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Work Experience

Associate Professor, Bioinformatics group lead, Single-Cell Research Center, 2011/05-present

Qingdao Institute of Bioenergy and Bioprocess Technology, Chinese Academy of Sciences (QIBEBT-CAS)

Principal Investigator, NVIDIA CUDA Research Center at QIBEBT-CAS, 2013/10-present

Visiting Scholar, University of California, San Diego, 2016/08-2016/11

Senior Research Associate, City University of Hong Kong, 2014/06-2014/07

Visiting Assistant Professor, Ruhr-University Bochum, Germany, 2013/06-2013/07

Education

Ph.D. Candidate in Micro Biology - University of Chinese Academy of Sciences, 2015- present

M.S. in Computer Science - State University of New York at Stony Brook, 2009 - 2011

B.E. in Computer Science and Technology -Wuhan University, 2005- 2009

Publications

1. Zhou[1], **Su[1]**, et al. RNA-QC-chain: comprehensive and fast quality control for RNA-Seq data. *BMC Genomics* 2018.

2. Jing, **Su***, et al. Parallel-META 3: Comprehensive taxonomical and functional analysis platform for efficient comparison of microbial communities. *Scientific Reports* 2017.

3. **Su**, et al. Application of Meta-Mesh on the analysis of microbial communities from human associated-habitats. *Quantitative Biology* 2015.

4. **Su**, et al. GPU-Meta-Storms: Computing the structure similarities among massive amount of microbial community samples using GPU. *Bioinformatics* 2014.

5. **Su**, et al. Rapid comparison and correlation analysis among massive number of microbial community samples based on MDV data model, *Scientific Reports* 2014.

6. **Su**, et al. Parallel-META 2.0: Enhanced Metagenomic Data Analysis with Functional Annotation, High Performance Computing and Advanced Visualization. *PLoS One* 2014.

7. Zhou[1], **Su[1]**, et al. Assessment of the quality control approaches for metagenomic data, *Scientific Reports* 2014.

8. Cheng[1], **Su[1]**, et al. Biological ingredient analysis of traditional Chinese medicine preparation based on high-throughput sequencing: the story for Liuwei Dihuang Wan. *Scientific Reports* 2014.

9. **Su**, et al. Meta-Storms: Efficient Search for Similar Microbial Communities Based on a Novel Indexing Scheme and Similarity Score for Metagenomic Data. *Bioinformatics* 2012.

10. **X. Su**, et al. Parallel-META: efficient metagenomic data analysis based on high-performance computation. *BMC Systems Biology* 2012.

11. **X. Su**, et al. An Open-source Collaboration Environment for Metagenomics Research. *IEEE International Conference on E-Science.* 2011.

12. P. Yang, **X. Su**, et al. Microbial community pattern detection in human body habitats via ensemble clustering framework, *BMC Systems Biology* 2013.

13. Q. Zhou, **X. Su**, et al. QC-Chain: Fast and Holistic Quality Control Method for Next-Generation Sequencing Data, *PLoS ONE* 2013.

14. B. Song, **X. Su** and K. Ning. MetaSee: An interactive and extendable visualization toolbox for metagenomic sample analysis and comparison, *PLoS One* 2012.