Jiyang Jiang, Ph.D.

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SUMMARY

Versatile Data & Bioinformatics Scientist with dual expertise in advanced analytics and multi-omics data interpretation. Specializing in applying machine learning and deep learning approaches to complex biomedical datasets across multiple modalities in clinical settings. Combines strong computational skills with solid domain knowledge in oncology, immunology, and microbiology to extract meaningful insights from high-dimensional biological data.

Github: https://github.com/jjyjoy1?tab=repositories

CORE STRENGTHS

- **Advanced Machine Learning & Deep Learning Applications**: Implemented sophisticated ML/DL algorithms (scikit-learn, TensorFlow, PyTorch) for biomarker discovery, phenotype prediction, and multi-omics data integration. Developed end-to-end predictive modeling pipelines for classification, regression, and survival analysis tasks.
- **Multi-Omics Data Integration and Analysis**: Expert in integrating diverse biological datasets using advanced ML models, including variational autoencoders (VAE). Implement sophisticated feature selection, dimensionality reduction, and model optimization strategies to enhance model performance and extract interpretable biological insights from complex multi-modal data.
- **Comprehensive Bioinformatics Pipeline Development**: Designed and deployed reproducible workflows (Snakemake, Nextflow) for genomics analysis, including innovative cfDNA target sequencing pipelines for oncology with enhanced sensitivity for cancer biomarker detection.
- **Single-Cell Analytics Expertise**: Specialized in analyzing high-resolution cellular data (scRNA-seq, scATAC-seq, CITE-seq, TCR/BCR V(D)J) using integrative algorithms (Seurat, scVI-tools) to uncover cellular heterogeneity relevant to disease mechanisms.
- **Technical Infrastructure Management**: Proficient in configuring and optimizing bioinformatics tools within high-performance computing and cloud environments, ensuring computational scalability for data-intensive projects.
- **Custom NGS Assay Development**: Developed UMI-based NGS assays with enhanced variant detection capabilities through optimized bioinformatics strategies and multiple variant caller integration.
- **Programming & Computational Proficiency**: Advanced skills in Python, R, and shell scripting for data science and bioinformatics applications.
- **Specialized Genomics Applications**: Expert in designing custom primers/probes and implementing targeted approaches for specialized genomic/metagenomic research initiatives with applications in precision oncology.

Employer Name: Sysmex-SII, Baltimore MD	Feb 2022 – Present
Title:	Bioinformatics Scientist

- Led the development of cfDNA detection kits, from target primers/probe designing to cfDNA target sequencing pipelines validation, enhancing biomarker detection sensitivity through advanced data analysis
- Proficient in using Streamlit, Plotly Dash for efficient data processing, interactive visualization, and streamlined data management in web-based applications
- Skilled in UMI-based data analysis, with expertise in accurately quantifying gene expression, reducing PCR bias, and improving data quality; Experienced in leveraging UMIs to enhance the precision and reliability of high-throughput sequencing results
- Developed an innovative amplicons aligner that enhances alignment accuracy for PCR-based target sequencing
- Leveraging machine learning models to integrate multi-omics datasets, conduct comprehensive data analyses, and develop insightful visualizations, facilitating the discovery of biological patterns and actionable insights.

Employer Name: FDA CFSAN, Cold Spring, MD Feb 2021 – Nov 2022
Title: Bioinformatician

- Led bioinformatics and Lab Information Management System(LIMS) support for high-throughput NGS data analysis, work as LIMS project manager
- Implementing ML-driven approaches to optimize quality control and annotation processes.
- Built predictive models for food safety datasets, using clustering and classification techniques to analyze microbial diversity patterns and assess public health risks

Employer Name: SAIC/Engility Corp, Cold Spring, MD May 2014 – Feb 2021
Title: Senior Bioinformatician

- Served as an HPC application administrator, specializing in the management HPC/Cloud working environment.
- Developed and maintained Snakemake, NextFlow, and Bash-based pipelines for NGS data analysis, including WGS, WES, metagenomics, and single-cell RNA-seq.
- Optimized WGS/WES pipelines for comprehensive data processing, from quality control to genome assembly and annotation, with a focus on variant identification and genotype-phenotype association study
- Designed and implemented metagenomics pipelines using QIIME, mothur, and phyloseq, integrating machine learning algorithms to analyze multi-omics data and identify microbial species and strain-level variations.
- Proficient in single-cell RNA-seq analysis, with extensive experience using Seurat, scverse, and Bioconductor R packages, applying ML techniques for denoising, feature selection, dimensionality reduction, clustering, visualization, and multi-dataset integration.
- Skilled in scRNA-seq, scATAC-seq, CITE-seq, and TCR/BCR V(D)J analysis, leveraging tools like Seurat and Harmony to uncover cellular diversity and key pathways in infectious disease research

