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EDUCATION

- M.S. Computer Science, University of California, Irvine, 2021 - 2024
B.S. Automation & Computer Science (Dual Degree), Zhejiang University, 2016 - 2020

PUBLICATIONS

First Author Publications

- [7] **Duan, Z.**, Riffle, D., Li, R., Liu, J., Min, M. R., & Zhang, J. (2024). Impeller: a path-based heterogeneous graph learning method for spatial transcriptomic data imputation. *Bioinformatics*, btae339. doi:10.1093/bioinformatics/btae339
- [6] **Duan, Z.**, Xu, S., Sai Srinivasan, S., Hwang, A., Lee, C. Y., Yue, F., ... & Zhang, J. (2024). scENCORE: leveraging single-cell epigenetic data to predict chromatin conformation using graph embedding. *Briefings in Bioinformatics*, 25(2), bbae096. doi:10.1093/bib/bbae096
- [5] **Duan, Z.**, Lee, C., & Zhang, J. (2023). ExAD-GNN: explainable graph neural network for Alzheimer's disease state prediction from single-cell data. *APSIPA Transactions on Signal and Information Processing*, 12(5). doi:10.1561/116.00000239
- [4] **Duan, Z.**, Dai, Y., Hwang, A., Lee, C., Xie, K., Xiao, C., ... & Zhang, J. (2023). iHerd: an integrative hierarchical graph representation learning framework to quantify network changes and prioritize risk genes in disease. *PLoS Computational Biology*, 19(9), e1011444. doi:10.1371/journal.pcbi.1011444
- [3] **Duan, Z.**, Xu, H., Wang, Y., Huang, Y., Ren, A., Xu, Z., ... & Wang, W. (2022). Multivariate time-series classification with hierarchical variational graph pooling. *Neural Networks*, 154, 481-490. doi:10.1016/j.neunet.2022.07.032
- [2] **Duan, Z.**, Xu, H., Huang, Y., Feng, J., & Wang, Y. (2022). Multivariate time series forecasting with transfer entropy graph. *Tsinghua Science and Technology*, 28(1), 141-149. doi:10.26599/TST.2021.9010081
- [1] **Duan, Z.**, Wang, Y., Ye, W., Fan, Q., & Li, X. (2022). Connecting latent relationships over heterogeneous attributed network for recommendation. *Applied Intelligence*, 52(14), 16214-16232. doi:10.1007/s10489-022-03340-7

Other Publications

- [16] Wen, C., Margolis, M., Dai, R., Zhang, P., Przytycki, P. F., Vo, D. D., ..., **PsychENCODE Consortium**, ... & Gandal, M. J. (2024). Cross-ancestry atlas of gene, isoform, and splicing regulation in the developing human brain. *Science*, 384(6698), eadh0829. doi:10.1126/science.adh0829
- [15] Deng, C., Whalen, S., Steyert, M., Ziffra, R., Przytycki, P. F., Inoue, F., ..., **PsychENCODE Consortium**, ... & Pollard, K. S. (2024). Massively parallel characterization of regulatory elements in the developing human cortex. *Science*, 384(6698), eadh0559. doi:10.1126/science.adh0559

