Shaopeng Liu

Ph.D. candidate
Bioinformatics

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🛈 State College, PA, 16803

🌐 PDF: Curriculum vitae

Keywords ——————

1. Bioinformatician
2. Genomic data scientist
3. Metagenomics
4. Biomedical knowledge graphs

Skills ——————

Python

Shell

Genomics & NGS

Git

Statistics

Algorithm

Docker & Singularity

Markdown & YAML & HTML

SQL

Summary

Passionate bioinformatician with 5+ years experience coping with genomic datasets and computational tasks. Developed comprehensive pipelines for bioinformatic workflow, and implemented novel algorithms for sketching-based data analysis. Seeking to leverage efficient algorithms, multi-omic data, artificial intelligence, and biomedical knowledge graphs to address health-related issues.

Education

2019-2024	Ph.D. in Bioinformatics & Genomics	Pennsylvania State University
2016-2017	M.Sc. in Biostatistics	Washington University in St. Louis
2010-2014	B.Sc. in Biology	Wuhan University

Experience

1. Bioinformatic intern (2022.5-8, Gilead Sciences)

- explored, implemented and benchmarked alignment-based and k-mer-based methods for HBV genotyping.

2. Doctoral researcher in computational biology (2020-2024, PSU)

- proved, implemented and benchmarked a truncation-based containment MinHash algorithm CMash, which can efficiently estimate multi-resolution Jaccard and containment indices, in metagenomic analysis;
- worked in the ARAX team that aims at providing a graph-based reasoning tool to explore biomedical questions;
- developed novel methods and comprehensive pipelines to explore the "microbial dark matter".

3. Bioinformatician (2017-2019, WUSTL)

- collaborated with varioius groups and performed bioinformatic analysis on genomic and epigenomic datasets, including ChIP-seq, RNA-seq, WGBS, ATAC-seq, and single-cell RNA;
- worked in the Data Coordination Center (DCC) of TaRGET II Consortium, streamlined and setup the routine pipelines for RNA-seq, ChIP-seq, WGBS, and ATAC-seq data; and processed part of data with preliminary quality analysis;
- developed AIAP, an advanced ATAC-seq analysis pipeline for comprehensive analysis of ATAC-seq dataset; and also implemented the pipeline into Docker and Singularity

Publication

2022	ARAX: a graph-based modular reasoning tool for translational biomedicine. *bioRxiv*
2022	*CMash: fast, multi-resolution estimation of k-mer-based Jaccard and containment indices. *Bioinformatics*
2021	*AIAP: A Quality Control and Integrative Analysis Package to Improve ATAC-seq Data Analysis. *Genomics, Proteomics & Bioinformatics*
2021	Deconstructing Stepwise Fate Conversion of Human Fibroblasts to Neurons by MicroRNAs. *CELL STEM CELL*
2020	Comparison of differential accessibility analysis strategies for ATAC-seq data. *Scientific reports*

*: first author

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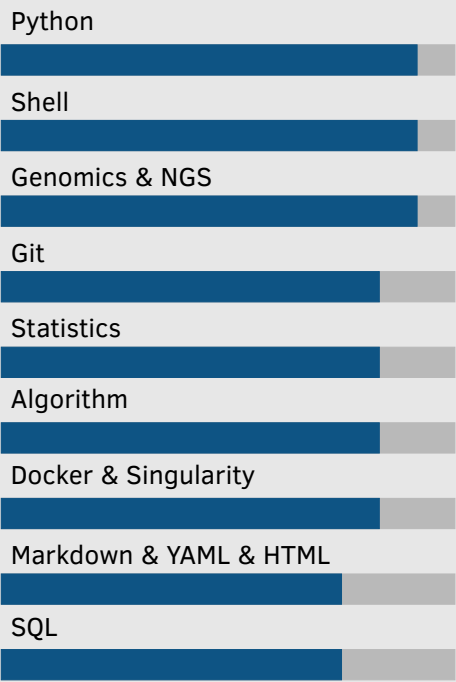✉ sml6467@psu.edu

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2019	Conditional Activation of NF-κB Inducing Kinase (NIK) in the Osteo-lineage Enhances Both Basal and Loading-Induced Bone Formation. *Journal of Bone and Mineral Research*
2018	The role of Twist1 in mutant huntingtin-induced transcriptional alterations and neurotoxicity. *Journal of Biological Chemistry*
2017	Regulatory networks specifying cortical interneurons from human embryonic stem cells reveal roles for CHD2 in interneuron development. *Proceedings of the National Academy of Sciences*
2014	Multistage Regulator Based on Tandem Promoters and CRISPR/Cas. *ACS Synthetic Biology*

Awards

2019-2021	The Graham Endowed Fellowship	Pennsylvania State University
2019	The J. Lloyd Huck Graduate Fellowship	Pennsylvania State University
2019	The Braddock Scholarship	Pennsylvania State University
2016	WU Scholarship and Grants	Washington University in St. Louis
2013	Golden medal	International Genetically Engineered Machine (IGEM)
2010-2012	College Scholarship	Wuhan University