

Nathan T. Lawlor

Email: Nathan.lawlor03@gmail.com

Website: <https://nlawlor.github.io> ♦ LinkedIn: [linkedin.com/in/nathan-lawlor-01707280/](https://www.linkedin.com/in/nathan-lawlor-01707280/)

ABOUT ME

Accomplished cellular biologist and data scientist with 4+ years of hands-on laboratory, bioinformatics, data mining, programming, and software development experience. Currently developing and applying data analytic strategies to decipher the underlying causes of human diseases such as Type 2 diabetes and aging. My mission is to provide data-driven translational solutions for the improved diagnosis, treatment, and prevention of these diseases to maximize patient health and wellness.

EDUCATION

Master of Science in Microbial Systems Analysis

University of Connecticut / Storrs, CT / December 2015

Bachelor of Science in Biology; Minor: Environmental Studies

Boston College / Chestnut Hill, MA / May 2014

SKILLS

Programming Languages: R (Fluent), Python (Intermediate), SQL (Intermediate), JAVA (Beginner)

Integrated Development Environments: RStudio (R), Jupyter Notebook (Python)

Software: Trimmomatic, BWA, TopHat, Bowtie, STAR, Cufflinks, RSEM, QoRTs, SAMtools, HOMER, Picard Tools

Data Science Libraries: ggplot2, dplyr, tidyr, shiny, Seurat, Matrix, monocle, cicero, pandas, scikit-learn (sklearn)

Online Genetic Resources: NCBI PubMed, BLAST, OMIM, ClinVar, GEO, SRA, and UCSC Genome Browser

RESEARCH AND WORK EXPERIENCE

Research Data Analyst II

The Jackson Laboratory for Genomic Medicine / Farmington, CT / January 2018 – Present

- Facilitate collaborations between laboratories to reduce funding costs by 25% while maintaining project efficiency
- Create 5 software packages and R shiny web applications for analysis and visualization of genomics data
- Provide bioinformatics, programming, and data analysis training to 5-10 graduate students and staff scientists

Research Data Analyst I

The Jackson Laboratory for Genomic Medicine / Farmington, CT / January 2016 – January 2018

- Implemented R, Python, SQL and UNIX shell software for interpretation of over 100 genomics datasets
- Produced the lab's first scientific publication (currently cited over 100 times) and wrote 4 first-author papers in the first two years of joining the lab
- Responsible for processing, analysis, and visualization of chromatin interaction (Hi-C, ChIA-PET), epigenome (ChIP-seq, ATAC-seq), genetic (exome, eQTL), and single cell omics (sc-RNA-seq, sc-ATAC-seq) data

Co-Op Associate Intern

The Jackson Laboratory for Genomic Medicine / Farmington, CT / May 2015 – Aug 2015

- Analyzed 14 distinct human cancer gene expression datasets to identify patterns associated with clinical outcome
- Developed a Bioconductor R package (*multiClust*) to streamline analysis
- Presented research findings to department of 10-15 computer scientists and later published the work in a scientific journal

Graduate Student Research Associate

University of Connecticut / Storrs, CT / Sept 2014 – May 2015, Sept 2015 – Dec 2015

- Extracted RNA and DNA from 5-10 mammalian tissues for RT-PCR and gel electrophoresis
- Operated confocal microscope to characterize unique cell types and image 50-100 slides each week
- Trained 3-5 graduate students in de-novo genome assembly strategies and beginner-level bioinformatics

SELECT PUBLICATIONS

“(Epi)genomic heterogeneity of pancreatic islet function and failure in type 2 diabetes”. N. Lawlor and M. L. Stitzel. *Molecular Metabolism*. 2019 Sept. <https://www.sciencedirect.com/science/article/pii/S2212877819305629?via%3Dihub>

“Multiomic Profiling Identifies cis-Regulatory Networks Underlying Human Pancreatic β Cell Identity and Function” N. Lawlor, E. J. Marquez, P. Orchard, N. Narisu, M. S. Shamim, *et al.*. *Cell Reports*. 2019 Jan 15. [https://www.cell.com/cell-reports/fulltext/S2211-1247\(18\)32043-6](https://www.cell.com/cell-reports/fulltext/S2211-1247(18)32043-6)

“Genomics of Islet (Dys)function and Type 2 Diabetes” N. Lawlor, S. Khetan, D. Ucar, and M. L. Stitzel. *Trends in Genetics*. 2017 Feb 25. <https://www.ncbi.nlm.nih.gov/pubmed/28245910>

“Single-cell transcriptomes identify human islet cell signatures and reveal cell-type-specific expression changes in type 2 diabetes” N. Lawlor*, J. George*, M. Bolisetty, R. Kursawe, L. Sun, Sivakamasundari V, I. Kycia, P. Robson, and M. L. Stitzel. *Genome Research*. 2016 Nov 18. <https://genome.cshlp.org/content/early/2017/01/16/gr.212720.116> [* equal contributor]