Ruifeng Hu, Ph.D. (Permanent resident)

Current position: Yale School of Medicine, Research Scientist (Research rank faculty)
Contact: 1 (979) 264-7270 huruifeng.cn@hotmail.com
Links: https://github.com/huruifeng / https://huruifeng.github.io

EDUCATION

2012.9 – 2017.7	**Ph.D. Bioinformatics & Computational Biology** Peking Union Medical College & Chinese Academy of Medical Sciences, Tsinghua University, Beijing, China
2008.9 – 2012.6	**B.Eng. Computer Science and Technology** College of Computer Science and Technology, Nanjing Forestry University, Nanjing, China

FOCUS & SKILLS

I would like to apply advanced statistical and machine learning methods to analyze multi-modal data aiming to potential biomarker/target identification and MoA (mechanism of action) insights. In the past, I leveraged high-throughput data and multi-omics integration in a variety of contexts including tumor-intrinsic cancer resistance, personalized diagnose, Parkinson's disease, and infectious diseases

- Proficient in analyzing multi-omics data (e.g., bulk/single-cell RNASeq, genetics data, WG CRISPR screen data, Spatial transcriptomics)
- Proficient in Python, C/C++, Go, R, and Linux shell language and large-scale data calculation (Rich experience with local HPC or cloud computing environment (*e.g.* AWS, GCP, Verily), rich experience with Nextflow, AirFlow, and proficient in code managements via GitHub and Docker).
- Proficient in various algorithms of deep learning, including CNN, RNN, DNN, VAE and Generative models, and using them to develop prediction algorithms. Proficient understanding and practical expertise in LSTM, Transformer, and Attention models. (Extensive experience using PyTorch, TensorFlow, and Keras).
- Proficient in common regression, clustering, and classification algorithms of machine learning, including Linear/Logistics regression, SVM, k-means, decision tree, random forest, *et.al.* Rich experience in data modeling, DevOps, and AI/ML Ops
- Proficient in constructions of bioinformatics statistical modeling and data analysis pipelines.
- Rich experience with several public genomic data atlas (*e.g.* ENCODE, TCGA, DepMap, GTEx, CELLxGENE).
- Proficient in the construction of bioinformatics webserver platforms, application interfaces (APIs) design for data visualization, extractions and transfers (*e.g.* React, Vite, html5/CSS, TailwindCSS, Material UI, Express.js, FastAPI, Flask, Django, MySQL, PostgreSQL, MongoDB).
- Deep knowledge of cancer genetics and rich practical experience in cancer genomics.
- I excel in collaborative environments and project leadership and mentoring.

EXPERIENCE

Yale School of Medicine, New Haven, CT **2024.10 – Current**

Research Scientist, Research rank faculty

- In summary: working as an advanced member of a research group. I focus on several projects in supporting of the PI, my responsibilities involve the combination of project management, research execution, data and pipeline management, research staff/trainee training and supervision, leading or assisting in the development of papers for publication and conference presentations, and supporting the preparation of grant applications and reports to funding agencies.
- Core member of ASAP (Aligning Science Across Parkinson's) Multi-omics Meta-analysis (MoMa) Working Group: Data is submitted from 32 ASAP teams, I am working closely with other teams independently or under the PI's guidance, my duties include:(1) Developing and managing project plans; (2) Meeting with collaborators to understand their samples, data and protocols, and propose the data submission standards to the ASAP committee to ensure compatibility and consistency across cohorts and omics layers; (3) Conducting statistical univariate and multivariate data analysis, interpreting the results and delivering and presenting final analysis report in manuscript-level quality; (4) Developing predictive models that leverage ML/AI for cross-omics feature integration, identifying key drivers of biological variation; (5) Building collaborative frameworks to engage domain experts in co-interpretation of outputs, ensuring insights are actionable.
- Developing automated, efficient internal data analysis pipelines for standard NGS datasets, including genomics, transcriptomics, epigenomics, proteomics, etc. at bulk, single-cell or spatial level. (Include setting up cross-cohort data Q/C, data harmonization, and result reporting, maintaining the codes via GitHub/Docker with well-documented README as well as developing or adapting novel algorithms, statistical modeling, and workflow to support customized data analysis. Nextflow and Airflow were mainly used.)
- Creating exploratory data portal platform for data deposit, data management and building intuitive visualization and querying of relationships across data modalities; Providing strategic solution to accelerate the store/read ST and SC data to/from database.
- Leading/Assisting an AI + Omics club within the department for sharing thoughts and advanced AI and ML techniques applied in healthcare area.
- Communicating with other parties in projects (incl. wet lab, sequencing core, study coordinator, other data scientist, and PIs etc.). Creating the standard / SOP of data management, data delivery, QC merit and reporting.
- Other research activities: Assisting the PI to provide basic and advanced bioinformatics training to the junior members in the team; Establishing the lab GitHub with curated core compute pipelines and maintaining the bioinformatics resources; Managing the lab server or HPC storage space and developing strategic plan to fulfill the lab computational needs. Drafting of the research plan, writing of research SOPs, application and renewal of grants. Staying current with advancements in the field to incorporate emerging technologies.

