

Melyssa Minto | Computational Biologist

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Education & Training

Duke University , Durham NC <i>Doctor of Philosophy in Computational Biology and Bioinformatics</i>	October 2022
Meredith College , Raleigh NC <i>Bachelor of Science, Magna cum laude, Mathematics & Biology</i> <i>Honors Program Scholar</i>	May 2017
Trainings: AWS Technical Essentials, Building Data Lakes, Building Batch Data Analytics Solutions, AWS Data Access and Cloud Computing Workshop, National Center for Biological Information Project Management Training, Duke DEVELOPMNT Clinical Research Education in Genome Science, Icahn School of Medicine at Mt. Sinai Certificate in Integrative Genomics, Summer Institute in Statistical Genetics UW-Seattle Certificate in MCMC for Statistical Genetics, Summer Institute in Statistical Genetics UW-Seattle	July 2022 Nov 2021 Spring 2021 Fall 2021 July 2018 July 2018

Research Experience

Bioinformatics Scientist — RTI International <ul style="list-style-type: none">Use and modify existing workflows, develop new pipelines to analyze high dimensional genomic data from a variety of biological experimentsImplemented integrative and statistical techniques to inform gene ranking for drug repurposing in substance use disorder patients.Developed appropriate statistical frameworks to understand brain region specific DNA methylation in alcohol use disorder patients.	Oct 2022 – Present
Ph.D. Graduate Candidate — Duke University <i>Dissertation: Systematic examination of epigenomic regulation of neuronal plasticity</i> <ul style="list-style-type: none">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 cerebellumConducted 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.	Dec 2018-Oct 2022
Computational Toxicology Intern — ScitoVation <ul style="list-style-type: none">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 prioritizationDemonstrated 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.	Jan 2017 – Jan 2018
Invertebrate Research Intern – NC Museum of Natural Sciences <ul style="list-style-type: none">Collected morphometric data from hundreds of samples from both the NC Museum of Natural Sciences and the	Jun 2016 – May 2017

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, *Monolnc*, 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. **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*](#). (In preparation)
2. Vijyendra Ramesh, Fang Liu, **Melyssa Minto**, Urann Chan, Anne West [*Bidirectional changes in postmitotic H3K27me3 distributions underlie cerebellar granule neuron maturation dynamics*](#). BioXiv (2022).
3. 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)
4. 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)
5. 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)
6. 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)
7. 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
8. **Melyssa Minto**, Michele Josey, Clarlynda Williams-DeVane. [*Monolnc: Monotonic Increasing*](#). R package version 1.1. (2016)

Mentorship Experience

Benjamin Goldstein, Duke University B.S. Mathematics

Summer 2021

Provide training in analytical techniques for high-throughput sequencing experiments, R/Tidy programming, git version control, and scientific writing.

Noelia Rodriguez, Meredith College, B.S. Biology & B.A Mathematics

2018 - present

Mentor on internship opportunities, leadership, and research activities

Pamela Gonzalez, Meredith College, B.A. Psychology (Mathematics, Social Work minors)

2017-present

Meet with semesterly to discuss time management, career path, and success strategies for coursework

Conferences & Symposia

- **Integrative modeling of Zic binding to reveal novel roles in chromatin remodeling 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 – Current
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

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

Teaching Experience

Integrative Genomics Workshop	August 2022
<ul style="list-style-type: none"> • Developed a workshop for graduate students to learn how to integrate epigenomic (ATAC-seq, ChIP-seq, Hi-C) data with transcriptomic data. • Created code-a-longs 	
Data Carpentries Teacher's Assistant	August 2019, August 2018, August 2021
<ul style="list-style-type: none"> • Assisted during a Bootcamp for a University program for genomics and genetics at Duke University. • This Bootcamp included curriculum that covered Unix command line, programming in python using jupyter, data and project organization, and version control with Git. 	
HackBio Instructor	April 2021
<ul style="list-style-type: none"> • Instructor for Neuro-transcriptomics course for Hackbio • Topics covered included introduction to neurobiology, transcriptomics pipelines, and practicum for performing transcriptomic analysis on neuronal data. 	