CURRICULUM VITAE

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EDUCATION

2017-2023	**Doctor of Philosophy in Bioinformatics**
	Zhejiang University, Hangzhou, China
2013-2016	**Master of Philosophy in Biomedical Engineering**
	Tianjin Medical University, Tianjin, China
2009-2013	**Bachelor of Science in Biomedical Engineering**
	Shandong First Medical University (Shandong Academy of Medical Sciences), Taian, China

EXPERIENCE

2023-	**Research Associate**
	College of Life Sciences, Zhejiang University, Hangzhou, China
2016-2017	**Research Assistant**
	School of Biomedical Engineering, Tianjin Medical University, Tianjin, China

ACADEMIC HONORS & AWARDS

2017-	Bioinformatics Society of Zhejiang Province of China, membership
2019	Zhejiang University Award of Honor for Graduate
2018	Zhejiang University First-Class Scholarship for Doctoral Mid-term Examination (¥20,000)
2018	Zhejiang University Award of Honor for Graduate
2017	Zhejiang University Excellent Doctoral Freshman Scholarship (¥10,000)
2017	Certificate of Reviewing for *Computational Biology and Chemistry*
2014	The Sixth National Conference on Bioinformatics & Systems Biology of China, Second-Class Prize for Excellent Poster
2011	Shandong First Medical University & Shandong Academy of Medical Sciences, Second-Class Scholarship
2010	Shandong First Medical University & Shandong Academy of Medical Sciences, Third-Class Scholarship

JOURNAL PEER REVIEW

Science China Life Sciences, *Bioinformatics*, IEEE Journal of Biomedical and Health Informatics, *Frontiers in Neuroscience*, *Molecular Neurobiology*, *Scientific Reports*, *Frontiers in Neurology*, *Current Bioinformatics*, *International Journal of Intelligent Systems*, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, *BMC Medical Genomics*, *Journal of Molecular Neuroscience*, *Computational Biology and Chemistry*, *Cell Biochemistry and Biophysics*, *IEEE Open Journal of the Computer Society*

PUBLICATIONS & PREPRINTS

1. **YS Hu**[#]*, YH Chen[#], YM Hu, M Chen* (*To appear on* ***bioRχiv***). Decrypting human biological pathway crosstalk landscape in a deep learning architecture.
   DOI: 10.1186/s12xxx-0x4-01939-x
2. **YS Hu***, B She, Z Yin, X Yu, W Wu, M Chen*. Systems biology framework unravels molecular substrates underlying comorbidity between Parkinson's and Crohn's disease. ***medRχiv***, 2025.10.01.25337087.
   DOI: 10.1101/2025.10.01.25337087
3. **YS Hu***, ZX Wang, YM Hu, C Feng, QY Fang, M Chen*. AWmeta empowers adaptively-weighted transcriptomic meta-analysis. ***bioRχiv***, 2025.05.06.650408.
   (*Under Review*, ***Nature Communications***, IF = ***17.2***)
   DOI: 10.1101/2025.05.06.650408
4. YY Zhu[#], LY Liu[#], YM Hu[#], SD Li, EY Liu, **YS Hu**, S Zhang, HY Chao, Q Fang, H Yu, M Chen*. InTxDB: interaction data between gram-negative bacteria secreted effectors and host proteins.
   (*Major Revision*, ***Database***, IF = ***4.2***)
   DOI: 10.xxxxx/s12915-024-01376-1
5. YM Hu[#], LY Liu[#], YY Zhu[#], EY Liu, HY Chao, SD Li, C Feng, **YS Hu**, YH Chen, S Zhang, Y Chen, L Xie, YJ Wang, M Chen*. HPInet: Interpretable prediction of Host-Pathogen protein–protein Interactions using a transformer-based neural network. ***bioRχiv***, 2025.08.02.668281.
   DOI: 10.1101/2025.08.02.668281
6. YM Hu[#], MQ Yan[#], Y Zhu, H Chao, S Li, Q Ni, **YS Hu**, EY Liu, LY Liu, Y Chen, Z Zhou, Y Chen, S Zhang, Y Wang, C Feng*, M Chen*. Improved Prediction of Bacterial Type VI Secretion Effector Proteins Using an Integrated Convolutional Neural Network Model Combining N-terminal Signal Sequences, Evolutionary Information and Pre-Trained Protein Language Features. ***bioRχiv***, 2025.03.07.642067.
   (*Major Revision*, ***mSystems***, IF = ***6.1***)
   DOI: 10.1101/2025.03.07.642067
7. S Li, Z Wang, **YS Hu**, Q Ni, C Feng, Y Hu, S Zhang, M Chen*. Benchmarking alternative polyadenylation detection in single-cell and spatial transcriptomes. ***bioRχiv***, 2024.10.15.618405.
   (*Under Review*, ***Briefings in Bioinformatics***, IF = ***8.7***)
   DOI: 10.1101/2024.10.15.618405
8. LY Liu[#], EY Liu[#], YM Hu, S Li, S Zhang, H Chao, **YS Hu**, Y Zhu, Y Chen, L Xie, Y Shen, L Wu, M Chen*. ncPlantDB: A plant ncRNA database with potential ncPEP information and cell type-specific interaction. ***Nucleic Acids Research***, 2024, baac051. (IF = ***16.6***)
   DOI: 10.1093/nar/gkae1017
9. C Feng[#], RX Tie[#], SG Xin[#], Y Chen, S Li, Y Chen, X Hu, Y Zhou, Y Liu, Y Hu, **YS Hu**, H Pan, Z Wu, H Chao, S Zhang, Q Ni, J Huang, W Luo*, H Huang*, M Chen*. Systematic single-cell analysis reveals dynamic control of transposable element activity orchestrating the endothelial-to-hematopoietic transition. ***BMC Biology***, 2024, 22(1):143. (IF = ***5.4***)
   DOI: 10.1186/s12915-024-01939-5
10. Z Wu[#], C Feng[#], **YS Hu**, Y Zhou, S Li, S Zhang, Y Hu, Y Chen, H Chao, Q Ni, M Chen*. HALD, a human aging and longevity knowledge graph for precision gerontology and geroscience analyses. ***Scientific Data***, 2023, 10(1):851. (IF = ***8.9***)
    DOI: 10.1038/s41597-023-02781-0
11. Y Chen[#], **YS Hu**[#], X Hu, C Feng, M Chen*. CoGO: a contrastive learning framework to predict disease similarity based on gene network and ontology structure. ***Bioinformatics***, 2022, 38(18):4380-4386.
    (IF = ***7.6***)
    DOI: 10.1093/bioinformatics/btac520