Bristol Myers Squibb, Cambridge, MA **2023.6 – 2024.6**

Principal Scientist, Computational Reverse Translation

- Lead the project of utilizing/customizing/training genomics foundation models (*e.g.*, Geneformer, scGPT) to decipher the genomics data, and map patient samples to reductionist models.

- Analyze multi-omics (*e.g.,* bulk/scRNAseq, Spatial transcriptomics) data for potential drug targets/biomarkers identification from PDAC, NSCLC patient and model samples.
- Involved in the development of the spatial data portal framework which can help biologists to browse and visualize analyzed results.
- Whole-genome CRISPR data analysis to find the vulnerability genes of cancer cell lines under conditions.
- Collaboration with the MoCR TRC (Mechanisms of Cancer Resistance Thematic Research Center) teams on lung cancer R&D.

Harvard Medical School - BWH, Boston, MA **2021.3 – 2023.6**

Senior Research Associate

- Lead the project of discovering and replicating the differentially expressed genes from RNAseq data analysis to find potential diagnosis biomarkers in PPMI and PDBP cohorts.
- Build classification models for prediction of the Parkinson’s Disease status utilizing the multi-omics data (transcriptomics, genetics, and clinical data)
- Investigation of advanced machine learning/deep learning models (Autoencoder, DNN, LSTM, Transformer) for Parkinson’s Disease status prediction and UPDRS regression.
- Analysis of RNAseq data obtained from a time-series experimental design to find the potential diagnosis biomarkers for PD patients at different development stages.
- Build scRNAseq data analysis pipeline using Nextflow, and analyze the scRNAseq data for PD organoid samples
- Others: Running jobs on HPC with LSF, Slurm; Internal Linux server management.

School of Biomedical Informatics, UT Health Science Center, Houston, TX **2017.10 – 2021.3**

Postdoctoral Research Fellow

- Develop, implement, and maintain next-generation sequencing (NGS) data processing pipelines or modules to perform standard data analysis in an automated fashion for researchers and clinicians to explore the results. (TCGA cancer RNAseq/mutation data analysis, survival analysis, *et.al*)
- Development of novel computational methods/solutions for biomedical problems utilizing machine learning and deep learning models. (Drug response prediction, HLA-antigen prediction, Mutation effects, *et.al*)
- Constructions of biomedical knowledgebases and web servers for research communities (Mutation-drug response database, Cell-type enrichment analysis web server, *et.al*).
- Implement sequence-based models for exploring biological insights (Finding sequence motifs, *et.al*)
- Mentor or train junior investigators in the Center for Precision Health.
- Others: collaborate with wet labs and clinicians to provide technical expertise to lead in the development of study design, sample or data collection, pipeline development, data analysis, results interpretation, manuscript writing, and grant proposal preparation.

DATABASES/TOOLS/WEBSERVERS

* Website pages and function codes were totally built/completed by myself (Ruifeng Hu).

