

Hanrui Zhang, PhD candidate,
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Summary

- Strong research-oriented third-year Ph.D. student with experience in 9 publications (4 first author)
- Rich experience and background in bioinformatics and machine learning model development
- Independently organized winning team for international bioinformatics competitions

Education

2020-present Ph.D. candidate in Bioinformatics at the University of Michigan, Ann Arbor
2017-2019 Bioinformatics Master's program at University of Michigan, Ann Arbor
2016-2016 Columbia University, New York City, NY
2015-2015 University of California, Berkeley, CA
2014-2017 Base Class of Biotechnology and Application, Sun Yat-sen University, Guangzhou, Guangdong, China

Research experiences

2018-present Graduate Research Assistant, Yuanfang Guan Lab, department of Computerized Medicine and Bioinformatics, University of Michigan. Supervisor: Prof. Guan Yuanfang, gyuanfan@umich.edu

- Developed various machine learning models for solving different biomedical problems, including
 - Developed a Parkinson's disease diagnostic model using **DCNN** from accelerometry and voice recorded by mobile phones. Abstracted digital biomarkers of Parkinson's diseases using AI interpretation methods such as **saliency maps**.
 - Developed an automatic sleep stage segmentation and apnea/arousal detection model using **multi-task learning** and **U-Net**.
 - Developed machine learning models (**linear regression, GPR, XGboost, Random Forest, and LightGBM**) for predicting artemisinin resistance in malaria across different platforms and *in vivo, ex vivo*, and *in vitro* conditions, and identified top ART resistance-related genes and pathways by **SHAP analysis**.
 - Developed *Timesias* package predicting outcomes and top contributing factors from time-series data including EHR. This method was the **first place** algorithm in the 2019 DII Sepsis challenge.
 - Developed a rule-based hierarchical clustering algorithm for cell lineage reconstruction from real-life experimental datasets. This method won the **top-performing** algorithm in the 2020 Allen Institute Cell Lineage Reconstruction DREAM Challenge.
 - Developed a machine learning model for optimizing personalized anticancer treatment using **LightGBM** by incorporating **multi-facet information** including multi-omics profiles, drug-gene interaction, tissue-specific biological networks, mode of actions, and chemical structure of drugs, achieving experimental replication level performances.
 - Proposed a complete risk evaluation algorithm for predisposed Type 1 diabetes patients by integrating state-of-the-art survival models with machine learning, which won the **"Outside T1D"** award and was a **finalist** for the 2021 T1D d-challenge.

2018-2018 Research Assistant, Department of Computational Medicine and Bioinformatics, University of Michigan. Supervisor: Prof. Sartor Maureen, sartorma@umich.edu

- Pulled significant transcriptional targets from raw ChIA-PET data and compared the performances of ChIA-PET processing tools, Mango and ChiAPET2

2016-2016 Volunteer Research Assistant, Tobias Hohl Lab, Memorial Sloan Kettering Cancer Center. Supervisor: Dr. Zhai Bing, zhaib@mskcc.org

- Helped construct a metabarcoding pipeline to identify pathogenic gut fungi

2016-2016 Summer Intern, Beijing Genomics Institute (BGI) Diagnosis Technology Co. Ltd, Medical Bioinformatics and Technology Optimizing Distribution. Supervisor: Junqing Chen, chenjunqing@genomics.cn

- Developed an automatic pipeline for generating diagnostic reports for HCV drug resistance variations

2015-2016 Undergraduate Research Assistant, Lab of Plant Evolution and Genetics, Sun Yat-sen University. Supervisor: Prof. Yingjuan Su, suyj@mail.sysu.edu.cn

- Designed chloroplast microsatellite markers for an endangered endemic species in China, *Pseudotaxus chienii*

