Jiajian Zhou

Bioinformatics Analyst
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Academic career:

2012-now: Research Assistant, Dept. of Chemical Pathology, the Chinese University of HongKong

2010-2012: Research Fellow, Beijing Genomics Institute Shenzhen.

2011-now: Master of Science, CUHK-BGI Innovation Institute of Trans-omics.

2008-2010: Research Fellow, Plant Physiology Lab, South China Agricultural University.

2006-2010: Bachelor of Science in Biotechnology, College of Life Science, South China Agricultural University(SCAU).

Participating/participated Research Group:

2012-now   Department of Chemical Pathology, CUHK
My research interests focus on long no-coding RNA regulation and using NGS tools to get insight into the mechanism of C2C12 myogensis. Based on Next-generation sequencing dataset (RNA-seq, Chip-seq etc.), we try to construct transcriptional regulatory network to interpret the regulation and control mechanism of C2C12 differentiation.

2011-2012   Microbial Research Group, BGI shenzhen
Design NGS(Next-generation sequencing) solution for pathogen project, write pipeline to deal with NGS data and analysis some biological problem cooperate with customers. Base on my biological background, I can find many differences between pathogenic and nonpathogenic bacteria/fungi by compare their genome. We can provide some clues contribute to the pathogenicity base on bioinformatics analysis.

2010-2011   Social Evolution Group, BGI shenzhen
Participate in the Acromyrmex echinatior genome project and Termite genome project. At the begining, I focus on gene prediction and function annotation, while I learn programing and use many tools to annotation a denovo genome. For later analysis, I do some comparative genomics analysis, we compared the sex determination related genes, Metabolism related genes and Odorant Binding proteins among several species. Some differences are responsible to its social lifestyle. After that, I take part on Cotton project, focus on Cotton genome expansion due to LTR insertion recently.

2008-2009   Plant Physiology Lab, College of Life Science, SCAU
Following my supervisor, I join a team to develop a method to delay Litchi go browning. I purify the key enzyme by Chromatography and SDS-PAGE gel. To get some sequence information about this enzyme, we do a mass spectrum analysis. Base on several fragment, I design primers to amplify it's gene from Litchi cDNA libary. Then, we design probes to perform Northern Blot to test this gene express level in different stage of browning. We found that this gene express leve is high in the early stage of browning.

Skills

Use perl/python to deal with Next-genetation sequencing data;
Master bioinfomatics tools to deal with NGS data;
Good communication skills, and willingness to work with a team;
Use MP/MPI and CUDA to perform pararell computation.

Interests

I like sport (play pingpong, hiking and basketball), cooking and reading science fiction.

Publications

Sanne Nygarrd, Guojie Zhang,...,Cai Li, Haofu Hu, Jiajian Zhou, Lu Ji, Feng Qiu, Hailin Pan,Jun Wang,et al. [The genome of the leaf-cutting ant Acromyrmex echinatior suggests key adaptations to advanced social life and fungus farming.](#) Genome Research. Epub 2011 June 30