1. *ImmuneApp: an AI-driven tool for HLA-I epitope prediction and interpretable clinical immunopeptidome analysis. https://bioinfo.uth.edu/iapp/
2. *DeepTR: Prediction and characterization of T cell response specificity by interpretable deep learning https://bioinfo.uth.edu/DeepTR
3. *WebCSEA: Web-based Cell-type Specific Enrichment Analysis of Genes. https://bioinfo.uth.edu/webcsea
4. *Dr.VAEN: Drug response prediction using Variational Autoencoder based Elastic Net models. https://bioinfo.uth.edu/drvaen .
5. *MitoX: exploring mitochondrial heteroplasmy and gene expression from single-cell sequencing assays. https://github.com/huruifeng/MitoX
6. *CSEA-DB: Cell-type-Specific Enrichment Analysis DataBase. https://bioinfo.uth.edu/CSEADB
7. *KinaseMD: Kinase mutations and drug responses. https://bioinfo.uth.edu/kmd
8. *DeepFun: A tissue and cell type-specific deep learning sequence-based model to decipher noncoding variant effects. https://bioinfo.uth.edu/deepfun
9. 6mA-Finder: Computational prediction of 6mA sites in the DNA sequences. https://bioinfo.uth.edu/6mA_Finder
10. *TSEA-DB: A trait-tissue association map for human complex traits and diseases. https://bioinfo.uth.edu/TSEADB
11. VISDB: A knowledgebase containing the most comprehensive DNA virus integration sites and also the integration sites for several typical RNA retrovirus. https://bioinfo.uth.edu/VISDB
12. CleftGeneDB: The cleft gene annotation database aiming to provide a resource or reference for the midfacial development and related disease studies for mouse and human. https://bioinfo.uth.edu/CleftGeneDB
13. *ANCO-GeneDB: annotations and comprehensive analysis of candidate genes for alcohol, nicotine, cocaine and opioid dependence. https://bioinfo.uth.edu/ancogenedb
14. *TarNet: an evidence-based database for natural medicine research. https://github.com/huruifeng/TarNet
15. *LSCplus: a fast solution for improving long read accuracy by short read alignment. https://github.com/huruifeng/LSCplus
16. *lncRNATargets: A platform for lncRNA target prediction based on nucleic acid thermodynamics. https://github.com/huruifeng/lncRNATarget_local

PUBLICATIONS

1. Zheng, Mengqiu, Shaofeng Lin, Kunqi Chen, **Ruifeng Hu**, Liming Wang, Zhongming Zhao, and Haodong Xu. MetaDegron: multimodal feature-integrated protein language model for predicting E3 ligase targeted degrons. *Briefings in Bioinformatics* 25, no. 6 (2024): bbae519.
2. Haodong Xu, **Ruifeng Hu**[#], Xianjun Dong, Zhongming Zhao. ImmuneApp: an AI-driven tool for HLA-I epitope prediction and interpretable clinical immunopeptidome analysis. *Nature Communication*. 15 (1), 8926
3. Haodong Xu**, Ruifeng Hu#,** Xianjun Dong, Shengbao Suo, Zhongming Zhao. Prediction and characterization of T cell response specificity by interpretable deep learning. *Science Advances*. (Minor revision, Co-first author)
4. **Ruifeng Hu**, Ruoxuan Wang, Jie Yuan, Zechuan Lin, Elizabeth Hutchins, Barry Landin, Clemens Scherzer, Xianjun Dong. Early diagnosis biomarker discovery and modeling of Parkinson’s disease prediction with multi-omics data: a cross-sectional study. *(In submission).*

