program)

Work Experience

2023.07-present: Postdoctoral Research Association at Bioinformatics at Yale University, School of Medicine. Supervisor by Associate Prof. Xianjun Dong

2023.05-present: Affiliate Faculty Member of Broad institute of Harvard and MIT, Cambridge, MA, USA.

2023.05-2023.06: Postdoctoral Research Fellow at Bioinformatics, Genomics and Bioinformatics Hub, Harvard Medical School and Brigham & Women's Hospital, Boston, MA, USA. (Project: Expression Quantification of Transposable Elements and Association Analysis in Neurodegenerative Diseases by Integrating Multi-omics

2022.10-2023.04: Professor at Department of crop genetic breeding, Guizhou University, China.

2021.07-2022.08: Drug Farm Co. Ltd (https://drug-farm.com), Shanghai, China as Bioinformatics & AI Scientist.

Major Courses/Training

Mathematical Methods of Statistics, Biostatistics: Theories and Applications; Linear Statistical Analysis; Genomics and Bioinformatics; Statistical Analysis and Data Mining of Omics Data; Methods and Applications of Evolutionary Genomics, Analysis and Applications of Microarray and Next-generation Sequencing Data, Analysis of Categorical Data and Survival Data, Text Mining, The Mathematical Theory and Algorithms for Machine Learning and Pattern Recognition, Big Data-Oriented Machine Learning Theory and Algorithms and etc.

Research Interests

Computational biology, Biological big data mining; Genomics, Revealing the unknown functions of the human genome and their roles in neurological diseases by applying and developing computational methods to integrate multi-dimensional multi-source data, Phylogenomic and comparative genomics; Bioinformatics software development; Genome assembly, Genome evolution such as whole genome duplications; Hybridization detection; Gene evolution and functional genomics.

Research Publications (H-index: 10; Citations: 789, [#]co-first author, [*]corresponding author, https://scholar.google.com/citations?user=o_uUXZkAAAAJ&hl=en)

[#] **[1] <u>Yiyong Zhao</u>**, Rong Zhang, Kai-Wen Jiang, Ji Qi, Yi Hu, Jing Guo, Renbin Zhu, Taikui Zhang, Ashley N. Egan, Ting-Shuang Yi, Chien-Hsun Huang, and Hong Ma, Nuclear phylotranscriptomics and phylogenomics support numerous polyploidization events and hypotheses for the evolution of rhizobial nitrogen-fixing symbiosis in Fabaceae. *__Molecular Plant__*, 2021. 14(5): p. 748-773. (Cover story & Featured article, **IF$_{2021}$=21.949**, reported in dozens of domestic and international mainstream media such as Guangming Daily, People's Daily, China News, Science Daily, Phy.org, etc., My contribution: for the cover article, based on the transcriptome and genome, I constructed the largest phylogenetic relationship of Leguminosae to date. Phylogenetic relationships were resolved for five subfamilies, about 30 genome-wide replication events were identified, the evolutionary history of the nitrogen-fixing gene family was explored, and the important role of a new gene in nitrogen fixation was proposed, providing an important basis for germplasm conservation and breeding in the legume family. (The full analyses presented in this article were conducted by me, drafted the original manuscript and made rebuttal.)

[#]**[2]** Liangsheng Zhang[#, *], Fei Chen[#], Xingtan Zhang[#], Zhen Li[#], **<u>Yiyong Zhao</u>**[#], Rolf Lohaus[#], Xiaojun Chang[#], Wei Dong, Simon Y. W. Ho, Xing Liu, Aixia Song, Junhao Chen, Wenlei Guo, Zhengjia Wang, Yingyu Zhuang, Haifeng Wang, Xuequn Chen, Juan Hu, Yanhui Liu, Yuan Qin, Kai Wang, Shanshan Dong, Yang Liu, Shouzhou Zhang, Xianxian Yu, Qian Wu, Liangsheng Wang, Xueqing Yan, Yuannian Jiao, Hongzhi Kong, Xiaofan Zhou, Cuiwei Yu, Yuchu Chen, Fan Li, Jihua Wang, Wei Chen, Xinlu Chen, Qidong Jia, Chi Zhang, Yifan Jiang, Wanbo Zhang, Guanhua Liu, Jianyu Fu, Feng Chen, Hong Ma, Yves Van de Peer, and Haibao Tang, The water lily genome and the early evolution of flowering plants. *__Nature__*, 2020. 577(7788): p. 79-84. (**IF$_{2020}$=49.962, ESI highly cited paper**), (my contribution involved in the assembly, annotation, and correction of transcriptome data of the first aquatic early angiosperm genome. Based on 115 transcriptome and genome-wide data, a highly supported phylogenetic tree of flowering plants was constructed, and molecular clock analysis revealed that early angiosperms originated in the early Cretaceous, while highly supporting the phylogenetic relationships within the Water Lily family. Low-copy nuclear