12. H Chen, X Hu, **YS Hu**, J Zhou, M Chen*. CoVM^2: Molecular Biological Data Integration of SARS-CoV-2 Proteins in a Macro-to-Micro Method. ***Biomolecules***, 2022, 12(8):1067. (IF = ***5.4***)
    DOI: 10.3390/biom12081067
13. B Tan, S Xin, **YS Hu**, C Feng*, M Chen*. LBD: a manually curated database of experimentally validated lymphoma biomarkers. ***Database***, 2022, Volume 2022, baac051. (IF = ***4.2***)
    DOI: 10.1093/database/baac051
14. WY Wu, Y Wu, DH Hu, YC Zhou, **YS Hu**, YJ Chen, M Chen*. PncStress: a manually curated database of experimentally validated stress-responsive non-coding RNAs in plants. ***Database***, 2020, Volume 2020, baaa001. (IF = ***4.2***)
    DOI: 10.1093/database/baaa001
15. TY Wang, P Song, TT Zhong, XJ Wang, XP Xiang, Q Liu, HY Chen, T Xia, H Liu, YM Niu, **YS Hu**, L Xu, YK Shao, LJ Zhu, HY Qi, J Shen, TJ Hou, R Fodde*, JM Shao*. The inflammatory cytokine IL-6 induces FRA1 deacetylation promoting colorectal cancer stemness and malignancy. ***Oncogene***, 2019, 38:4932-4947. (IF = ***7.5***)
    DOI: 10.1038/s41388-019-0763-0
16. **YS Hu,** J Xin, Y Hu, L Zhang*, J Wang*. Analyzing the genes related to Alzheimer's disease via a network and pathway-based approach. ***Alzheimer's Research & Therapy***, 2017, 9(1):29. (IF = ***9.2***)
    DOI: 10.1186/s13195-017-0252-z
    🏆 Highly Cited Paper (**>110 citations**)
17. **YS Hu,** Z Pan, Y Hu, L Zhang*, J Wang*. Network and Pathway-Based Analyses of Genes Associated with Parkinson's Disease. ***Molecular Neurobiology***, 2017, 54(6):4452-4465. (IF = ***5.1***)
    DOI: 10.1007/s12035-016-9998-8
18. Y Hu, Y Yang, Z Fang, **YS Hu**, L Zhang*, J Wang*. Detecting pathway relationship in the context of human protein-protein interaction network and its application to Parkinson's disease. ***Methods***, 2017, 131:93-103. (IF = ***4.2***)
    DOI: 10.1016/j.ymeth.2017.08.001
19. ZH Fang, YC Yang, **YS Hu**, MD Li*, J Wang*. GRONS: a comprehensive genetic resource of nicotine and smoking. ***Database***, 2017, Volume 2017, bax097. (IF = ***4.2***)
    DOI: 10.1093/database/bax097
20. TY Ling, YC Zhou, CF Xu, XT Shao, **YS Hu**, KF Ding*, M Chen* (*In Preparation*). Colorectal cancer computer-aided image analysis: the teenager in the new era of deep learning.
21. YC Zhou, **YS Hu**, DH Hu, C Feng, MA Ahsan, YJ Liu, TY Ling, SD Li, XC Yang, R Hofestädt, M Chen* (*In Preparation*). DaTo: a repertoire dedicated to biological online resources.
22. YC Zhou, JT Xue, MA Ahsan, DH Hu, **YS Hu**, Y Liu, Y Jiang, W Ni, M Chen* (*In Preparation*). CytoSEE: a web-based toolkit for automatic computation and evaluation of cytometry data.
23. **YS Hu***, ZH Fang, J Wang*, M Chen* (*In Preparation*). A systems biology framework identifies latent molecular relationships between Alzheimer's and Parkinson's disease.