5. Qingfu Zhu, **Ruifeng Hu$^{\#}$,** Xiaodan Dai, Luke Lee, Xianjun Dong, Fei Liu. Transcriptional dynamics of human iPSC-derived extracellular vesicles in dopamine neuron differentiation. *Nature Neuroscience.* (*In submission*, Co-first author)
6. Mallik, Saurav, Junichi Iwata, **Ruifeng Hu**, and Tapas Si. Deep learning for disease prediction in next-generation sequencing and biomedical imaging data. *Frontiers in Genetics* 14 (2023): 1260940.
7. Haodong Xu, **Ruifeng Hu$^{\#}$**, and Zhongming Zhao. DegronMD: Leveraging evolutionary and structural features for deciphering protein-targeted degradation, mutations, and drug response to degrons. *Molecular Biology and Evolution*, 40.12 (2023): msad253. (Co-first author).
8. Mo Liu , An Xu , **Ruifeng Hu**, Mo-Fan Huang , Yang Zhang , Ying Liu , Julian Gingold , Chian-Shiu Chien , Chih-Wei Hsu , Feng Xiong , Peilin Jia , Yi-Ping Yang , Danielle Bazer , Wenbo Li , Francesca Aguilo , Shih-Hwa Chiou , Nathan Boles , Mien-Chie Hung , Zhongming Zhao , Ruiying Zhao, Dung-Fang Lee. Rewired m6A epitranscriptomic networks link mutant p53 to neoplastic transformation. *Nature Communication.* 14 (1), 1694.
9. Jia, Peilin, **Ruifeng Hu$^{\#}$**, and Zhongming Zhao. Benchmark of embedding-based methods for accurate and transferable prediction of drug response. *Briefings in Bioinformatics*. 24 (3), bbad098(Co-first author).
10. Jia, Peilin, **Ruifeng Hu**, Fangfang Yan, Yulin Dai, and Zhongming Zhao. scGWAS: landscape of trait-cell type associations by integrating single-cell transcriptomics-wide and genome-wide association studies. *Genome Biology,* 2022(23): 220.
11. Yulin Dai$^{\#}$, **Ruifeng Hu$^{\#}$**, Peilin Jia, Zhongming Zhao. WebCSEA: Web-based Cell-type Specific Enrichment Analysis of Genes. *Nucleic acids research,* 2021, 50(W1), W782-W790 (Co-first author).
12. Jian Tu, Zijun Huo, Yao Yu, Dandan Zhu, **Ruifeng Hu**, An Xu, Ruoyu Wang, Haidan Luo, Julian A. Gingold, Jie Su, Mo-Fan Huang, Kuang-Lei Tsai, Ruoji Zhou, Hui-Ming Chen, Weiling He, Shu-Hsia Chen, Thomas R. Webb, Huiling Yang, Peilin Jia, Jason T. Yustein, Lisa L. Wang, Mien-Chie Hung, Zhongming Zhao, Ruiying Zhao, Chad D. Huff, Jingnan Shen, & Dung-Fang LeeHereditary retinoblastoma iPSC model reveals aberrant spliceosome function driving bone malignancies. *Proceedings of the National Academy of Sciences,* 2021,119 (16), e2117857119
13. Mendez, Emily F., Haichao Wei, **Ruifeng Hu**, Laura Stertz, Gabriel R. Fries, Xizi Wu, Katherine E. Najera et al. Angiogenic gene networks are dysregulated in opioid use disorder: evidence from multi-omics and imaging of postmortem human brain. *Molecular psychiatry,* 2021, 26(12): 7803-7812.
14. Andi Liu, Yulin Dai, Emily F Mendez, **Ruifeng Hu**, Gabriel R Fries, Katherine E Najera, Shan Jiang, Thomas D Meyer, Laura Stertz, Peilin Jia, Consuelo Walss-Bass, Zhongming Zhao. Genome-wide correlation of DNA methylation and gene expression in postmortem brain tissues of opioid use disorder patients. *International Journal of Neuropsychopharmacology*, 2021, 24 (11), 879-891.
15. Guangsheng Pei$^{\#}$, **Ruifeng Hu$^{\#}$**, Zhongming Zhao, Peilin Jia. DeepFun: a deep learning sequence-based model to decipher non-coding variant effect in a tissue-and cell type-specific manner. *Nucleic Acids Research*, 2021. 49 (W1), W131-W139. (Co-first author)
16. Lucca Pizzato Tondo, Thiago Wendt Viola, Gabriel R Fries, Bruno Kluwe-Schiavon, Leonardo Mello Rothmann, Renata Cupertino, Pedro Ferreira, Alexandre Rosa Franco, Scott D Lane, Laura Stertz, Zhongming Zhao, **Ruifeng Hu**, Thomas Meyer, Joy M Schmitz, Consuelo Walss-Bass, Rodrigo Grassi-Oliveira. White matter deficits in cocaine use disorder: convergent evidence from in vivo diffusion tensor imaging and ex vivo proteomic analysis. *Translational Psychiatry*, 2021.1-10

