Melyssa Minto | Computational Biologist

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Education & Training

Duke University, Durham NC   October 2022
Doctor of Philosophy in Computational Biology and Bioinformatics
Meredith College, Raleigh NC   May 2017
Bachelor of Science, Magna cum laude, Mathematics & Biology
Honors Program Scholar
Trainings:

AWS Technical Essentials, Building Data Lakes, Building Batch Data Analytics Solutions, **AWS**	July 2022
Data Access and Cloud Computing Workshop, ***National Center for Biological Information***	Nov 2021
Project Management Training, **Duke DEVELPMNT**	Spring 2021
Clinical Research Education in Genome Science, ***Icahn School of Medicine at Mt. Sinai***	Fall 2021
Certificate in Integrative Genomics, ***Summer Institute in Statistical Genetics UW-Seattle***	July 2018
Certificate in MCMC for Statistical Genetics, ***Summer Institute in Statistical Genetics UW-Seattle***	July 2018

Research Experience

Bioinformatics Scientist —RTI International   Oct 2022 – Present

- Created and implemented existing workflows, develop new pipelines to analyze high dimensional genomic data from a variety of biological experiments.
- Led genomic and statistical analyses to uncover alcohol-related DNA methylation disparities in prefrontal cortex and nucleus accumbens, contributing to NIH/NIAAA-funded research on Alcohol Use Disorder.
- Played a pivotal role in the Integrative Omics Center for Accelerating Neurobiological Understanding of Opioid Addiction, employing RNAseq summary statistics to scrutinize expression level differences in postmortem dorsolateral prefrontal cortex (DLPFC) brain tissue of opioid addiction patients.
- Developed frameworks for network replication testing across studies to rank genes based on phenotype significance, facilitating compound prioritization and cataloging genes and compounds for potential therapeutic use.

Ph.D. Graduate Candidate — Duke University   Dec 2018-Oct 2022
Dissertation: Systematic examination of epigenomic regulation of neuronal plasticity

- Developed a modular and scalable in-house pipeline to process raw next generation sequencing data on a high-performance computing cluster. This pipeline was widely implemented across the lab for alignment of DNase, ChIP-seq, RNA-seq, and other sequencing data.
- Developed integrative workflow to analyze and interpret gene expression and chromatin data. Used chromatin data to determine regulatory regions around induced genes as a search space for transcription factor (TF) binding. Cross-validated enriched transcription factor motifs with transcriptional enrichment to determine putative TFs regulating neuronal plasticity in a stimulus dependent manner.
- Used this integrative workflow to predict TFs that regulated amphetamine induced transcription in Pvalb+ interneurons and TFs in collaboration with the Zic TFs to regulated developmental gene expression in the maturing mouse cerebellum
- Conducted a multiomic time-course analysis of ChIP-seq of two histone modifications in the developing cerebellum. Established that histone markers H3K27ac and H3K27me3 in the developing cerebellum tend to regulate the same genes but in different genomic regions.
- Integrated publicly available single cell RNA-seq into workflows to identify cell type specific transcription factors.

Computational Toxicology Intern — ScitoVation   Jan 2017 – Jan 2018

- Efficiently balanced multiple projects from within and outside of the computational toxicology team manner to meet each quarterly deadline. Each project was clearly documented, and version controlled.
- Harmonized ~45,000 chemical-assay plate data from and bioactivity, and chemical property data (i.e. SMILES, Cramer Classification, Population Exposure rates) from multiple sources, including U.S. EPA funded Collaborative Estrogen Receptor Activity Prediction Project, for chemical testing risk prioritization
- Demonstrated the need for fit for purpose assays for compounds with high vapor pressure based on the proportionally low hits in conventional plate assays and their high risk in neurological and hepatic systems.
- Performed differential expression and enrichment analysis to determine genes and pathways dysregulated by several chemical compounds in R to identify targets for stakeholders.
- Created a pipeline to perform a systematic literature search in Python using the PubMed API to curate publicly

available data on a compound's bioactivity as well as common terms discussed in the abstract of research articles to assess the need for risk testing.

Invertebrate Research Intern – NC Museum of Natural Sciences   Jun 2016 – May 2017
- Collected morphometric data from hundreds of samples from both the NC Museum of Natural Sciences and the Smithsonian Museum of Natural History.
- Trained regression models using selected morphometric data and genotype data to delimit crayfish species to help lead conservation efforts.
- Incorporated machine learning algorithms to automate morphometric analysis and aid in identification of characteristics that can be used to distinguish crayfishes.

