

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, International Journal of Intelligent Systems, Frontiers in Neuroscience, Molecular Neurobiology, Scientific Reports, Frontiers in Neurology, Current Bioinformatics, IEEE/ACM Transactions on Computational Biology and Bioinformatics, PLOS ONE, BMC Medical Genomics, Journal of Molecular Neuroscience, Computational Biology and Chemistry, Cell Biochemistry and Biophysics, BMC Neurology, BMC Genomic Data, Mammalian Genome

PUBLICATIONS & PREPRINTS

1. **YS Hu**[#], YH Chen[#], YM Hu, M Chen* (To appear on [bioRxiv](#)). Decrypting human biological pathway crosstalk landscape in a deep learning architecture.
DOI: [10.1186/s12xxx-0x4-01939-x](#)
2. **YS Hu**^{*}, ZX Wang, YM Hu, C Feng, QY Fang, M Chen* (To appear on [bioRxiv](#)). AWmeta empowers adaptively-weighted transcriptomic meta-analysis.
(Invited by [Nature Methods](#) after presubmission inquiry, IF = 45.6)
DOI: [10.1186/s12915-024-xxxxxx-5](#)
3. **YS Hu**^{*}, BT She, ZN Yin, XJ Yu, W Wu, M Chen* (To appear on [medRxiv](#)). Systems biology framework unravels molecular substrates underlying comorbidity between Parkinson's and Crohn's disease.
DOI: [10.xxxxx/s12915-024-01939-5](#)
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.
(Submitted, [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*. HPI-net: Interpretable prediction of Host-Pathogen protein-protein Interactions using a transformer-based neural network. (Under Review, [Briefings in Bioinformatics](#), IF = 7.9)
DOI: [10.xxxxx/s12915-024-01361-8](#)
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. [bioRxiv](#), 2025.03.07.642067.
(Under Review, [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. [bioRxiv](#), 2024.10.15.618405.
(Under Review, [Genome Biology](#), IF = 16.5)
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*. CoVM²: 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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/10.1186/s13195-017-0252-z)
 Highly Cited Paper (>100 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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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

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