17. Peilin Jia[#], **Ruifeng Hu**[#], Guangsheng Pei, Yulin Dai, Yinying Wang, Zhongming Zhao. Deep generative neural network for accurate drug response imputation. *Nature Communication,* 2021. 12 (1), 1-16 (<u>Co-first author</u>)
18. Hao-Dong Xu, Fangfang Yan, **Ruifeng Hu**, Akiko Suzuki, Chihiro Iwaya, Peilin Jia, Junichi Iwata*, Zhongming Zhao*. CleftGeneDB. a manually curated cleft-related gene resource. *Science Bulletin,* 2021. 66 (23), 2340-2342
19. **Ruifeng Hu**[#], Haodong Xu[#], Peilin Jia, Zhongming Zhao. KinaseMD: Kinase mutations and drug responses in pan-cancer. *Nucleic Acids Research,* gkaa945.
20. Yulin Dai[#], **Ruifeng Hu**[#], Peilin Jia, Zhongming Zhao. CSEA-DB: an omnibus for human complex trait and cell type associations, *Nucleic Acids Research,* gkaa1064 (<u>Co-first author</u>)
21. Guangsheng Pei[#], **Ruifeng Hu[#],** Yulin Dai, Astrid M Manuel, Zhongming Zhao, Peilin Jia. Predicting regulatory variants using a dense epigenomic mapped CNN model elucidated the molecular basis of trait-tissue associations. *Nucleic Acids Research,* gkaa1137(<u>Co-first author</u>)
22. Guangsheng Pei, **Ruifeng Hu**, Yulin Dai, Zhongming Zhao, Peilin Jia. Decoding whole-genome mutational signatures in 37 human pan-cancers by denoising sparse autoencoder neural network. *Oncogene*. 2020, 39, 5031–5041. (Responsible for VAE Model construction).
23. Hao-Dong Xu, **Ruifeng Hu**, Peilin Jia, Zhongming Zhao. 6mA-Finder: a novel method for identifying DNA N6-methyladenine sites in genome. *Bioinformatics,* 2020, 36 (10), 3257-3259.
24. Yulin Dai, **Ruifeng Hu**, Zhongming Zhao, Peilin Jia. Diverse types of genomic evidence converge on alcohol use disorder risk genes. *Journal of Medical Genetics*. 2020 Mar 13.
25. Peilin Jia, Yulin Dai, **Ruifeng Hu**, Guangsheng Pei, Astrid Marilyn Manuel, and Zhongming Zhao. TSEA-DB: a trait–tissue association map for human complex traits and diseases. *Nucleic Acids Researh*. 2020, 48(D1):D1022-D1030.
26. Deyou Tang, Bingrui Li, Tianyi Xu, **Ruifeng Hu**, Daqiang Tan, Xiaofeng Song, Peilin Jia, and Zhongming Zhao. VISDB: a manually curated database of viral integration sites in the human genome. *Nucleic Acids Research*. 2020, 48(D1):D633-D641.
27. **Ruifeng Hu**, Guangsheng Pei, Peilin Jia, and Zhongming Zhao. Decoding regulatory structures and features from epigenomics profiles: a Roadmap-ENCODE Variational Auto-Encoder (RE-VAE) model. *Methods*. 2021, 189: 44-53.
28. **Ruifeng Hu**, Yulin Dai, Peilin Jia, and Zhongming Zhao. ANCO-GeneDB: annotations and comprehensive analysis of candidate genes for alcohol, nicotine, cocaine and opioid dependence. *Database* (Oxford). 2018, bay121.
29. Ke Yang, Yun Luo, Shan Lu, **Ruifeng Hu**, Yuyang Du, Ping Liao, Guibo Sun, and Xiaobo Sun. Salvianolic acid B and ginsenoside Re synergistically protect against Ox-LDL-induced endothelial apoptosis through the antioxidative and antiinflammatory mechanisms. *Frontiers in Pharmacology*. 2018, 9:662.
30. **Ruifeng Hu**, and Xiaobo Sun. Design of new traditional Chinese medicine herbal formulae for treatment of type 2 diabetes mellitus based on network pharmacology. *Chinese Journal of Natural Medicines*. 2017, 15(6):436-441.
31. Dan Yang, Junjie Shao, **Ruifeng Hu**, Haimei Chen, Ping Xie, and Chang Liu. Angiotensin II promotes the anticoagulant effects of rivaroxaban via angiotensin type 2 receptor signaling in mice. *Scientific Reports*. 2017, 7(1):369.
32. **Ruifeng Hu**, Guibo Sun, and Xiaobo Sun. LSCplus: a fast solution for improving long read accuracy by short read alignment. *BMC Bioinformatics*. 2016, 17(1):451.

