

Nathan T. Lawlor

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EDUCATION

University of Connecticut, Storrs, CT

December 2015

Professional Science Master's in Microbial Systems Analysis

Boston College, Chestnut Hill, MA

May 2014

Bachelor of Science in Biology

Minor: Environmental Studies

TECHNICAL SKILLS

Languages: R (Fluent), Python (Intermediate), Perl (Intermediate), JAVA (Beginner), MATLAB (Beginner), HTML (Beginner)

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

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

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

RESEARCH AND WORK EXPERIENCE

The Jackson Laboratory for Genomic Medicine, Farmington, CT

January 2018 – Present

Laboratories of Michael Stitzel, Ph.D. and Duygu Ucar, Ph.D.

Position: *Research Data Analyst II*

- Co-lead bioinformatics analyst for a Human Cell Atlas project associated with the Chan Zuckerberg Initiative (CZI)
- Develop, publish, and maintain R packages (*iasva*, *BiFET*) on Bioconductor/GitHub via Git version control
- Explore and mine large single cell genomics datasets consisting of > 30,000 single cells
- Use high performance computing (HPC) LINUX environment and TORQUE resource manager for analyses
- Create R shiny web applications for sharable and interactive browsing/visualization of genomic data

The Jackson Laboratory for Genomic Medicine, Farmington, CT

January 2016 – January 2018

Laboratory of Michael Stitzel, Ph.D.

Position: *Research Data Analyst I*

- Responsible for processing, analysis, and visualization of chromatin interaction (Hi-C, ChIA-PET), epigenome (ChIP-seq, ATAC-seq) and transcriptome (RNA-seq) next generation sequencing (NGS) data
- Organized, maintained, and deposited NGS data in NCBI public repositories
- Implemented R, Python, and UNIX shell software for interpretation of NGS data
- Applied tools in Adobe Illustrator and Photoshop to design artwork for manuscript publications

The Jackson Laboratory for Genomic Medicine, Farmington, CT

May 2015 – Aug 2015

Laboratory of Krishna Karuturi, Ph.D.

Position: *Co-Op Associate Intern, Computational Sciences*

- Used statistical and data clustering methods in R to identify cancer gene expression patterns associated with clinical outcome
- Created and developed a Bioconductor R package (*multiChust*) to streamline data analysis

University of Connecticut, Storrs, CT

Sept 2014 – May 2015, Sept 2015 – Dec 2015

Laboratory of Spencer Nyholm, Ph.D.

Position: *Graduate Student Research Associate*

- Extracted RNA and DNA from mammalian tissues for reverse-transcriptase PCR and gel electrophoresis
- Library preparation and next generation sequencing of bacterial isolates on an Illumina MiSeq
- Operated confocal microscope to characterize unique cell types in mammalian tissue

SELECT PUBLICATIONS

“A Common Type 2 Diabetes Risk Variant Potentiates Activity of an Evolutionarily Conserved Islet Stretch Enhancer and Increases C2CD4A and C2CD4B Expression” I. Kycia, B. Wolford, J. Huyghe, C. Fuchsberger, S. Vadlamudi, R. Kursawe, *et al.* (N. Lawlor). *American Journal of Human Genetics* 102, no. 4 (April 5, 2018): 620–35. <https://doi.org/10.1016/j.ajhg.2018.02.020>

“Alpha TC1 and Beta-TC-6 genomic profiling uncovers both shared and distinct transcriptional regulatory features with their primary islet counterparts” N. Lawlor*, A. Youn*, R. Kursawe, D. Ucar, and M. L. Stitzel. *Scientific Reports*. 2017 Sept 20. <https://www.nature.com/articles/s41598-017-12335-1> [* equal contributor]

“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]