

Melyssa Minto

PhD Candidate in Computational Biology and Bioinformatics

Personal Info

E-mail

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Soft Skills

Leadership

Communication

Logistical

Creativity

Mentorship

Project Management

Hard Skills

R

Python

Bash/Shell

MATLAB

HTML

CSS

Java

Markdown

Git

SLURM

HTML Scrubbing

Data Cleaning

Bayesian Stats

Grant Writing

Language

Spanish

Objective

My research interests lie at the intersection of computational biology, epigenomics, and human health. Long-term, my goal is to study epigenomics in the context of health disparities and to make findings in this field more accessible especially to marginalized populations. To achieve this goal, I enrolled in the Computational Biology and Bioinformatics PhD program at Duke University and joined Anne West's lab where I am developing the statistical and computational skills to work with (epi)genomic data. Thanks to large-scale sequencing projects, there exists a plethora of genomic and epigenomic data; however the field needs integrative approaches to finding relevant biological information within these data. During my PhD, I am building statistical models to elucidate transcription factor binding patterns that regulate the maturation of cerebellar granule neurons, thus advancing understanding of brain development. This training will equip me to be a leader in epigenomics, and with the resources and training of the HHMI Gilliam Fellowship, I look forward to collaborating with like-minded scientists to both advance knowledge and to tear down systemic barriers in STEM.

Education and Certificates

Current

July 2018

July 2018

May 2017

Ph.D. in Computational Biology and Bioinformatics | Duke University

Cert in Integrative Genomics | Summer Institute for Statistical Genetics

Cert in MCMC for Statistical Genetics | Summer Institute for Statistical Genetics

B.S. in Mathematics and B.S. in Biology, Meredith College, Raleigh, NC

Leadership and Involvement

2020

2019 – 2020

2019 – Current

2019

2019 – 2020

2019

2018 – Current

2018 – Current

2018 – Current

2018

2018

2018

Project Manager | Duke Data+ *Environmental Public Health Tracking*

Mentor | Durham Public School Women in Math Program

President | Triangle Science Share

Graduate Student Q&A [YouTube Live](#) | Duke Graduate School

Seminar Planning Committee | Computational Biology & Bioinformatics

Alumni Networking Panel & Reception Committee | Bouchet Society

Few-Glasson Alumni Society Selection Committee | Duke Graduate School

Faculty Mentor Award Selection Committee | Duke Graduate School

Dean's Awards Selection Committee | Duke Graduate School

Gordon G. Hammes Teaching Selection Committee | Duke Graduate School

Retreat Planning Committee | Computational Biology & Bioinformatics

Graduate Student [Welcome Panel](#) | Duke Graduate School

Honors and Awards

2017 – Current

2017

2017

2016

2016

2016

2016

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

August 2018/

August 2019

2017 – Current

Data Carpentries Teacher's Assistant

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.

Tech Assistant/Instructor, *Black Girls Code*

Volunteer to help organize, set up, and teach girls ages 7-17 about the basic principles behind coding, computer science, and engineering. Serve as a role model for girls by sharing my expertise and relevant experience.

Seminar/Conference Presentations

Sep 2020

Sep 2019

April 2019

February 2017

November 2016

May 2016

May 2016

Zic regulates cerebellar granule neuron maturation in late developmental stages through noncanonical binding | Cold Spring Harbor Labs – Epigenetics and Chromatin

Computational methods to model the dynamic binding of the Zic Transcription Factor in Postnatal Development of the Cerebellum | Duke Neurobiology Retreat and Duke Computational Biology and Bioinformatics Retreat

Bioinformatic analysis of H3K27me3 and H3K27ac dynamics of postnatal development of cerebellum | IRTG Dissecting and Reengineering the Regulatory Genome

Cray Cray Morphometrics: Advancing Morphometric Delimitation of Species of Crayfish | Shaw University Research Symposium