33. **Ruifeng Hu**, and Xiaobo Sun. lncRNATargets: A platform for lncRNA target prediction based on nucleic acid thermodynamics. *Journal of Bioinformatics and Computational Biology*. 2016, 14(4):1650016.
34. **Ruifeng Hu**, Guomin Ren, Guibo Sun, and Xiaobo Sun. TarNet: an evidence-based database for natural medicine research. *PLoS One*. 2016,11(6):e0157222.
35. Leilei Zhang, Jing Jin, Lijing Zhang, **Ruifeng Hu**, Li Gao, Xiaowei Huo, Dongyu Liu et al. Quantitative analysis of differential protein expression in cervical carcinoma cells after zeylenone treatment by stable isotope labeling with amino acids in cell culture. *Journal of Proteomics*. 2015, 126:279-87.
36. Qidi Ai, Guibo Sun, Yun Luo, Xi Dong, **Ruifeng Hu**, Xiangbao Meng, and Xiaobo Sun. Ginsenoside Rb1 prevents hypoxia-reoxygenation-induced apoptosis in H9c2 cardiomyocytes via an estrogen receptor-dependent crosstalk among the Akt, JNK, and ERK 1/2 pathways using a label-free quantitative proteomics analysis. *RSC Advance*. 2015, 5:26346-26363.
37. **Ruifeng Hu**, Xiaoyan Xing, Guibo Sun and Xiaobo Sun. The prospect of using bioinformatics technology in the field of biological medicine in the era of big data. *Acta pharmaceutica Sinica*. 2014, 49(11):1512-9.
38. **Ruifeng Hu**, Xu Zeng, Weiwei Gao, Qian Wang, and Zhihua Liu. HRAS: a webserver for early warning of human health risk brought by aflatoxin. *Molecular Biology Reports*. 2013, 40(2):1181-7.

PRESENTATIONS/CONFERENCES/ABSTRACTS

1. **Ruifeng Hu**, Ruoxuan Wang, Jie Yuan, Zechuan Lin, Elizabeth Hutchins, Barry Landin, Clemens Scherzer, Xianjun Dong. Early diagnosis biomarker discovery and modeling of Parkinson’s disease prediction with multi-omics data: a cross-sectional study. BWH Neuroscience Day, 02-07-2023.
2. Yulin Dai[#], **Ruifeng Hu[#],** Peilin Jia, Zhongming Zhao WebCSEA: Web-based Cell-type Specific Enrichment Analysis of Genes. The American Society of Human Genetics, Los Angeles, CA, USA, October 25-29, 2022. [selected for plenary presentation]
3. Qingfu Zhu, **Ruifeng Hu[#],** Xiaodan Dai, Luke Lee, Xianjun Dong, Fei Liu. Transcriptional dynamics of human iPSC-derived extracellular vesicles in dopamine neuron differentiation. Ann Romney Center for Neurologic Diseases-ADPD SEMINAR SERIES 2022, 12-13-2022, Departmant of Neuroscience, Brigham and women’s hospital.
4. Emily Mendez, Haichao Wei, **Ruifeng Hu**, Laura Stertz, Gabriel R Fries, Xizi Wu, Katherine Najera, Karla Moriel, Thomas Meyer, Sudhakar Selvaraj, Antonio Teixeira, Zhongming Zhao, Jiaqian Wu, Cristian Coarfa, Preethi Gunaratne, Consuelo Walss-Bass .Cell-Type Specific Effects of Opioid Exposure in Human Brain. *Neuropsychopharmacology* 46 (SUPPL 1), 444-444
5. Emily Mendez, Laura Stertz, Gabriel Fries, **Ruifeng Hu**, Thomas Meyer, Zhongming Zhao, Consuelo Walss-Bass. Molecular Signatures of Cocaine Neurotoxicity in Human Brain Models. *Journal of Clinical and Translational Science*, 5 (s1), 115-115. 2021
6. Emily Frances Mendez, Laura Stertz, Gabriel Fries, **Ruifeng Hu**, Thomas Meyer, Zhongming Zhao, Consuelo Walss-Bass. Molecular Signatures of Cocaine Toxicity in Postmortem Human Brain and Neurons. *Journal of Clinical and Translational Science,* 4 (s1), 140-140. 2021
7. Rodrigo Grassi-Oliveira, Lucca Pizzato Tondo, Thiago W Viola, Gabriel Fries, Bruno Kluwe-Schiavon, Leonardo Mello Rothmann, Renata Cupertino, Pedro Ferreira, Alexandre Rosa