Transcriptomics Research Intern | ENBYSIS Lab — NC State University   Summer 2016
- Evaluated differential gene expression in Arabidopsis plant undergoing lignin biosynthesis in R to determine the genes and pathways that are regulated by this process.
- This data was integrated into a differential equations model to simulate the expression of molecules in the lignin biosynthesis pathway with the aim of designing a synthetic system to create lignin, an important molecule in biofuels

Research Technician | Biomedical Research Institute—NC Central University   Jun 2015 – Dec 2016
- Served as a lead statistician on a dynamic team for a research project analyzing growth data, epigenetic data, and genetic data.
- Created R package, MonoInc, to clean monotonic data such as child growth data, that flags data that is either outside of a user-input range or non-monotonic and performs a single or weighted imputation. Imputation methods include nearest neighbor, regression, last observation carried forward.
- Helped to develop the study design and statistical methodology for a behavioral zebrafish study that modeled fetal alcohol syndrome where multiple measures of social anxiety were captured.

Publications

1. Javan K. Carter, Bryan C. Quach, Caryn Willis, **Melyssa S. Minto,** PGC-SUD Epigenetics Working Group, Dana B. Hancock, Janitza Montalvo-Ortiz, Olivia Corradin, Ryan W. Logan, Consuelo Walss-Bass, Brion S. Maher, Eric Otto Johnson. Identifying novel gene dysregulation associated with opioid overdose death: A meta-analysis of differential gene expression in human prefrontal cortex. (medRxiv 2024)
2. Julie D. White, **Melyssa S. Minto**, Caryn Willis, Bryan C. Quach, Shizhong Han, Ran Tao, Amy Deep-Soboslay, Lea Zillich, Shaunna L. Clark, Edwin J. C. G. van den Oord, Thomas M. Hyde, R. Dayne Mayfield, Bradley T. Webb, Eric O. Johnson, Joel E. Kleinman, Laura J. Bierut, Dana B. Hancock. Alcohol Use Disorder-Associated DNA Methylation in the Nucleus Accumbens and Dorsolateral Prefrontal Cortex (medRxiv 2024)
3. Jeran K. Stratford, Megan U. Carnes, Caryn Willis, **Melyssa S. Minto**, Logain E. Elnimeiry, Ravi M. Mathur, Matthew S. Schu, Bryan C. Quach, Javan C. Carter, Tracy N. Nolen, Nathan V. Vandergrift, Thomas K. Kosten, Eric O. Johnson, Bradley T. Webb. Identifying compounds to treat opiate use disorder by leveraging multi-omic data integration and multiple drug repurposing databases.(medRxiv 2024)
4. Caryn Willis, Julie D. White, **Melyssa S. Minto**, Bryan C. Quach, Shizhong Han, Ran Tao, Joo Heon Shin, Amy Deep-Soboslay, Thomas M. Hyde, R. Dayne Mayfield, Bradley T. Webb, Eric O. Johnson, Joel E. Kleinman, Laura J. Bierut, Dana B. Hancock.. Gene expression differences associated with alcohol use disorder in human brain. (medRxiv 2024)
5. **Melyssa Minto**, Emiliano Sotelo, Vijyendra Ramesh, Anne West. *Bioinformatic Investigation of the Zic1/2 binding reveals novel co-factors in Zic-mediated gene regulation in the cerebellum*. (bioRxiv 2024)
6. Vijyendra Ramesh, Fang Liu, **Melyssa Minto**, Urann Chan, Anne West *Bidirectional changes in postmitotic H3K27me3 distributions underlie cerebellar granule neuron maturation dynamics.* eLife (2023).
7. Chantel I. Nicolas, Matthew W. Linakis, **Melyssa Minto**, Kamel Mansouri, Rebecca A. Clewell, Miyoung Yoon, Martin B. Phillips, John F. Wambaugh, Grace Patlewicz, Patrick D. McMullen, Melvin E. Andersen, and Harvey J. Clewell III. *Estimating Provisional Margins of Exposure for Data-Poor Chemicals Using High-Throughput Computational Methods*. *Frontiers in Pharmacology (2022)*
8. Jenea I. Adams, Taylor Ferebee, **Melyssa Minto**, Kayla K. Pennerman, Nyasha Chambwe. *10 Simple Rules for Creating a Global Network in Computational Biology*. PLoS Comp Bio (2022)
9. David Gallegos, **Melyssa Minto**, Fang Liu, Mariah F. Hazlett, S. Aryana Yousefzadeh, Luke C. Bartelt, Anne E. West. *Cell-type specific transcriptional adaptations of nucleus accumbens interneurons to amphetamine.* Molecular Psychiatry (2022)
10. Chantel I Nicolas, Kevin Bronson, Salil N Pendse, Alina Efremenko, Jeremy M Fitzpatrick, **Melyssa S Minto**, Kamel Mansouri, Miyoung Yoon, Martin B Phillips, Rebecca A Clewell, Melvin E Andersen, Harvey J Clewell III, Patrick D McMullen. *The TTC Data Mart: an interactive browser for Threshold of Toxicological Concern calculations*. *Computational Toxicology* (2020)
11. Patrick D. McMullen, Melvin E. Andersen, Brian Cholewa, Harvey J. Clewell, Katherine M. Dunnick, Jessica K. Hartman, Kamel Mansouri, **Melyssa S. Minto**, Chantel I. Nicolas, Martin B. Phillips, Scott Slattery, Miyoung Yoon, Rebecca A. Clewell, *Evaluating opportunities for advancing the use of alternative methods in risk assessment through the development of fit-for-purpose in vitro assays*. *Toxicology* in Vitro (48).2018