- [14] Huuki-Myers, L. A., Spangler, A., Eagles, N. J., Montgomery, K. D., Kwon, S. H., Guo, B., ..., **PsychENCODE Consortium**, ... & Maynard, K. R. (2024). A data-driven single-cell and spatial transcriptomic map of the human prefrontal cortex. *Science*, 384(6698), eadh1938. doi:10.1126/science.adh1938
- [13] Ruzicka, W. B., Mohammadi, S., Fullard, J. F., Davila-Velderrain, J., Subburaju, S., Tso, D. R., ..., **PsychENCODE Consortium**, ... & Kellis, M. (2024). Single-cell multi-cohort dissection of the schizophrenia transcriptome. *Science*, 384(6698), eadg5136. doi:10.1126/science.adg5136
- [12] Emani, P. S., Liu, J. J., Clarke, D., Jensen, M., Warrell, J., Gupta, C., ..., **Duan, Z.**, ... & Gerstein, M. (2024). Single-cell genomics and regulatory networks for 388 human brains. *Science*, 384(6698), eadi5199. doi:10.1126/science.adi5199
- [11] Dai, R., Chu, T., Zhang, M., Wang, X., Jourdon, A., Wu, F., ..., **PsychENCODE Consortium**, ... & Liu, C. (2024). Evaluating performance and applications of sample-wise cell deconvolution methods on human brain transcriptomic data. *Science Advances*, 10(21), eadh2588. doi:10.1126/sciadv.adh2588
- [10] Pratt, H. E., Andrews, G., Shedd, N., Phalke, N., Li, T., Pampari, A., ..., **PsychENCODE Consortium**, ... & Weng, Z. (2024). Using a comprehensive atlas and predictive models to reveal the complexity and evolution of brain-active regulatory elements. *Science Advances*, 10(21), eadj4452. doi:10.1126/sciadv.adj4452
- [9] Xia, Y., Xia, C., Jiang, Y., Chen, Y., Zhou, J., Dai, R., ..., **PsychENCODE Consortium**, ... & Chen, C. (2024). Transcriptomic sex differences in postmortem brain samples from patients with psychiatric disorders. *Science Translational Medicine*, 16(749), eadh9974. doi:10.1126/scitranslmed.adh9974
- [8] Lee, C. Y., Riffle, D., Xiong, Y., Momtaz, N., Lei, Y., Pariser, J. M., ..., **Duan, Z.**, ... & Zhang, J. (2024). Characterizing dysregulations via cell-cell communications in Alzheimer's brains using single-cell transcriptomes. *BMC neuroscience*, 25(1), 24. doi:10.1186/s12868-024-00867-y
- [7] Zhang, R., **Duan, Z.**, Lee, C. Y., Riffle, D., Min, M. R., & Zhang, J. (2023). Turtling: A Time-aware Neural Topic Model on NIH Grant Data. *Bioinformatics Advances*, vbado96. doi:10.1093/bioadv/vbado96
- [6] Lee, C. Y., Chen, Y., **Duan, Z.**, Xu, M., Girgenti, M. J., Xu, K., ... & Zhang, J. (2022). Venus: An efficient virus infection detection and fusion site discovery method using single-cell and bulk RNA-seq data. *PLOS Computational Biology*, 18(10), e1010636. doi:10.1371/journal.pcbi.1010636
- [5] Wang, Y., **Duan, Z.**, Huang, Y., Xu, H., Feng, J., & Ren, A. (2022). MTHetGNN: A heterogeneous graph embedding framework for multivariate time series forecasting. *Pattern Recognition Letters*, 153, 151-158. doi:10.1016/j.patrec.2021.12.008
- [4] Xu, H., **Duan, Z.**, Wang, Y., Feng, J., Chen, R., Zhang, Q., & Xu, Z. (2021). Graph partitioning and graph neural network based hierarchical graph matching for graph similarity computation. *Neurocomputing*, 439, 348-362. doi:10.1016/j.neucom.2021.01.068
- [3] Liao, Z., Yang, Y., Sun, C., Wu, R., **Duan, Z.**, Wang, Y., ... & Xu, J. (2021). Image-based prediction of granular flow behaviors in a wedge-shaped hopper by combining DEM and deep learning methods. *Powder Technology*, 383, 159-166. doi:10.1016/j.powtec.2021.01.041
- [2] Wang, B., Zhou, C., **Duan, Z.**, Zhu, Q., Wu, J., & Xiong, R. (2020). Untethered quadrupedal hopping and bounding on a trampoline. *Frontiers of Mechanical Engineering*, 15, 181-192. doi:10.1007/s11465-019-0559-5
- [1] Wang, Y., **Duan, Z.**, Liao, B., Wu, F., & Zhuang, Y. (2019, July). Heterogeneous attributed network embedding with graph convolutional networks. In *Proceedings of the AAAI conference on artificial intelligence* (Vol. 33, No. 01, pp. 10061-10062). doi:10.1609/aaai.v33i01.330110061

INVITED TALKS

- "scENCORE, a computationally method to reconstruct chromatin compartments from the more affordable and widely accessible single-cell epigenetic data."
13th Annual Symposium, Southern California Systems Biology May 2024
- "iHerd, a hierarchical graph representation learning method for identifying key driver genes by analyzing gene network changes across different conditions."
2023 SCORCH Consortium Meeting Dec 2023

AWARDS AND HONORS

- Dean's Fellowship, University of California, Irvine 2021
- Research and Innovation Scholarship, Zhejiang University 2019
- Academic Excellence Scholarship, Zhejiang University 2017 - 2019

TEACHING

- *Reader*, University of California, Irvine Spring 2022
ICS 6D: Discrete Mathematics for Computer Science
- *Reader*, University of California, Irvine Winter 2021
ICS 178: Machine Learning and Data Mining
- *Reader*, University of California, Irvine Fall 2021
ICS 178: Machine Learning and Data Mining

SERVICES

Journal Reviewer

Computers in Biology and Medicine
Gene
IEEE Transactions on Pattern Analysis and Machine Intelligence
Information Science
Knowledge and Information Systems
Knowledge Based Systems
Neural Networks
Neurocomputing
Pattern Recognition
Pattern Recognition Letters
Reliability Engineering & System Safety
The Journal of Supercomputing

Conference Reviewer

The International Conference on Intelligent Systems for Molecular Biology (ISMB)
IEEE International Conference on AI for Medicine, Health, and Care (AIMHC)

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