CONFERENCE PROCEEDINGS

1. **YS Hu***, J Wang*, M Chen. Analyzing the genes related to Alzheimer's disease via a network and pathway-based approach. ***First Sino-Russian Workshop on Integrative Bioinformatics and Systems Biology (WIBSB-2018)*** @ Novosibirsk, Russia
    DOI: 10.18699/WIBSB-2018-28
2. **YS Hu**, Z Pan, Y Hu, J Wang*. Network and pathway based analyses of genes associated with Parkinson's disease. ***The Seventh National Conference on Bioinformatics and Systems Biology*** @ Chengdu, China
    Availability: ResearchGate Link

3. Y Hu, **YS Hu**, Y Yang, Z Fang, J Wang*. Uncovering the common pathogenesis in neurodegenerative and psychiatric disorder via network approaches. ***The Seventh National Conference on Bioinformatics and Systems Biology*** @ Chengdu, China
   Availability: ResearchGate Link
4. Z Fang, Y Yang, Y Hu, **YS Hu**, J Wang*. Identifying the enriched biological pathways in genes related to nicotine dependence via a network-based gene-weighting algorithm. ***The Seventh National Conference on Bioinformatics and Systems Biology*** @ Chengdu, China
   Availability: ResearchGate Link
5. **YS Hu**, R Fan, X Li, M Liu, X Liu, X Yi, T Zhang, J Wang*. Common characteristics of Alzheimer's disease and Parkinson's disease based on AlzGene and PDGene databases. ***The Sixth National Conference on Bioinformatics and Systems Biology*** @ Nanjing, China
   Availability: ResearchGate Link
6. X Liu, X Li, M Liu, R Fan, **YS Hu**, Y Hu, X Yi, T Zhang, J Wang*. Computing the phenotype similarity based on OMIM database and MESH vocabulary. ***The Sixth National Conference on Bioinformatics and Systems Biology*** @ Nanjing, China
   Availability: ResearchGate Link
7. X Li, M Liu, X Liu, R Fan, **YS Hu**, Y Hu, X Yi, T Zhang, J Wang*. TarPriGO: a new method to prioritize miRNA targets based on Gene Ontology. ***The Sixth National Conference on Bioinformatics and Systems Biology*** @ Nanjing, China
   Availability: ResearchGate Link
8. M Liu, X Liu, X Li, R Fan, **YS Hu**, Y Hu, X Yi, T Zhang, J Wang*. A comprehensive pathway and network analysis of candidate genes associated with nicotine addiction. ***The Sixth National Conference on Bioinformatics and Systems Biology*** @ Nanjing, China
   Availability: ResearchGate Link
9. R Fan, M Liu, X Li, X Liu, **YS Hu**, Y Hu, X Yi, T Zhang, J Wang*. The functional divergence analysis of neuronal nicotinic acetylcholine receptor subunits. ***The Sixth National Conference on Bioinformatics and Systems Biology*** @ Nanjing, China
   Availability: ResearchGate Link

ACADEMIC TALKS

09/2019 Zhejiang University-Bielefeld University Joint Symposium @ Bielefeld, Germany

08/2018 First Sino-Russian Workshop on Integrative Bioinformatics and Systems Biology (WIBSB-2018) @ Novosibirsk, Russia

POSTERS

1. **YS Hu**, Z Pan, Y Hu, J Wang*. Network and pathway based analyses of genes associated with Parkinson's disease. ***The Seventh National Conference on Bioinformatics and Systems Biology*** @ Chengdu, China
   DOI: 10.13140/RG.2.2.20162.27844
2. **YS Hu**, R Fan, X Li, M Liu, X Liu, X Yi, T Zhang, J Wang*. Common characteristics of Alzheimer's disease and Parkinson's disease based on AlzGene and PDGene databases. ***The Sixth National Conference on Bioinformatics and Systems Biology*** @ Nanjing, China
   DOI: 10.13140/RG.2.2.14971.82725

PATENTS

1. 一种生化通路串话识别方法 (Chinese Patent)
   Inventor: 陈铭，**胡言石（YS Hu）**，陈俞皓
   Application number: 2023107816823
   Filing date: 2023-06-28
   Publication number: CN116959588A
   Publication date: 2023-10-27
   Link: China National Intellectual Property Administration (CNIPA) Patent Page