Edmund A. **Miller**

COMPUTATIONAL BIOLOGIST · SOFTWARE DEVELOPER

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Experience

Functional Genomics Lab(Prof. Tae Hoon Kim)   *Richardson, Texas*

RESEARCHER   *Jul 2015 - PRESENT*

- Created a pipeline to reproduce and create new nacent RNA predictions using Snakemake.
- Mentored undergraduates in rewriting nacent RNA pipeline following nf-core standards
- Used techniques such as containers, conda environments, and high-performance computing clusters.
- Performed RNA isolation from cells that were treated with LPS-particles and used qPCR to quantify eRNA transcript levels.

Element Biosciences   *San Diego, California (Remote)*

BIOINFORMATICS ENGINEERING ASSOCIATE   *Aug 2021 - February 2023*

- Gave a talk at Nextflow Summit 2022 on secondary analysis automation.
- Maintaining internal pipelines and automating secondary analysis.
- RNA-seq tertiary analysis.
- Creation of TumorNormal pipeline.

Element Biosciences   *San Diego, California (Remote)*

BIOINFORMATICS ENGINEERING INTERN   *June 2021 - Aug 2021*

- Converted Internal Whole Genome Sequencing Pipeline from Jupyter and bash scripts to nextflow.
- Performed variant calling for COVID-19 samples.
- Processed 10x spatial transcriptomics data.
- Created internal standards for nextflow modules, multiqc, and pipeline testing.
- Analyzed ERCC spike-in data.

Olypsis Technologies   *Dallas, Texas (Remote)*

BLOCKCHAIN SOFTWARE DEVELOPER   *May 2018 - May 2020*

- Lead developement and design of completing tasks including, creating a functioning test suite for legacy code, containerizing the entire system, designing and implementing 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 DAWN protocol to transfer files in a peer to peer fashion, that is decentralized and does not rely on a 3rd party to be trusted using Whisper, IPFS, AES256, and React.

Skills

Tools	Nextflow, Nix/OS, Snakemake, Conda, Slurm
Programming	Python, Node.js, Rust, R, Solidity, Bash/ZSH, Clojure
DevOps	Docker, Kubernetes, GitHub Actions, AWS, GitLab-CI
Front-end	React, Vue, Nextjs, Gatsby, Redux, Hugo, HTML5, CSS

Education

University of Texas at Dallas   *Richardson, Texas*

PH.D. IN MOLECULAR AND CELL BIOLOGY   *Aug 2020 - PRESENT*

- Fall 2021 - TA for Genes to Genomes
- Summer 2021 - Co-created Course material and TA for Applied Genomics
- Fall 2020 - Spring 2021 - TA for Biochemistry I

University of Texas at Dallas   *Richardson, Texas*

M.S. IN BIOTECHNOLOGY   *Aug 2018 - Dec 2019*

- Fast-Track Program

University of Texas at Dallas   *Richardson, Texas*

B.S. IN MOLECULAR BIOLOGY   *Aug 2015 - Aug. 2018*

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

Projects

mlf-core   *Preprint*

Core   *Jan 2021 - PRESENT*

- Deterministic machine learning project templates based on MLflow.

nf-core   *GitHub Page*

Maintainer   *Mar 2020 - PRESENT*

- Maintaining nf-core/nascent
- Hackathon organizing team and mentor
- Modules Team
- Lead creation of unit and e2e tests and CI refactoring for DSL2 Modules.
- Implementing nf-test into modules and pipelines.

Doom-Emacs   *GitHub*

Contributor   *Mar 2018 - PRESENT*

- Worked on Reference, Conda, and Solidity modules.
- Maintaining several personal modules such as Snakemake and LSP language support.

edgePy   *GitHub*

Contributor   *Sep 2018 - PRESENT*

- A Python implementation of edgeR for differential expression analysis.
- Implementing code and testing standards to the repo.

emacs-jest   *GitHub*

Maintainer   *Dec 2018 - PRESENT*

- A package to run Jest testing inside of emacs with a magit popup.