genes from the whole genome confirmed that saprophytic camphor was the earliest differentiated angiosperm. Meanwhile, using a comparative genomics approach, the Blue Star water lily was identified as a potential hybrid parent of two cultivars, laying the foundation for genomics in molecular cultivation breeding. (The related analyses of Phylogenomic relationships and divergence time estimations of angiosperms in Figure 1 were conducted by me and drafted the corresponding part manuscript and made rebuttal.)

[#][3] Angiosperm-wide analysis of fruit and ovary evolution aided by a new nuclear phylogeny supports association of the same ovary type with both dry and fleshy fruits. Yezi Xiang[#], Taikui Zhang[#], **Yiyong Zhao**[#], Hongjin Dong, Hongyi Chen, Yi Hu, Ji Qi, Chien-Hsun Huang, Jun Xiang[*], and Hong Ma[*]. *Journal of Integrative Plant Biology*, 2024, 00: 1-24. (**IF$_{2022}$=11.4**) (My contributions including examined available datasets and chose the high-quality datasets for 423 angiosperm species, representing all major angiosperm lineages and nearly all orders. Due to large scale of hundreds of angiosperm species and many thousands of genes, the molecular evolutionary analyses took a lot of steps and a lot of time. I was able to generate the appropriate gene phylogenies and summarized the results for the purpose of reporting gene duplications at key nodes in the angiosperm phylogeny as reported in this paper.)

[*][4] Dandan Li[#], Mingjin Huang[#, *], Qunwei Han, Dachang Wanag, Kaijie Li, Qiuyue Yang, Ronghui Gu, Guangchong Zhou, Songtao He, Houlin Yu, Lin Cheng, **Yiyong Zhao**[*]. A high-quality chromosomal-level reference genome of *Dendrobium nobile* L. provides new insights into the biosynthesis and accumulation of picrotoxane-type sesquiterpenoid alkaloids, 2024. https://doi.org/10.1016/j.indcrop.2024.118243. *Industrial Crops and Products* (**IF$_{2022}$=5.9**) (My contribution in Conceptualization, Data curation, Investigation, Writing/review/editing & handled revisions and rebuttals.)

[*][5] Lin Cheng, Qunwei Han, Fei Chen, Mengge Li, Tiago Santana Balbuena, and **Yiyong Zhao**[*], Phylogenomics as an effective approach to untangle cross-species hybridization event: A case study in the family Nymphaeaceae. *Frontiers in Genetics* (section in computational genomics), 2022. 13. (**IF$_{2022}$=3.7**) (My contributions in conducting nearly all analyses, drafted the original manuscript, and handled revisions and rebuttals.)

[*][6] Lin Cheng[#], Mengge Li[#], Yachao Wang[#], Qunwei Han, Yanlin Hao, Zhen Qiao, Wei Zhang, Lin Qiu, Andong Gong, Zhihan Zhang, Tao Li, Shanshan Luo, Linshuang Tang, Daliang Liu, Hao Yin, Song Lu, Tiago Santana Balbuena, and **Yiyong Zhao**[*], Transcriptome-based variations effectively untangling the intraspecific relationships and selection signals in Xinyang Maojian tea population. *Frontiers in Plant Science*, 2023. 14. (**IF$_{2022}$=5.6**) (My contributions in conceptualization and supervision and handled revisions and rebuttals.)

[*][7] Daliang Liu, Zhihan Zhang, Yanlin Hao, Mengge Li, Houlin Yu, Xingruo Zhang, Haoyang Mi, Lin Cheng[*], **Yiyong Zhao**[*]. Decoding the complete organelle genomic architecture of *Stewartia sinensis*: An early-diverging species in Theaceae with phylogenetic implications. 25, 114 (2024). *BMC Genomics* (**IF$_{2022}$=4.4**) (My contribution in conceptualization and supervision and handled revisions and rebuttals.)