Cleaning Electronic Medical Records Using Novel R Package Monolnc | Annual Biomedical Research Conference for Minority Students

Monolnc: An R Package | North Carolina Central University

A Study of the Risks of Teenage Pregnancy in the U.S. | Meredith College Celebrating Student Achievement Day (CSA Day)

Research Experience

DISSERTATION RESEARCH

My current research involves an integrative approach to determine regulators or psychostimulant induced genomic changes in Parvalbumin (PV) Interneurons as well as transcriptional regulators of maturation in Cerebellar Granule Neurons (CGNs) in Dr. Anne West's Lab. Since research from the lab has already shown that PV cells are integral in forming addictive like behaviors, understanding the genomic regulation that occurs in these cells will reveal insights as to how addiction is formed on a biological level and novel targets to treat addiction. As for my primary project, looking at how genome regulation changes throughout maturity in a post mitotic cell population opens the door to understanding how transcription factors and the 3D genome play a role driving cell maturation. I will be developing a Bayesian graphical model to learn the variation of TF binding throughout a time course such that it will reveal how TFs are changing their binding patterns over time. This will have mechanistic implications outside of CGNs.

INDUSTRY EXPERIENCE

JANUARY 2017 – August 2017 | **ScitoVation** | Efficiently balanced multiple projects from within and outside of the computational toxicology team manner to meet each quarterly deadline. Projects included curating chemical-assay plate data, performing gene expression/enrichment analysis, creating a pipeline to perform a systematic literature search with the goal of curating publicly available data on a compound's bioactivity. Each project was clearly documented, and version controlled.

UNDERGRADUATE RESEARCH

June 2016 – 2016 | **Prairie Ridge Ecostation, North Carolina Museum of Natural Sciences** | Collected data from both the NC Museum of Natural Sciences and the Smithsonian, used morphometric and genotype data to delimit crayfish species. Incorporated machine learning algorithms to automate morphometric analysis and aid in identification of characteristics that can be used to distinguish crayfishes.

June 2016 – August 2016 | **ENBISYS Lab, North Carolina State University** | Found gene targets to upregulate the synthesis of lignin, a biofuel, by differential analysis in R. These findings were used to further develop a computational model based on the lignin biosynthesis pathway to better understand how to increase the production of biofuels.

June 2015 – Dec 2016 | **Biomedical/Biotechnology Research Institute, North Carolina Central University** | 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 longitudinal data – It flags data that is either outside of a range or non-monotonic and performs a single or weighted imputation. Helped to develop the study design and statistical methodology for a behavioral zebrafish study that modeled fetal alcohol syndrome.

May 2015 – May 2016 | **Meredith College** | *The Implications Associated with the Perceptions of Farmwork and Agriculture* Distributed a survey and used R to analyze the awareness of farmworkers among Meredith College community. Determined the steps to increase awareness the unfair conditions of farmworkers. *A Study of the Risks of Teenage Pregnancy in the U.S.* Conducted statistical analyses to identify risk factors for teenage pregnancy using data provided by the National Survey for Family Growth.

May 2014 – August 2014 | **DREAM STEM, North Carolina Central University** | Under the tutelage of Dr. Goalin – Milledge, analyzed the genetic risk for type-2 diabetes using various statistical tests conducted in R. This resulted in SNP targets for type-2 diabetes.

Publications

IN PREPARATION

1. David Gallegos, **Melyssa Minto**, Fang Liu, Aryanna Yousefzadeh, Mariah Hazlett, Greg Crawford, Anne E West. Psychostimulant-regulated transcriptional plasticity in Nucleus Accumbens fast-spiking interneurons. *In Preparation*

PUBLISHED

1. 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
2. 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
3. **Melyssa Minto**, Michele Josey, Clarlynda Williams-DeVane. *Monolnc: Monotonic Increasing*. (2016). R package version 1.1. <https://CRAN.R-project.org/package=Monolnc>