Zijun Zhang

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https://zj-zhang.github.io/

Education

2014-2019

Ph.D. in Bioinformatics; UCLA (Los Angeles, USA)

(expected)

2010-2014 B.Sc. in Bioinformatics; Zhejiang University (Hangzhou, China)

Publications

- **Zhang, Zijun**; Park, Eddie; Lin, Lan; Xing, Yi; A panoramic view of RNA modifications: exploring new frontiers (Genome Biology, 2018)
- Park, Eddie; Pan, Zhicheng; Zhang, Zijun; Lin, Lan; Xing, Yi; The expanding landscape of alternative splicing variation in human populations (American Journal of Human Genetics, 2018)
- Zhang, Zijun; Xing, Yi; CLIP-seq analysis of multi-mapped reads discovers novel functional RNA regulatory sites in the human transcriptome (Nucleic acids research, 2017)
- Liu, Lili; **Zhang, Zijun**; Sheng, Taotao; Chen, Ming; DEF: an automated dead-end filling approach based on quasi-endosymbiosis (Bioinformatics, 2017)
- Liu, Lili; Mei, Qian; Yu, Zhenning; Sun, Tianhao; Zhang, Zijun; Chen, Ming; An integrative bioinformatics framework for genome-scale multiple level network reconstruction of rice (Journal of integrative bioinformatics, 2013)
- Liu, Lili; **Zhang, Zijun**; Mei, Qian; Chen, Ming; PSI: a comprehensive and integrative approach for accurate plant subcellular localization prediction (PLoS One, 2013)

Projects

CLAM CLIP-seq Analysis of Multi-mapped reads

Open-source python package for calling peaks in CLIP/RIP-seq data.

DARTS Deep learning augmented Analysis of RNA-seq Transcript Splicing

Bayesian inference utilizing deep-learning prediction informative prior

Skills

- Programming languages: Python, R, scikit, Keras, Tensorflow, Theano, Matlab, AWS, HTML,
 CSS, PHP, Jekyll, SQL, C/C++, Unix/SGE, Git
- Statistics: Regularized regression, Bayesian statistics and Bayesian inference, Causal Inference, Hierarchical modeling, MCMC, multivariate analysis
- Machine/Deep learning: Supervised(CNN, LSTM, adaboost/xgboost, SVM, random forest), Unsupervised(clustering, autoencoder, factor analysis), Reinforcement(controller network)