Celine Manigbas

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Research Experience

Icahn School of Medicine at Mount Sinai, Sharp Lab   New York, NY

Bioinformatician, **Genetics and Genomics | September 2022 - Present**
- Designed and optimized custom data pipelines, enabling high-throughput genomic analyses for large cohorts
- Led phenome-wide association studies (PheWAS) on over 160,000 tandem repeats across 410,000 European individuals, analyzing over 30,000 clinically significant phenotypes in the UKBiobank.
- Performed analysis to identify functional repeats that impact local gene expression and DNA methylation
- Presented research findings at major conferences, effectively communicating genomic analyses and their clinical relevance to diverse audiences
- Collaboration with Dr. Rebecca Birnbaum into investigating the role of TRs in Schizophrenia

Boyce Thompson Institute at Cornell University, Mueller Lab   Ithaca, NY

Research Intern, **BTI Computational Biology Center | June 2018 - June 2019**
- Selected for the 2018 NSF REU Plant Genome Research Program (NSF 18-579)
- Led the genome assembly, error correction, and functional annotation of the *A. syriaca* (common milkweed) genome, ensuring high data quality for further research use
- Mapped RNA-seq data and performed *ab initio* gene predictions
- Conducted gene family expansion analyses to trace the evolution of pathways critical to cardiac glycoside biosynthesis, a key defense mechanism and an important drug used to treat heart conditions
- Utilized bioinformatics tools like *Arrow, Mikado, Maker* pipeline, *AUGUSTUS*, and *OrthoFinder*

New York University, Cardozo lab   New York, NY

Research Intern, **Biochemistry and Molecular Pharmacology | June - August 2017**
- Conducted molecular modeling simulations using *ICM-Browser Pro*, modeling crystal structures of bacteriophage T4 and investigating its interaction with E. coli's RNA polymerase (RNAP)
- Utilized Monte Carlo sampling techniques to model unknown protein loop structures, contributing to new insights into bacteriophage-host interactions
- Contributed to formal lab meetings and observed lectures by laboratory staff at the NYU Langone School of Medicine

Publications and Invited Presentations

Manigbas CA, Jadhav B, Garg P, Shadrina M, Lee W, Altman G, Martin-Trujillo A, Sharp AJ. A phenome-wide association study of tandem repeat variation in 168,554 individuals from the UK Biobank. *medRxiv* (PMID: 38343850). *Accepted in Nature Communications (November 18, 2024)*.

European Society of Human Genetics Conference   Berlin, Germany
Poster Presentation, Best Poster Session | June 2024
A phenome-wide association study of tandem repeat variation in 168,554 individuals from the UK Biobank

American Society of Human Genetics Annual Meeting   Denver, CO
Oral Platform Presentation | November 2024
A phenome-wide association study of tandem repeat variation in 168,554 individuals from the UK Biobank

Skills

- ***Programming Languages:*** R, Python, Unix (shell), C++, Java
- ***Tools & Analyses***: *REGENIE*, *METAL*, *PLINK*, fine-mapping, PheWAS, GWAS, eQTL, conditional analysis, linkage disequilibrium analysis, linear and logistic regression, principal component analysis, gene set enrichment analysis
- ***Cloud Computing & Data Management:*** Familiarity with cloud computing platforms and manipulating large-scale data banks, high-performance computing, pipeline optimization, data integrity management

Education

Massachusetts College of Liberal Arts (MCLA) | 2019   GPA: 3.88
- Bachelor of Science, Computer Science: Bioinformatics; *summa cum laude*

Bard High School Early College Queens | 2016   GPA: 3.54
- Associate of Arts Degree

Achievements and Leadership

Best Poster | *European Society of Human Genetics Conference 2024*
- Abstract among the best scored papers accepted for poster presentation
- Presented overview of work at the Best Posters Session

All-College Honors | *MCLA 2019*
- Successfully completed a rigorous, interdisciplinary academic program, which includes at least 18 credit hours of honors courses, including upper-level coursework

Ada Lovelace Computer Science Outstanding Student Award | *MCLA 2019*
- Awarded to top student in the Computer Science department

Alpha Chi National College Honor Society | *MCLA 2017-2019*

Student Government Executive Vice President | *MCLA 2017-2019*
- Collaborated with faculty on committees (All-College, Academic Policies, Curriculum), presenting student concerns and proposing policies to enhance the student experience.
- Collaborated with other board members to reach consensus on campus-wide decisions

Outstanding Senior Leader Award | *MCLA 2019*

Relevant Coursework

- **Science and Mathematics GPA: 3.97**
- ***Biological Sciences****: Genetics, Zoology, Cell & Molecular Biology, Biochemistry, Organic Chemistry
- ***Mathematics****: Biometry, Proof I & II, Discrete Mathematics
- ***Computer Science:*** Programming in Java/C++, Object Oriented Design, Database Development, Data Structures and Algorithms, Machine Learning