Edmund Miller

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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 developement 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.