Employer Name: American Type Culture Collection (ATCC) Dec, 2012 – Apr, 2014
Title: Senior Biologist in Biodefense and Emerging Infections Resources Program

- Bioinformatics Pipelines Setup. To design, develop and implement bioinformatics pipelines to: a) design universal primers and probes to detect influenza virus; and b) predict genomic signatures of upcoming seasonal influenza virus in order for early virus typing and detection.

- Comparative Genomics. To identify genomic patterns in prokaryote organisms through comparative genomics study.
- Target Gene Expression Detection. To develop, optimize and validate qPCR kits in order to detect the expression level of the target gene.
- General Support. To provide advanced bioinformatics training and support to peer scientists.
- Tools used: Perl, BioPerl, De Novo assemblers, multiple sequences alignment tools, BLAST, ProKKA, etc.

Employer Name: National Institutes of Health, Bethesda, MD Jun, 2007 – Jun, 2012
Title: IRTA Postdoctoral Fellow
Research includes:

- Protein Conserved Domain Identification. To identify conserved domains in HIV proteins through alignment of multiple sequences extracted from HIV sequence database.
- Protein Structure-Function Correlation. To predicate and validate HIV capsid proteins functions during replication based on their structure.

Employer Name: Vanderbilt University, Nashville, TN Dec, 2002 – May, 2007
Title: Research Associate
Research includes:

- Effect of Mutations on Drug-resistance of HIV strains. To identify the causality between mutations and drug-resistance of HIV strains, and predict mutations associated with reduced drug susceptibility.
- HIV Envelop Proteins Functions. To identify LLP1 domain in gp41 cytoplasmic tail plays an important role in regulating premature virion entry.

Employer Name: Peking University Health Science Center, Beijing, China Sept, 1999 – Jun, 2002
Title: Research Assistant, Department of Immunology

- Hematopoietic and Immune Reconstitution after Bone Marrow Transplantation.

Employer Name: Xinjiang Medical University, Xinjiang, China Jul, 1997- Aug, 1999
Title: Lecturer, Department of Pharmacology
Lesson taught:

- Pharmacology

EDUCATION

07/2002 Ph.D. Immunology, Health Science Center, Peking University, Beijing, China

07/1997 MS Pharmacology, Xinjiang Medical University, Urumqi, China

07/1994 MB (MD equivalent), Xinjiang Medical University, Urumqi, China

SELECTED PUBLICATIONS

1. **Jiang Jiyang,** Ablan Sherimay, *et al.* The interdomain linker region of HIV-1 capsid protein is a critical determinant of proper core assembly and stability. Virology. Dec 2011, 421(2):253-65.
2. **Jiyang Jiang**, Christopher Aiken. Maturation-dependent human immunodeficiency virus type 1 particle fusion requires a carboxyl-terminal region of the gp41 cytoplasmic tail. J Virol. 2007 Sep; 81(18):9999-10008.
3. Davis MR, **Jiang Jiyang**, Zhou J, Freed EO, Aiken C. A mutation in the human immunodeficiency virus type Gag protein destabilizes the interaction of the envelope protein subunits gp120 and gp41. J Virol. 2006 Mar; 80(5):2405-17.
4. **Jiyang Jiang** and Christopher Aiken. Maturation of the viral core enhances the fusion of HIV-1 particles with primary human T cells and monocyte-derived macrophages. Virology. 2006 Mar 15; 346(2):460-8.
5. Marjorie Pion, Jean-Francois Arrighi, **Jiyang Jiang**, Christopher A Lundquist, Oliver Hartley, Christopher Aiken and Vincent Piguet. Analysis of HIV-1-X4 Fusion with Immature Dendritic Cells Identifies a Specific Restriction that Is Independent of CXCR4 Levels. J Invest Dermatol. 2006 Aug 17
6. Wyma DJ, **Jiang Jiyang**, Shi J, Zhou J, Lineberger JE, Miller MD, Aiken C. Coupling of human immunodeficiency virus type 1 fusion to virion maturation: a novel role of the gp41 cytoplasmic tail. J Virol. 2004 Apr; 78(7):3429-35.