[*][8] Lin Cheng[#], Mengge Li[#], Qunwei Han, Zhen Qiao, Yanlin Hao, Tiago Santana Balbuena, and **Yiyong Zhao***, Phylogenomics resolves the phylogeny of Theaceae by using low-copy and multi-copy nuclear gene makers and uncovers a fast radiation event contributing to tea plants diversity.

Biology, 2022. 11(7): p. 1007. **(IF$_{2022}$=4.2)** (My contribution in conceptualization and supervision and handled revisions and rebuttals.)

[#][9] Yifan Jiang[#, *], Fei Chen[#], Aixia Song[#], **Yiyong Zhao**[#], Xinlu Chen, Yuan Gao, Guo Wei, Wanbo Zhang, Yaqin Guan, Jianyu Fu, Junhao Chen, Wenlei Guo, Zhengjia Wang, Tobias G. Köllner, Zhineng Li, Ning Liu, Shunzhao Sui, Liangsheng Zhang*, and Feng Chen*, The genome assembly of *Chimonanthus praecox* var. *concolor* and comparative genomic analysis highlight the genetic basis underlying conserved and variable floral traits of wintersweet. *Industrial Crops and Products*, 2023. 206: p. 117603. **(IF$_{2022}$=5.9)** (The related analyses of phylogenomic relationships and divergence time estimations of magnoliids in Figure 4 were conducted by me and drafted the corresponding part manuscript and made rebuttal.)

[10] Lin Zhang, Xinxin Zhu, **Yiyong Zhao**, Jing Guo, Taikui Zhang, Weichen Huang, Jie Huang, Yi Hu, Chien-Hsun Huang[*], and Hong Ma[*], Phylotranscriptomics resolves the phylogeny of Pooideae and uncovers factors for their adaptive evolution. *Molecular Biology and Evolution*, 2022. 39(2). **(IF= 16.24)** (My contributions including taxon samplings and sequencing, assistance in Lin's data analyses)

[11] Jing Guo, Weibin Xu, Yi Hu, Jie Huang, **Yiyong Zhao**, Lin Zhang, Chien-Hsun Huang, and Hong Ma, Phylotranscriptomics in Cucurbitaceae reveal multiple whole-genome duplications and key morphological and molecular innovations. *Molecular Plant*, 2020. 13: p. 1-17. **(IF=13.164)** (My contributions including taxon samplings and sequencing, assistance in Jing's data analyses)

[12] Chengpeng He[#], Zhiyu Chen[#], **Yiyong Zhao**, Yue Yu, Hongkuan Wang, Cong Wang, Gregory P. Copenhaver, Ji Qi[*], and Yingxiang Wang[*], Histone demethylase IBM1-mediated meiocyte gene expression ensures meiotic chromosome synapsis and recombination. *PLOS Genetics*, 2022. 18(2): p. e1010041. **(IF$_{2022}$=5.917)** (My contributions including all the gene expression quantification and differential gene expressions analyses from RNA-seq datasets)

[13] Jie Huang, Weibin Xu, Junwen Zhai, Yi Hu, Jing Guo, Caifei Zhang, **Yiyong Zhao**, Lin Zhang, Christopher Martine, Hong Ma, and Chien-Hsun Huang, Nuclear phylogeny and insights into whole-genome duplications and reproductive development of Solanaceae plants. *Plant Communications*, 2023. 4(4): p. 100595. **(IF$_{2022}$=10.5)** (My contributions including taxon samplings and sequencing, assistance in Jie's data analyses)

[14] Yinghai Liang, Shanshan Wang, Chenhui Zhao, Xinwei Ma, **Yiyong Zhao**, Jing Shao, Yuebo Li, Honglian Li, Hongwei Song, Hong Ma, Hao Li, Bingbing Zhang, and Liangsheng Zhang, Transcriptional regulation of bark freezing tolerance in apple (*Malus domestica* Borkh.). *Horticulture Research*, 2020. 7(1): p. 205**. (IF$_{2020}$=6.072)** (My contributions including the gene expression quantification and differential gene expressions analyses for RNA-seq data)

[15] Zhuang Meng, Jinlei Han, Yujing Lin, **Yiyong Zhao**, Qingfang Lin, Xiaokai Ma, Jianping Wang, Muqing Zhang, Liangsheng Zhang, Qinghui Yang, and Kai Wang, Characterization of a *Saccharum spontaneum* with a basic chromosome number of x = 10 provides new insights on genome evolution in genus *Saccharum*. *Theoretical and Applied Genetics*, 2020. 133(1): p. 187-199. **(IF$_{2020}$=5.699)** (My contributions including Phylogeny and divergence time estimation of Poaceae as in Figure 5.)