Franco, Scott D Lane, Laura Sterzt, Zhongming Zhao, **Ruifeng Hu,** Thomas Meyer, Joy M Schmitz, Consuelo Walss-Bass. Diffusion Tensor Imaging of Cocaine Users and Proteomic Analysis of Postmortem Brains of Subjects Reporting Cocaine Addiction Suggest White Matter Impairment in BA9 Region of Prefrontal Cortex. *Biological Psychiatry*, 2021

8. Emily Mendez, Haichao Wei, Laura Stertz, Gabriel Fries, **Ruifeng Hu**, Xizi Wu, Katherine Najera, Karla Moriel, Thomas Meyer, Zhongming Zhao, Jiaqian Wu, Consuelo Walss-Bass. Differential Regulation of Angiogenic Gene Networks in Postmortem Brains of Opioid Use Disorder Subjects. *Biological Psychiatry*, 2021
9. Zhongming Zhao, Peilin Jia, Yulin Dai, **Ruifeng Hu**, Guangsheng Pei, Astrid M Manuel (2020). A trait-tissue association landscape for human complex traits and diseases. AMIA 2020 Informatics Summit, Houston, TX, March 24, 2020 [selected for podium presentation]
10. **Ruifeng Hu**, Guangsheng Pei, Peilin Jia, and Zhongming Zhao (2019). Decoding regulatory structures and features from epigenomics profiles: a Roadmap-ENCODE Variational Auto-Encoder (RE-VAE) model. Presented at the 68th Annual Meeting of The American Society of Human Genetics, Houston, TX, USA, October 15-19, 2019, Abstract # 1515W [Reviewers' Choice Abstracts: The top 10% of poster abstracts]
11. Deyou Tang, Bingrui Li, Tianyi Xu, **Ruifeng Hu**, Zhongming Zhao (2019). VISDB: A comprehensive database for human disease-related virus integration sites. Presented at the 68th Annual Meeting of The American Society of Human Genetics, Houston, TX, USA, October 15-19, 2019, Abstract # 1567T
12. Peilin Jia P, Guangsheng Pei, **Ruifeng Hu**, Zhongming Zhao (2019). A variational autoencoder model for accurate imputation of drug response. Presented at the 68th Annual Meeting of The American Society of Human Genetics, Houston, TX, USA, October 15-19, 2019, Abstract # 834W
13. Consuelo Walss-Bass, **Ruifeng Hu**, Laura Stertz, Gabriel Fries, William Russell, Nicholas Crist, Glenn Sandberg, Zhongming Zhao, and Thomas Meyer. (2019) Proteomics of addiction: Postmortem brain analyses of cocaine and opioid disorder. Presented at the 68th Annual Meeting of The American Society of Human Genetics, Houston, TX, USA, October 15-19, 2019, Abstract # 1824W [Reviewers' Choice Abstracts: The top 10% of poster abstracts]
14. Consuelo Walss-Bass, **Ruifeng Hu**, Laura Stertz, Gabriel Fries, William Russell, Nicholas Crist, Glenn Sandberg, Zhongming Zhao, and Thomas Meyer (2019). Proteomics of addiction: Postmortem brain analyses of cocaine and opioid disorder. Presented at the XXVIIth World Congress of Psychiatric Genetics (WCPG), Los Angeles, CA, USA, October 26–31, 2019.
15. Consuelo Walss-Bass, Laura Stertz, Gabriel R Fries, **Ruifeng Hu**, William Russell, Glenn Sandberg, Zhongming Zhao, Rodrigo Grassi-Oliveira, Thomas Meyer (2019). Proteomics Analysis Suggests Demyelination as a Mechanism of Cocaine-Induced Neurotoxicity: Postmortem Brain Analyses of Cocaine Use Disorder. Neuropsychopharmacology 44 (Suppl 1), 511-512
16. **Ruifeng Hu,** Peilin Jia, Zhongming Zhao (2018). ANCO Genes: Annotations and comprehensive analysis of candidate genes for alcohol, nicotine, cocaine, and opiate (ANCO) dependence. Presented at the 67th Annual Meeting of The American Society of Human Genetics, San Deigo, CA, USA, October 16-20, 2018, Abstract #1397F.
17. **Ruifeng Hu,** Guomin Ren, Guibo Sun, Xiaobo Sun. Research on Chinese herbal compounds based on network pharmacology -- a case study of Chinese herbal compounds on the treatment