12. **Melyssa Minto**, Michele Josey, Clarlynda Williams-DeVane. *MonoInc: Monotonic Increasing*. R package version 1.1. (2016)

Conferences & Symposia

- **Differential gene regulation associated with alcohol use disorder in human nucleus accumbens and dorsolateral prefrontal cortex.** The American Society of Human Genetics (Nov 2023) *Poster Presentation*
- **Tissue-specific DNA methylation signatures of alcohol use disorder in human brain.** National Institute for Drug Abuse Genetics and Epigenetics Cross-Cutting Research Team Meeting (May 2023) *Poster Presentation*
- **Integrative modeling of Zic binding to reveal novel roles in chromatin remolding and gene regulation**. CSHL Biology of Genomes (May 2022). *Poster presentation*
- **Bioinformatic Investigation of Zic Family of Transcription Factors in the Mature Cerebellum**. Sema4 BIPOC Initiative Genomics Symposium (April 2022). *Poster presentation*
- **Beyond PWMs: Modeling sequence in context to reveal the multimodality of transcription factor binding and activity**. Cold Spring Harbor Labs – Genome Informatics (Nov 2021). Poster presentation
- **Modeling transcription factor dynamics of postnatal development in the cerebellum.** Black Women in Computational Biology Summit (May 2021). *Oral presentation*
- **Using genomic sequence to determine the mechanistic changes to Zic TF binding in the maturing cerebellum.** Annual NC Women of Color Research Network Symposium (May 2021). *Oral presentation*
- **Zic regulates cerebellar granule neuron maturation in late developmental stages through noncanonical binding.** Cold Spring Harbor Labs – Epigenetics and Chromatin (Sep 2020). *Poster presentation*
- **Bioinformatic analysis of H3K27me3 and H3K27ac dynamics of postnatal development of cerebellum.** IRTG Dissecting and Reengineering the Regulatory Genome (Apr 2019). *Poster presentation*
- **Cray Cray Morphometrics: Advancing Morphometric Delimitation of Species of Crayfish.** Shaw University Research Symposium (Feb 2017). *Poster presentation*
- **Cleaning Electronic Medical Records Using Novel R Package MonoInc**. Annual Biomedical Research Conference for Minority Students (Nov 2016). *Poster presentation*
- **MonoInc: An R Package**. North Carolina Central University Graduate & Undergraduate research symposium (May 2016). *Oral presentation*
- **A Study of the Risks of Teenage Pregnancy in the U.S**. Meredith College Celebrating Student Achievement Day (May 2016). *Poster presentation*

Leadership & Professional Service

Education subcommittee | Duke Racial Equity Advisory Council	2021
Panelist | ISCB Great Lakes Bioinformatics Conference 2021 EDI panel	2021
Leadership Team | Black Women in Comp Bio Network	2020 – Current
Project Manager | Duke Data+ Environmental Public Health Tracking	May 2020 – Aug 2020
Alumni Networking Panel & Reception Committee | Duke Bouchet Society	2019
Few-Glasson Alumni Society Selection Committee | Duke Graduate School	2018 – 2020
Faculty Mentor Award Selection Committee | Duke Graduate School	2018 – 2020
Dean's Awards Selection Committee | Duke Graduate School	2018 – 2020
Gordon G. Hammes Teaching Selection Committee| Duke Graduate School	2018,2021
Retreat Planning Committee | Computational Biology & Bioinformatics	2018

Outreach & Volunteer Experience

Technology Judge | NC Science & Engineering Fair – Region 3B	2021
Panelist | Tufts T-TRIPODS Diamonds Data Science Panel	2021
STEM Instructor | The Prevailing Girl Camp	2021
Panelist | Golden Door Scholars Career Hour	2021
Mentor | Durham Public School Women in Math Program	Sep 2019 – Mar 2020
President | Triangle Science Share	2020
Graduate Student Q&A YouTube Live | Duke Graduate School	2019
Graduate Student Welcome Panel | Duke Graduate School	2018

Awards & Honors

Highly Published Author Award | RTI International, 2023
RISE Spot Award for High Quality and Initiative in Review ECHO | RTI International, 2022
Precision Genomics Collaboratory Pilot Grant | Duke University
Duke BioCoRE Scholar
Deborah K. Smith Award for Achievement in Biology | Meredith College
Ford Foundation Fellowship Honorable Mention
Who's Who Among Students in American Universities and Colleges
Beta Beta Beta | National Biological Honor Society
Pi Mu Epsilon | National Mathematics Honor Society
Outstanding Student Researcher of the Year | NC Central University