

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

- 2023-2024 **Research Assistant**
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

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.
2. **YS Hu**^{*}, YM Hu, M Chen* (To appear on [bioRxiv](#)). AWmeta empowers adaptively-weighted meta-analysis for gene expression data.
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.
4. 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](#)
5. 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](#)
6. 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](#)
7. 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](#)
8. 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](#)
9. 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](#)
10. 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](#)
11. **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](#)
12. **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](#)
13. 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](#)
14. 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)

15. 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.
16. 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.
17. 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.
18. **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
Application number: 2023107816823
Filing date: 2023-06-28
Publication number: CN116959588A
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Link: [China National Intellectual Property Administration \(CNIPA\) Patent Page](#)