JINGLIE ZHOU

PhD, Computational Biology Postdoc Fellow,

DOE Joint Genome Institute, Walnut Creek, CA (Berkeley Lab)

* Do not need company support for visa or work permission

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SUMMARY

I am a Postdoc Fellow with background of both analysis of huge DNA data and experiment experience. Strong research background on metagenomic study. Years of experiences in different sequencing technologies (e.g. 454, Illumina and PacBio) and analysis of metagenomic data including but not limited to assemblies, binning, annotation and phylogenies. Creative, highly self-motivated and multidisciplinary researcher, fast learner, team player with excellent communication skills. Seeking the opportunity to work as bioinformatician/data scientist with a forward-looking group.

SKILLS

Programming & Data analysis

Python (Pandas, Numpy, networkx, SciPy, scikit-learn) and R (DEseq2, edgeR)

Data Visualization   **Metagenomic Web-based Tools**

Matplotlib, Seaborn and ggplot   ggKbase, Kbase and JGI Genome Portal

Molecular biology techniques

Cross-flow ultrafiltration, Bioanalyzer Automated Electrophoresis and PCR, etc

PROFESSIONAL EXPERIENCES

Led study of microbial diversity and carbon cycling in South bay salt ponds. Itag and shotgun data analysis of microbes from 38 samples including phylogenies, abundance normalization (DEseq2), correlation, occurrence network and PCoA/CCA/NMDS (Dissimilarity: Bray–Curtis/unifrac), assembly, annotation, binning, visualization, importance selection using Lasso and LDA.

Led discovery of virophage genomes from public IMG metagenomes. *In silicons* creening genomes based on construction of hmm models of the marker gene, followed by annotation, SNP detection, prediction of hosts based on occurrence and visualization.

EDUCATION AND EXPERIENCE

2019.1 – 2019.4   Data Science Immersive, Galvanize

2016.7 – present   Computational biology postdoc fellow, Joint Genome Institute, Berkeley lab

2012.8 – 2016.7   Ph.D in Microbiology, Auburn University

PUBLICATIONS

Zhou, J., Sun, D., Childers, A., McDermott, T. R., Wang, Y., & Liles, M. R. (2015). Three novel virophage genomes discovered from Yellowstone Lake metagenomes. **Journal of virology**, 89(2), 1278-1285

Zhou, J., Zhang, W., Yan, S., Xiao, J., Zhang, Y., Li, B., ... & Wang, Y. (2013). Diversity of virophages in metagenomic data sets. **Journal of virology**, 87(8), 4225-4236. ***Spotlight paper. F1000Prime Recommended***