


# Edmund Miller


 hello@edmundmiller.dev  edmundmiller.dev  @edmundmiller  Edmund Miller

PhD Candidate | nf-core Core Member

## Experience

### Bioinformatics Engineering Associate

*Element Biosciences*


 Aug 2021 — Feb 2023

 Remote

- Designed and created a system for internal pipelines and automating secondary analysis.
- Contributed in converting Loop Genomics pipeline from Python and Azure API calls to Nextflow reducing cost from \$500 per sample to \$40 per sample.
- Restructured tertiary analysis.

### Bioinformatics Engineering Intern

*Element Biosciences*


 Jun 2021 — Aug 2021

 Remote

- Converted the internal whole genome sequencing pipeline from former Jupyter notebooks and bash scripts to Nextflow.
- Performed variant calling for COVID-19 AmpliSeq samples.
- Processed 10x spatial transcriptomics data.
- Created internal standards for Nextflow modules, MultiQC, and pipeline testing.
- Analyzed ERCC spike-in data.

### Software Engineer

*Olypsis Technologies*

 Jun 2018 — Jun 2020


 Dallas, Tx


- Lead development and design of BlockNKey completing tasks such as created the functioning test suite for legacy code, containerized the entire system, designed and implemented a REST API and smart contracts for the system.
- Created a novel ERC20 payment splitter smart contract in Solidity for Digital Assets Foundry.
- Developed the decentralized DAWN protocol to transfer files in a peer to peer fashion, eliminating the need for a 3rd party in the transaction.
- Worked with a variety of Web3 technologies including Whisper, IPFS, AES256, and React.

## Education

### PhD - Molecular and Cell Biology

*University of Texas at Dallas*


 Aug 2020 — Dec 2024

 Richardson, Tx

- Designed and taught the *Applied Genomics* course during summer semesters, which is now a required course for the Genomics Certificate.

### MS - Biotechnology


*University of Texas at Dallas*

 Aug 2018 — Dec 2019

 Richardson, Tx

### BS - Molecular Biology

*University of Texas at Dallas*


 Aug 2015 — Aug 2018


 Richardson, Tx

- Academic Excellence Scholarship 2015-2019
- President's Scholarship 2016-2017
- Continuing Student Scholarship 2017-2018


## Publications

### Scalable and efficient DNA sequencing analysis on different compute infrastructures aiding variant discovery

 2023-07-19


 bioRxiv


### Sequencing by avidity enables high accuracy with low reagent consumption

 2023-05-25

 Nature Biotechnology

### mlf-core: a framework for deterministic machine learning

 2023-04-03

 Bioinformatics

## Speaking

### Nextflow Summit

- *Workflow automation: Using the Aviti benchtop sequencing system and Nextflow Tower* - Oct 2022
- *nf-test at nf-core: empowering scalable and streamlined testing* - Oct 2023
- *Nextflow and database uses: powering data engineering, exploring DuckDB, and beyond* - Nov 2023

### Juliacon

- *Exploring the State of Machine Learning for Biological Data* - July 2023
- *Unlocking the Power of Genomic Analysis in Julia* - July 2023

### nf-core/bytesize

- *nf-test* - Jul 2023
- *nascent* - Nov 2022
- *Pytest-workflow/Github actions* - Jun 2021

## Projects

### nf-core/nascent

Nascent Transcription Processing Pipeline

### nextflow-mode

A Emacs mode for syntax highlighting for Nextflow based on snakemake-mode.