[16] Weichen Huang, Lin Zhang, J. Travis Columbus, Yi Hu, **Yiyong Zhao**, Lin Tang, Zhenhua

Guo, Wenli Chen, Michael McKain, Madelaine Bartlett, Chien-Hsun Huang, De-Zhu Li, Song Ge, and Hong Ma, A well-supported nuclear phylogeny of Poaceae and implications for the evolution of C_4 photosynthesis. *__Molecular Plant__*, 2022. 15(4): p. 755-777. **(IF$_{2022}$= 27.5)** (My contributions including taxon samplings and sequencing, assistance in Weichen's data analyses)

[17] Fanjuan Meng, Li Liu, Mu Peng, ZhongKui Wang, Chao Wang, and **__Yiyong Zhao__**, Genetic diversity and population structure analysis in wild strawberry (*Fragaria nubicola* L.) from Motuo in Tibet Plateau based on simple sequence repeats (SSRs). *__Biochemical Systematics and Ecology__*, 2015. 63: p. 113-118. **(IF$_{2015}$=1.381)** (My contributions including taxon samplings and sequencing, assistance in Mu's data analyses)

[18] Ye Zheng, **__Yiyong Zhao__**, Lihua Wu, Juan Lin. Study on copy number variation and differentiated expression pattern of *CaCA* family genes in *Capsella*. 2020. http://www.jns.fudan.edu.cn/#/digest?ArticleID=1178, *__Chinese Journal of Fudan University (Natural Science)__* [J], 59, No.1:1-31 (My contributions including the gene expression quantification and differential gene expressions analyses for RNA-seq data)

*__**[19]**__ Yiyong Zhao[#, *], Daliang Liu[#], Hao Yin, Tao Li, Liang Wang, Quanzhi Zhao[*]. The origins of cultivated rice and genomic signature of heterosis for yield traits in super-hybrid rice. 2024. doi: https://doi.org/10.1101/2024.03.19.585738. *__bioRxiv__*. (**__BMC Biology__**, **Unver Review)** My contribution in conceptualization and supervision, assistance in Daliang's data analyses, drafted the initial manuscript)

[20] Lin Cheng[#], Yanlin Hao[#], Qunwei Han, Zhen Qiao, Mengge Li, Daliang Liu, Hao Yin, Tao Li, Wen Long, Shanshan Luo, Ya Gao, Zhihan Zhang, Houlin Yu, Xinhao Sun, **__Yiyong Zhao*__**. The origin and evolution of orphan genes: a case study in tea plant family. *__bioRxiv__* 2024.02.01.578514; doi: https://doi.org/10.1101/2024.02.01.578514 (*__Communications Biology__*, **IF$_{2022}$=5.9,** under revision) My contribution in conceptualization and supervision and handled revisions and rebuttals.)

Programming Skills

Proficient in Linux, Python, R and other programming languages for big data mining.

Developing Software/Web

PhyloTracer: A Versatile Toolkit for Comparative Genomics and Phylogenomic Analysis. Module features as follows:

1) **PhyloTree_CollapseExpand**: To transform a phylogenetic tree with Newick format into a 'comb' structure based on a predefined support value threshold. It can also revert the 'comb' structure to the binary tree, allowing meet the standard software analysis requirements.

2) **PhyloSupport_Scaler**: To recalibrate support values (bootstrap/posterior probability) for a phylogenetic tree, scaling them between [0,1] and [1,100] ranges for computational requirements.

3) **BranchLength_NumericConverter**: To convert values of branch length with string

format to numeric format for a phylogenetic tree, critical for quantitative analysis and computational operations.

4) **Phylo_Rooter**: Enables an accuracy method for gene tree rooting and enhancing the downstream evolutionary genomic analysis.

5) **OrthoFilter_LB**: To prune phylogenomic noises from single-copy and multi-copy gene family trees by removing the tips with long branch lengths.

