

JOHN PABLO MENDIETA

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SUMMARY

Computational Biologist with 10+ years of experience specializing in **high-throughput multi-omics integration, single-cell regulatory logic, and machine learning (ML) modeling**. Expert in architecting production-ready computational pipelines (Nextflow, Snakemake) to translate complex scRNA/ATAC-seq data into **tunable gene editing targets**. Proven track record of leading cross-functional teams to develop patent-pending genomic technologies and publishing high-impact research in **Cell, Science and Nature**.

EDUCATION

University of Georgia

PhD in Genetics

March 2024

Athens, Georgia

University of Colorado

Bachelor of Arts in Molecular and Cellular Biology

Dec 2015

Boulder, Colorado

SKILLS

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|---|---|--|---|
| – Languages: Python (Pandas, Scanpy, PyTorch), R (Tidyverse, edgeR), Rust, Unix/Bash | (scRNA/ATAC-seq, ChIP-seq, WGBS), Variant Calling, Motif Enrichment | (CNNs/GNNs), Ensemble Methods, Statistics | Git/GitHub |
| – Bioinformatics: NGS | – ML/Modeling: G2P Modeling, Deep Learning | – Engineering: AWS (S3, EC2), Docker, Nextflow, Snakemake, SLURM/HPC, | – Experimental: CRISPR/Cas system design, Functional Genomics, High-throughput screening |

WORK EXPERIENCE

Computational Biologist

Inari Agriculture

October 2024 – Present

Cambridge, Massachusetts

- **Platform Development:** Co-developed patent-pending technology for **tunable genomic editing**, integrating ML-based computational target discovery with high-throughput in vivo validation.
- **ML Data Strategy:** Architected ingestion and standardization of 15+ large-scale multi-omic datasets (public and internal), expanding the feature space for **genotype-to-phenotype (G2P) models** used in target selection.
- **Engineering:** Led transition of experimental editing workflows into **production-ready R&D methodologies**, facilitating rapid, iterative hypothesis testing across diverse biological systems.
- **Data-to-Decision Workflows:** Designed robust computational frameworks that bridge multi-omic "dry lab" predictions with experimental "wet lab" assay development, accelerating target validation cycles.
- **Cross-functional Leadership:** Advised R&D strategy for functional genomics (e.g., ATAC-seq, RNA-seq), optimizing experimental design to feed high-resolution training data into predictive ML models.

Post-doctoral Researcher

University of Georgia

April 2024 – October 2024

Athens, Georgia

- **Deep Learning Integration:** Applied deep learning architectures to model **cell-type aware gene regulation**, identifying key regulatory logic governing complex developmental traits.
- **High-Throughput Editing:** Spearheaded collaborative CRISPR-Cas projects to validate regulatory elements, generating high-resolution datasets to inform functional genomic understanding.
- **Mentorship:** Led a team of junior scientists in computational biology, emphasizing software engineering best practices and reproducible, scalable data analysis.

Graduate Student Researcher

University of Georgia

August 2018 – March 2024

Athens, Georgia

- **Single-Cell Innovation:** Developed robust, species-agnostic methods for the analysis of single-cell multi-omic assays (RNA-seq and ATAC-seq), published in **Cell** and **Science**.
- **Pipeline Engineering:** Designed and deployed scalable **Nextflow and Snakemake pipelines** for large-scale data processing on HPC/Cloud environments, significantly improving data integrity and throughput.
- **Algorithm Development:** Created innovative computational tools for chromatin accessibility analysis, identifying cell-type-specific regulatory elements across diverse eukaryotic systems.
- **Reproducible Science:** Authored comprehensive single-cell analysis tutorials and open-source software, utilized by the broader genomic research community to standardize data QC and integration.

Bioinformatics Analyst I

Boyce Thompson Institute

May 2017 – July 2018

Ithaca, New York

- **Genome Assembly:** Spearheaded de novo assembly and annotation of five diverse species using PacBio long-read and short-read WGS data.
- **Variant Discovery:** Generated high-quality variant libraries (SNPs/Indels) for population-scale genomic analysis and evolutionary modeling.

PUBLICATIONS

1. JP Mendieta, X Zhang, Z Luo, AP Marand, H Yan, H Jang, S Bang, MAA Minow, RJ Schmitz- (2025) A spatially resolved multi-omic single-cell atlas of soybean development. *Cell*
2. AP Marand, L Jiang, F Gomez-Cano, MAA Minow, X Zhang, JP Mendieta, Z Luo, S Bang, H Yan, C Meyer, et al.- (2025) The genetic architecture of cell type-specific cis regulation in maize. *Science*
3. H Yan, JP Mendieta, X Zhang, Z Luo, AP Marand, Y Liang, MAA Minow, Y Zhong, Y Jin, H Jang, et al.- (2025) A single-cell rice atlas integrates multi-species data to reveal cis-regulatory evolution. *Nature Plants*
4. JP Mendieta, X Tu, A. Marrand, S Zhong, R Schmitz- (2024) Investigating the cis-Regulatory Basis of C3 and C4 Photosynthesis in Grasses at Single-Cell Resolution. *PNAS*
5. JP Mendieta, A Sangra, H Yan, M Minow, R Schmitz- (2023) Exploring Plant Cis-Regulatory Elements at Single-Cell Resolution: Overcoming Biological and Computational Challenges to Advance Plant Research. *The Plant Journal*
6. H Yan, M Sun, Z Zhang, Y Jin, A Zhang, C Lin, B Wu, M He, B Xu, J Wang, P Qin, JP Mendieta, G Nie, J Wang, C Jones, G Feng, R Srivastava, X Zhang, A Bombarély, D Luo, L Jin, Y Peng, X Wang, Y Ji, S Tian, L Huang (2023) Pangenomic analysis identifies structural variation associated with heat tolerance in pearl millet. *Nature Genetics*
7. A Murry, JP Mendieta, C Vollmers, R Schmitz- (2022) Simple and accurate transcriptional start site identification using Smar2C2 and examination of conserved promoter features. *The Plant Journal*
8. JP Mendieta, W Ricci, A Marrand, X Zhang, R Schmitz- (2021) Leveraging histone modifications to improve genome annotations. *Genes|Genome|Genetics*
9. CS Smith, S Tittes, JP Mendieta, E Collier-zans, H Rowe, LH Rieseberg, NC Kane- (2018) Genetics of alternative splicing evolution during sunflower domestication. *Proceedings of the National Academy of Sciences*
10. D Vergara, H Baker, K Clancy, KG Keepers, JP Mendieta, CS Pauli, S Tittes, KH White, NC Kane (2016) Genetic and genomic tools for Cannabis sativa. *Critical Reviews in Plant Sciences*