of type II diabetes mellitus. Proceedings of Traditional Chinese Medicine Informatics Meeting in China (2014), page 129-134. China Information of Traditional Chinese Medicine Congress, Nov 22-23 2014, Beijing, China. [Second Prize of Excellent Paper]

JOURNAL REVIEWER

Nucleic Acids Research, Briefings in Bioinformatics, Bioinformatics, Biomedicine, Brain Science, Computers in Biology and Medicine, Journal of Biology, Journal of Biomedical Informatics, Database, BMC Genomics, BMC Supplements, Experimental Biology and Medicine, Frontiers in Genetics, Healthcare, PLoS ONE, Scientific Reports. Journal of Personalized Medicine, International Journal of Environmental Research and Public Health, Viruses, Mathematics, Cancers, International Journal of Molecular Sciences, Entropy, Journal of Clinical Medicine.

CONFERENCE REVIEWER

International Conference on Intelligent Biology and Medicine 2020, International Conference on Intelligent Biology and Medicine 2022, The 12th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB), American Medical Informatics Association (AMIA) 2021 Virtual Informatics Summit, AMIA 2022 Virtual Informatics Summit. ASHG 2019 Essay Contest. Computational Biology and Bioinformatics,*et.al.*

CONFERENCE COMMITTEE MEMBER

The International Society for Computational Biology-ISMB/ECCB 2023, International Conference on Intelligent Biology and Medicine 2022

JOURNAL EDITOR

Frontiers in Genetics - Computational Genomics; Frontiers in Bioinformatics – Integrative Bioinformatics; Genomics; Biology;

AWARDS & SCHOLARSHIPS

2016.10	National Scholarship for Graduate Students, from Chinese Ministry of Education and Ministry of Finance (CAMS&PUMC) (the highest scholarship for graduate students)
2014 & 2015	First Prize Scholarship for Academic Excellence (CAMS&PUMC)
2010.10, 2011.10	National Encouragement scholarship
2009.10	National Scholarship for Undergraduate Students, from Chinese Ministry of Education and Ministry of Finance (NJFU) (the highest scholarship for undergraduate students)
2010, 2011	The First Prize Scholarship of Nanjing Forestry University

SELECTED HONORS

2014, 2015, 20016	Outstanding Graduate Students of PUMC
2012.6	Outstanding Undergraduates of NJFU
2011.10	Excellent Student Cadre, Advanced Class in Jiangsu Province, China
2010	Second Prize, Mathematical Contest in Modeling (Jiangsu, China); Second Prize, MCM/ICM (Mathematical Contest In Modeling & Interdisciplinary Contest In Modeling)
2010, 2011	Second Prize, National Software Talent Contest (Finals), China
2009, 2010, 2011	Merit Student of Nanjing Forestry University, China (For three consecutive years)

OTHERS

1. I developed SoilClassfy v2 which is available in App Store. This App is developed with Prof. Lin Li from Tennessee State University. Geotechnical engineer (civil engineer) can use this app to classify the soil based on two soil classification systems AASHTO and USCS.

2. I developed https://CaseGreen.info which is a website to crawl the USCIS case status, visualize the case status data, and make data-driven analysis to result in a reliable prediction of the status change date. The website is running on AWS automatically, and there are ~50k page views monthly.