6) **OrthoFilter_Mono**: To prune phylogenomic noise from single-copy and multi-copy gene family trees. It removes outliers and paralogs based on predefined taxonomic constraints (e.g., ensuring members from taxa such as families or orders form monophyletic groups). Caution: Groupings should be selected with care, prioritizing well-established relationships unless otherwise required for specific objectives.

7) **TreeTopology_Summarizer**: To enumerate the frequency of both absolute and relative topologies for single-copy gene trees or interested predefined clades.

8) **Tree_Visualizer**: To visualize and integrate gene duplication detection results into the species tree.

9) **GD_Detector**: To identify gene duplication events by reconciliation of gene family trees to a species tree.

10) **GD_Visualizer**: To visualize gene duplication detection on the context of a species tree.

11) **GD_Loss_Tracker**: To track the gene duplication loss event starting across each nodes/tips from a specific GD burst event in the species tree.

12) **GD_Loss_Visualizer**: To visualize the summary of gene duplication loss event counts for each nodes/tip on the context of the species tree.

13) **Ortho_Retriever**: To rapid infer putative single-copy orthologs by splitting paralogs from large-scale gene family trees across multiple species.

14) **Hybrid_Tracer**: To detect hybridization signals for each potential GD burst event across species tree by using the D-statistic (ABAB-BABA) test.

15) **Hybrid_Visualizer**: To visualize hybridization signals, highlighting support from gene tree topologies and D-statistic signals.

16) **HaploFinder**: Distinguishing ancient genome recombination events including gene conversions and crossovers by tracing subgenome haplotypes through phylogenomic profiling.

Python version: https://github.com/YiyongZhao/PhyloTracer

Web version: http://www.bioinfordocker.com/PhyloTracer (Under construction)

HybridTracer-GNN (https://github.com/YiyongZhao/Hybrid_Tracer-GNN**)** enables inference of hybrid speciation and admixture with fast graph neural network.

FabGenomeGalaxy   (http://www.bioinfordocker.com/FabGenomeGalaxy/**)**:   An   Integrative Platform for Fabaceae Comparative Genomics and Gene Family Analysis.

Editorial Activities

- Ad-hoc Reviewer –
Frontiers in Bioinformatics, Frontiers in Genetics, Horticulture Research, Frontiers in Plant Science, Frontiers in Molecular Biosciences, Journal of Systematics and Evolution, BMC

Ecology and Evolution, Frontiers in Endocrinology, Open Medicine and Plant Genetic Resources.

- Editorial Roles –

2023 - present: As a member of Reviewer Board in MDPI academic press (https://www.mdpi.com)

2023 - present: Frontiers in Plant Science specialty section of Functional and Applied Plant Genomics. (Academic Editor)

2023 - present: Frontiers in Ecology and Evolution (Academic Editor)

2023 - present: Innovation (Academic Editor)

2022 - present: Tropical Plants (Academic Editor)

Faculty Academic Appointments

2023: Deputy Director and Technical & Academic Lead, Key Laboratory of Molecular Breeding of Grain and Oil Crops of Guizhou Province, College of Agriculture, Guizhou University, Guiyang 550025, China. (Responsibilities: Gene Mining for Significant Agronomic Traits in Crops).

Conferences or Training

[1] 2017.06.16-06.18: Bioinformatics and Intelligent Information Processing Academic Conference, Location: Minhang Campus, Shanghai Jiao Tong University.

[2] 2017.06.26-06.27: 2017 Pujiang Genetic and Molecular Diagnostics Industry-Academia Research Forum.

[3] 2017.06.25-07.02: The 13th Fudan University Summer Advanced Workshop on Ecology, Location: Ecology Building of Fudan University.

[4] 2017.07.02-07.07: 2017 Fudan University Big Data Institute Summer Course, Location: Fudan Guanghua Building.

[5] 2017.07.17-07.21: Microbial Genomics Training Course by Shanghai Majorbio Bio-pharm Technology Co., Ltd.

[6] 2017.07.23-07.29: XIX International Botanical Congress, Location: Shenzhen.

[7] 2017.11.01-11.03: 2017 IUFRO Genetics and Genomics of Fagaceae (as a volunteer).

[8] 2017.12: Fudan Science and Technology Innovation Forum, Location: Shanghai Wujiaochang.

[9] 2017.12.02-12.03: The 10th China-R Conference (Shanghai) and East China Data Science Conference, Location: East China Normal University.