Publications
<ol style="list-style-type: none"> 1. Zhang H, Guo J, Li H, Guan Y. 2022. Machine learning for artemisinin resistance in malaria treatment across in vivo-in vitro platforms. <i>iScience</i>. https://doi.org/10.1016/j.isci.2022.103910 2. Zhang H, Wang X, Li H, Mehendale S, Guan Y. 2021. Auto-annotating sleep stages based on polysomnographic data. <i>Patterns</i>. https://doi.org/10.1016/j.patter.2021.100371 3. Chou E, Zhang H, Guan Y. Protocol for using Ciclops to build models trained on cross-platform transcriptome data for clinical outcome prediction. <i>STAR Protoc</i>. 2022 Jul 20;3(3):101583. doi: 10.1016/j.xpro.2022.101583 4. Qin T, Lee C, Cavalcante R, Orchard P, Yao H, Zhang H, Wang S, Pati SI, Boyle AP, Sartor M. 2022 Comprehensive enhancer-target gene assignments improve gene set level interpretation of genome-wide regulatory data <i>Genome Biology</i>. https://doi.org/10.1186/s13059-022-02668-0 5. Deng K, Li Y, Zhang H, Wang J, Albin RL, Guan Y. 2022. Heterogeneous digital biomarker integration outperforms patient self-reports in predicting Parkinson's disease. <i>Communications Biology</i>. https://doi.org/10.1038/s42003-022-03002-x 6. Gong W*, Granados A*, Hu J*, Jones M*, Raz O, Martinez IS*, Zhang H*, Chow KK, Kwak IY, Retkute R, Prusokas A, Prusokas A, Khodaverdian A, Zhang R, Wang R, Rao S, Rennert P, Saipradeep V, Naveen S, Joseph T, Rao A, Srinivasan R, Peng J, Han L, Shang X, Garry DJ, Yu T, Chung V, Mason M, Liu Z, Guan Y, Yosef N, Shendure J, Telford M, Shapiro E, Elowitz MB, Meyer P. 2021. Benchmarked approaches for cell lineage reconstructions of in vitro dividing cells and in silico models of <i>Caenorhabditis elegans</i> and <i>Mus musculus</i> developmental trees. <i>Cell Systems</i>. doi: 10.1016/j.cels.2021.05.008. 7. Zhang H, Yi D, Guan Y. 2021. Timesias: A machine learning pipeline for predicting outcomes from time-series clinical records. <i>STAR Protoc</i>. doi: 10.1016/j.xpro.2021.100639 8. Zhang H, Deng K, Li H, Albin R, Guan Y. 2020. "Deep Learning Identifies Digital Biomarkers for Self-Reported Parkinson's Disease", <i>Patterns</i>. https://doi.org/10.1016/j.patter.2020.100042 9. Deng Q, Zhang H, He Y, Wang T, Su Y. 2017. "Chloroplast microsatellite markers for <i>Pseudotschus chienii</i> developed from the whole chloroplast genome of <i>Taxus chinensis</i> var. <i>mairei</i> (Taxaceae)." <i>Applications in Plant Sciences</i>. https://doi.org/10.3732/apps.1600153
* These authors contributed equally.
Technical skills
Programming Languages: Python, R, Shell, Perl, Pascal, C++, html; Machine learning platform: Keras, TensorFlow, Pytorch, Theano, sci-kit learn, NumPy, Pandas, Scipy; Research Skills: Manuscript preparation and data visualization
Awards and credits
2021 "Outside T1D" Award - Finalist for 2021 D-challenge for type 1 diabetes 2020 First Place in 2020 Allen Institute Cell Lineage Reconstruction DREAM Challenge 2016 Undergraduate Open Laboratory Research Grant, Sun Yat-sen University 2013 National Second Class Athlete in China; Sixth Place in Go Game Competition of Sichuan Province 2010 Second Grade Award in National Olympiad in Informatics in Provinces (NOIP) 2006 National Second Grade Player in China; First place in Go Game Competition of Sichuan Province
Community Services & Organizations
2022-present Lab manager at GuanLab at University of Michigan 2020-present Member on student PARC committee in DCMB, University of Michigan 2019-present Volunteer at Huron Valley Humane Society