# Sean Moore

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# **EDUCATION**

#### **PhD. Quantitative Life Sciences**

Montreal, CA | Sep 2022 - Present

McGill University

**BSc. Honours Computer Science and Biology, Minor in Mathematics** 

Montreal, CA | Sep 2018 - Apr 2022

McGill University

GPA: 3.79, First Class Honours

# RESEARCH EXPERIENCE

#### FRANCOIS LAB | PHD. ROTATION 3

Université de Montréal | Apr 2023 - Sept 2023

- Analyzing T-Cell responses to antigens to understand the dynamics of different antigen qualities.
- Using machine learning and generative modeling to quantify high dimensional time series data in a low dimensional latent space while preserving information.

#### WEBER LAB | PhD. ROTATION 2

McGill University | Jan 2023 - Apr 2023

- Replicated and extended current methods of simulating and analyzing multi-component phase separation.
- Developed and implemented methods to analyze the physics of phase separated droplets in live cells.
- Worked to verify and reproduce results that support current models of phase separation in nucleoli.

#### **VOGEL LAB | PhD. ROTATION 1**

McGill University | Sept 2022 - Dec 2022

- Developed program to analyze biases in intrinsically disordered regions of proteins based on the NARDINI algorithm.
- Used automated tracking pipeline to analyze microscope image data to obtain quantitative information about a system and develop a model to quantify cell division structures.

#### VYBIHAL LAB | VOLUNTEER

McGill University | Sept 2020 - Dec 2020

- Developed and published (https://github.com/ruitaiS/vybLab) novel machine learning models for online learning and unsupervised classification.
- Operated under strict time and space constraints as model was to be deployed on a robot with limited hardware and processing resources.

## **WORK EXPERIENCE**

## **GUARDIAN THERAPEUTICS | BIOINFORMATICS CONSULTANT**

Lexington, MA | Apr 2021 - Present

- Design and maintain a pipeline to process and analyze sequence data from laboratory experiments.
- Design and implement algorithms to process large amounts of RNA sequence data.
- Design, implement, and maintain a web server to facilitate the usage of above algorithms and efficiently store database files.

## IDEXX LABORATORIES | RAPID ASSAY PROJECT MANAGEMENT INTERN Westbrook, ME | Jun 2019 - Aug 2019

- Facilitated multiple parasitology prevalence studies for canine parasites.
- Worked with R&D to develop novel devices for onsite assays to increase parasite detection in household pets.

# OFFICE OF THE HARBORMASTER | Assistant to the Harbormaster Yarmouth, ME | Jun 2016 - Aug 2021

- Assisted the Harbormaster with his duties.
- Patrolled local waterways and warfs within the Harbormaster's jurisdiction.
- Managed the use of the town landing, licensing, and permitting with the public.

# PRIZES AND AWARDS

**GRAD EXCELLENCE AWARD | McGill University** 

\$8,000 | Jul 2022

QLS GRAD AWARD | QUANTITATIVE LIFE SCIENCE, McGILL UNIVERSITY

\$20,000 | Jul 2022

QLS 3MT COMPETITION 3RD PLACE | QUANTITATIVE LIFE SCIENCE, McGILL UNIVERSITY

Dec 2022

**IDEXX INTERN POSTER COMPETITION 1ST PLACE LIDEXX** 

Aug 2019

# LEADERSHIP

**VP FINANCE | QUANTITATIVE LIFE SCIENCES STUDENT ASSOCIATION** 

2023-2024

**BUDDY | QLS BUDDY PROGRAM** 

2023-2024

PRESIDENT | McGill Nordic Ski Team

2021-2022

VP FINANCE | McGill Nordic Ski Team

2020-2021, 2022-2023

# CONFERENCES AND WORKSHOPS

PHYSICAL BASIS OF CELLULAR MEMORY AND ADAPTION | CHAIR

April 2023

**QLS ANNUAL RESEARCH DAY | POSTER PRESENTATION** 

January 2023

# **PROJECTS**

**LLPSSIM ☑** 

SIMULATION, PHASE SEPARATION, JULIA

Developed a simulation in order to predict the number and composition of different phases that arise from specific component interaction strengths.

NARDS ☑ NULL MODEL, IDR, JULIA

Developed NARDS, (Nonrandom Arrangements of Residues in Disordered Shuffles) a tool for analyzing biases in the composition of intrinsically disordered regions of proteins. Originally, the program was written in python. I rewrote it in the Julia programming language to optimize for speed and flexability.

## R-GEN ☑

#### RUST, BAYESIAN INFERENCE, GENERATIVE MODELING

Developed a generative modeling framework written in the Rust programming language. Currently has support for arbitrary model construction and simple inference such as importance sampling. Currently working to improve api usability and out of the box support for more advanced algorithms such as Metropolis Hastings and particle filters.

TORAT 🔀 RUST. DATABASE

Developed a simple command line application written for the Office of the Maine State Treasurer. Allows for the screening and identification of out-of-state bank routing numbers to detect fraudulent COVID relief checks.

#### **OCEANIC MONITORING BUOY**

#### C, Arduino, Environment, Data Collection

Designed and deployed the electronic system on an oceanic monitoring buoy. Programmed an Arduino board to collect readings from temperature, turbidity, disolved oxygen, and electrical conductivity sensors at regular intervals and transmit the results over a 2G cellular network to the mainland.

# SKILLS

Programming Languages: Rust, Julia, Java, C++, Python, C#, Bash, C, R, Kotlin, OCaml Databases: SQL, MongoDB

Web Development: Vue, JavaScript, HTML/CSS

Technology: Git, DigitalOcean, Docker, LATEX

**Language:** English (Native), French (Intermediate)

Coursework: Honors Algorithms and Datastructures (COMP 252), Honors Algorithm Design (COMP 352), Probabilistic Programming (COMP 596), AI (COMP 424), Intro to Software Systems (COMP 206), Operating Systems (COMP 310), Intro to Computer Systems (COMP 273), Intro to Ecology and Evolution (BIOL 215), Intro to Phys Mol & Cell Biol (BIOL 219), Organic Chemistry 1 (CHEM 212), Basic Genetics (BIOL 202), Mathematical Models in Biology (BIOL 309), Comp. Biol. Methods & Research (COMP 561), Biodiversity and Ecosystems (BIOL 310), Eukaryotic Cell Biology (BIOL 313), Principles of Cellular Control (BIOL 551)