[10] 2017.12.20-12.21: The 2nd Conference on Artificial Intelligence for Precision Biomedical Informatics, Location: Wu Wenzheng Lecture Hall, Fudan Guanghua Building.

[11] 2018.01.31-02.04: Workshop on Molecular Paleobiology: Phylogeny and Divergence Time Estimation, Organizers: Yin Zongjun (NIGPAS) and Philip Donoghue (University of Bristol, UK), Location: Nanjing Institute of Paleontology.

[12] 2018.02.24-02.27: The 2nd Symposium of the International MAQC Society for Quality Control

of Omics Data, Location: Fudan University.

[13] 2018.04.29: Big History of Artificial Intelligence by Prof. Tiejun Huang, Location: Guanghua Building, Fudan University.

[14] 2018.04.09: Data Castle's Competition: Artificial Intelligence-based Drug Molecular Screening Competition.

[15] 2018.04.20-04.22: The 5th National Conference on Computational Biology and Bioinformatics and the 2nd Phoenix Genome Informatics Forum.

[16] 2018.06.24: Shanghai Workshop on Neuroimaging and Applications, Location: Zibin Building, Fudan University.

[17] 2018.09.11-09.12: International Summit on Computer Vision Technology and Applications (as a Volunteer), Location: Shanghai Putuo District.

[18] 2018.09.14: The 15th China Graduate Student Mathematical Modeling Competition.

[19] 2018.09.19: World Artificial Intelligence Conference, Sub-forum: Heterogeneous Computing, Standards Building, Industry Empowerment.

[20] 2018.10.21: The 8th Python Developers Conference PyConChina2018, Location: Shanghai Putuo District.

[21] 2018.10.26: Data Man Open Class: Big Data Business Application Analysis and Future Direction Outlook, Location: Room H6412, Fudan University.

[22] 2018.10.29: Data Castle's Competition: Car Destination Intelligence Prediction Contest.

[23] 2018.11.10: International Conference on the 10th Anniversary of the Institute of Plant Sciences, Location: Jiangwan Campus of Fudan University.

[24] 2018.12.01: Big Data and Artificial Intelligence 2018 Ph.D. Forum, Location: Zhangjiang Campus of Fudan University.

[25] 2018.12.08-12.09: The 11th China-R Conference (Shanghai) and East China Data Science Conference, Location: East China Normal University.

[26] 2018.12.13: Workshop on the Intersection of Artificial Intelligence and Biomedical Big Data, Location: Guanghua Building, Fudan University.

[27] 2019.03.30: AI Marketing-MobTech Precision Marketing, Location: 2F, Yuyu Building, Building 2, Huaxin Center, No. 711 Yishan Road, Xuhui, Shanghai.

[28] 2020.07.27-07.31: American Society of Plant Biologists: The Plant Biology 2020 Worldwide Summit, Location: USA.

[29] 2023.08.22-08.26: Eukaryotic mRNA Processing Conference, Topics: Mechanisms of RNA Splicing, Alternative Splicing: Mechanisms, Networks, and Biological Consequences, 3' End Processing, RNA Modifications, RNA Structure in Cells, Co-transcriptional RNA Processing: Dynamics of co-transcriptional RNA processing, RNA Turnover and Quality Control, Viruses and RNA Processing, RNA Processing in Disease, RNA-Protein Interactions/RNA Complexes; Location: Cold Spring Harbor Laboratory, NY, USA.

[30] 10 Year Anniversary Symposium, RNA Medicine 2024, April 25, 2024, Joseph B. Martin Conference Center, Beth Israel Deaconess Medical Center, Harvard Medical School.

[31] The Festival of Genomics & Biodata in Boston, Hall B2, Boston Convention & Exhibition Center, 415 Summer Street, Boston, MA 02210, USA

[32] 2024 Harvard Chinese Life Science Annual Symposium, September 14, 2024, Folkman Auditorium, Enders Building, Boston Children's Hospital, 320 Longwood Ave, Boston, MA 02115.

Foundation

Participated in two General Program of National Natural Science Foundation of China:

[1] National Natural Science Foundation of China, General Project, 31970224, Nuclear Gene-based Phylogenetic Reconstruction of Cucurbitaceae and Related Evolutionary Biology Studies, from 2020-01-01 to 2023-12-31, 580,000 RMB, Completed, as Participant.

