

CURRICULUM VITAE

Ruifeng Hu, Ph.D. (Permanent resident)

Current institute: Senior Research Associate, Precision Neurology Program, Brigham and Women's Hospital, Harvard Medical School.

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GitHub: <https://github.com/huruifeng>

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

INTERESTS & SKILLS

My interests are to develop methods to unveil the hidden biological circuitries underlying the biomedical data using advanced models with a focus on precision medicine, drug repurposing, immunotherapy, *et.al.* including (i) Decoding genomic sequence to decipher connections between sequence, functions, and phenotypes, especially leveraging sequence data and deep learning models (*e.g.*: Predict eQTLs, mutations effects); (ii) Using AI and machine learning to analyze large amounts of data and predict the effectiveness and safety of drugs (*e.g.*: Impute drug responses); (iii) Investigate the strategies to stimulate the immune system to fight cancer cells and other diseases (*e.g.*: Modeling HLA epitopes, HLA-peptide binding prediction, T-cell response); (iv) Developing data integration techniques, constructing databases, and creating web server platforms to facilitate access to research findings; (v) Multi-omics data analysis and a variety of bioinformatics statistical modeling. Ultimately, my goal is to contribute to the development of new drugs that can improve patient outcomes and alleviate human suffering.

- Proficient in analyzing multi-omics data (e.g. bulk/single-cell RNASeq, proteomics, or genetics data)
- Proficient in Python, C/C++, Go, R, and Linux shell language and large-scale data calculation (Rich experience with Unix/Linux and HPC environments, rich experience with Nextflow).
- Proficient in various algorithms of deep learning, including CNN, RNN, DNN, and Autoencoder, and using them to develop prediction algorithms. And well understanding and practices of 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*
- Proficient in the construction of bioinformatics web server platforms and databases (HTML, Python/Django/Web2Py, PHP, JS, CSS).
- Proficient in various bioinformatics statistical modeling and data analysis software.
- Rich experiences in various types of NGS data such as RNA-seq, ChIP-seq, ATAC-seq, et al.
- Rich experiences in modeling HLA epitopes, HLA-peptide binding prediction, Immunopeptidomics interpretation, and T-cell response prediction.
- Familiar with molecular biology techniques and experiments.

EXPERIENCE

Brigham and Women's Hospital, Harvard Medical School, Boston, MA, USA.

2021.3 – current

Senior Research Associate

- Discover and replicate 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 PD status utilizing the multi-omics data (transcriptomics, genetics, and clinical data)
- Investigation of advanced machine learning/deep learning models (Autoencoder, DNN, RNN, LSTM) for PD status prediction and UPDRS regression.
- Analysis of RNAseq data obtained from a time-series experimental design.
- Build scRNAseq data analysis pipeline using Nextflow.
- Others: running jobs on HPC with LSF, Slurm; Linux server management.

School of Biomedical Informatics, UT Health Science Center, Houston, TX, USA.

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

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

PUBLICATIONS

Manuscript in review/revision

1. **Ruifeng Hu**, Zhongming Zhao*. MitoX: exploring mitochondrial heteroplasmy and gene expression from single-cell sequencing assays. *Bioinformatics*. (Under review).
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 Computational Science*. (Minor revision, Co-first author)
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. *Nature Aging*. (Under review).
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*. (Under review, Co-first author)

Published/Accepted

1. 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*. (Accepted)

2. Jia, Peilin, **Ruifeng Hu**[#], and Zhongming Zhao. Benchmark of embedding-based methods for accurate and transferable prediction of drug response. *Briefings in Bioinformatics*. (Accepted, Co-first author).
3. 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.
4. 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).
5. 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 Lee Hereditary retinoblastoma iPSC model reveals aberrant spliceosome function driving bone malignancies. *Proceedings of the National Academy of Sciences*, 2021, 119 (16), e2117857119
6. 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.
7. 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.
8. 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)
9. 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
10. 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 (Co-first author)
11. 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
12. **Ruifeng Hu**[#], Haodong Xu[#], Peilin Jia, Zhongming Zhao. KinaseMD: Kinase mutations and drug responses in pan-cancer. *Nucleic Acids Research*, gkaa945.
13. Yulin Dai[#], **Ruifeng Hu**[#], Peilin Jia, Zhongming Zhao. CSEA-DB: an omnibus for human complex trait and cell type associations, *Nucleic Acids Research*, gkaa1064 (Co-first author)
14. 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(Co-first author)

15. 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).
16. 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.
17. 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.
18. 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.
19. 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.
20. **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.
21. **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.
22. 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.
23. **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.
24. 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.
25. **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.
26. **Ruifeng Hu**, and Xiaobo Sun. IncRNATargets: A platform for lncRNA target prediction based on nucleic acid thermodynamics. *Journal of Bioinformatics and Computational Biology*. 2016, 14(4):1650016.
27. **Ruifeng Hu**, Guomin Ren, Guibo Sun, and Xiaobo Sun. TarNet: an evidence-based database for natural medicine research. *PLoS One*. 2016,11(6):e0157222.
28. 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.
29. 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.

30. **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.
31. **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. [Awarded for excellent research work]
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, Department 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

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| 2014, 2015, 2016 | 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.