[2] National Natural Science Foundation of China, General Project, 31770242, Nuclear Gene-based Phylogenetic Reconstruction of the Brassicaceae and Analyzing the Evolutionary Pathway of Flower and Fruit Development and Stress-Resistant Genes in Different Lineages, from 2018-01-01 to 2019-12-31, 250,000 RMB, Completed, as Participant.

Selected Honors and Awards

[1] 2016-2021 The First Prize Graduate Academic Scholarship of Fudan University

[2] 2016 Northeast Forestry University "Outstanding Graduate" Award

[3] 2015 Third Prize in the Second Plant Classification Competition Summer Camp jointly organized by the Chinese Academy of Sciences Institute of Botany, Peking University, and Beijing Forestry University

[4] 2013-2014 Northeast Forestry University "Three Good Student" Award

[5] 2013 National Encouragement Scholarship

[6] 2012-2013 Northeast Forestry University First and Second Level Scholarships

[7] 2012 Northeast Forestry University "Hand-in-Hand" Outstanding Academic Scholarship

Key Contributions and Achievements at Drug Farm (2021-2022)

Role: Bioinformatics & Artificial Intelligence Scientist at Drug Discovery and Indication Predictions

[1] Indication Predictions:

   a) Spearheaded the examination and determination of drug indications, focusing on ailments such as Kawasaki disease, systemic lupus erythematosus, IgA nephropathy, diabetic nephropathy, atherosclerosis, acute myocardial infarction, ischemic stroke, idiopathic pulmonary fibrosis, PBI nephropathy (with UUO, adenine, Cisplatin treatment), type 2 nephropathy due to diabetes mellitus, vascular sheer stress and atherosclerosis, acute

myeloid leukemia, and myelodysplastic syndrome.

b) Employed natural language processing for swift data examination, accelerating the identification of potential indications for drugs.

[2] Drug Target Discovery:

a) Collaboratively introduced IDinvivo+, an innovative tool designed for the prompt discovery of novel drug targets. This tool harnessed the power of graph neural networks founded on natural language processing, amalgamating data from renowned databases such as PPI, GO, KEGG, MeSH, ChemBL, GEO, and more.

b) Conducted gene enrichment analyses rooted in curated databases, utilizing the most recent software and data sources. This ensured our enrichment assessments (pertaining to GO, KEGG, Diseases) were consistently in sync with the latest industry data.

c) Orchestrated a comprehensive Meta-Analysis using various datasets, combined with the P-value method, to assess the merits of distinct algorithms like Empirical Fisher's methods, Stouffer's Methods, among others. This led to the development of "Meta-analysis_V9_ZYY", an advanced automated meta-analysis program that integrates the Network Analyst for thorough data assessment.

d) Furthered our co-expression analyses by grasping different clustering algorithms, ultimately adopting the Fuzzy C-Means Clustering and K-means techniques to decipher the relationship between OSS shear force and atherosclerosis.

[3] Technical Mastery & Infrastructure Deployment:

a) Oversaw the deployment of a supercomputing cluster server optimized for GPU functionality, ensuring swift and seamless data computations.

b) Spearheaded web-crawling initiatives, gleaning valuable data from prominent sources such as NCBI, Malacards diseases, Pharmado, and the likes.

c) Demonstrated adeptness in deploying and leveraging a spectrum of biomedical databases including HGNC, Uniprot, DO disease, Europe_PMC, and more.

d) Cultivated expertise in crucial bioinformatics tools such as MetaMap, NetworkX, PubMed_parser, Bio.Medline, Bio.Entrez, Rank-In, and Network Analyst.

e) Achieved proficiency in deciphering single-cell sequencing datasets, diverse microarray, and transcriptome data processing.

During my tenure at Drug Farm, I immersed myself in a blend of cutting-edge methodologies and in-depth bioinformatics studies, continuously pioneering advancements in drug discovery.

Volunteer Experience

[1] June 2014 - August 2014: Participant in AIESEC Global Community Development Program

a) Actively engaged in the "Heart to Heart" project in collaboration with CFPA, aimed at poverty alleviation and educational support in poor area Yichun, Wuyiling, China.

b) Responsible for cultural exchange initiatives, enhancing community engagement through teaching experiences and proficiency in public speaking.

c) Completed volunteer service that fostered teamwork skills and provided in-depth

understanding of educational needs in underprivileged areas.

[2] Regular Blood Donor, Red Cross: Donated over 1000ml of blood, aiding critical medical needs and contributing to life-saving supplies.