Nathan T. Lawlor, M.S.
CURRICULUM VITAE

CONTACT INFORMATION

The Jackson Laboratory for Genomic Medicine
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EDUCATION

2014 – 2015 **Professional Science Master's in Microbial Systems Analysis**
University of Connecticut, Storrs, CT
Advisor: Joerg Graf, Ph.D.

2010 – 2014 **Bachelor of Science in Biology**
Boston College, Chestnut Hill, MA

PROFESSIONAL EXPERIENCE

2018 – present **Research Data Analyst II**
The Jackson Laboratory for Genomic Medicine, Farmington, CT
Supervisors: Michael Stitzel, Ph.D., and Duygu Ucar, Ph.D.

2016 – 2018 **Research Data Analyst I**
The Jackson Laboratory for Genomic Medicine, Farmington, CT
Supervisor: Michael Stitzel, Ph.D.

2015 – 2015 **Co-op Associate Intern, Computational Sciences**
The Jackson Laboratory for Genomic Medicine, Farmington, CT
Supervisors: Joshy George, Ph.D., Krishna Karuturi, Ph.D.,

2014 – 2015 **Graduate Student Research Associate**
University of Connecticut, Storrs, CT
Advisor: Spencer Nyholm, Ph.D.

2013 – 2014 **Undergraduate Student Research Associate**
Boston College, Chestnut Hill, MA
Advisors: YingYing He, Ph.D., and David Newburg, Ph.D.

RESEARCH EXPERIENCE

Research Data Analyst II January 2018 – present
The Jackson Laboratory for Genomic Medicine, Farmington, CT
Simultaneously manage data analysis strategies in the type 2 diabetes lab as well as co-lead a project involving characterizing human immune cell types for the Chan-Zuckerberg Initiative and Human Cell Atlas Project.

Research Data Analyst I January 2016 – January 2018
The Jackson Laboratory for Genomic Medicine, Farmington, CT
Main data analyst in a lab studying the (epi)genomic and environmental bases of type 2 diabetes. Responsible for analysis and visualization of all next-generation sequencing data produced in the lab.

Co-op Associate Intern May 2015 – August 2015
The Jackson Laboratory for Genomic Medicine, Farmington, CT
Created an R package (*multiClust*) for convenient comparison of gene ranking and data clustering strategies and applied this software to identify cancer gene expression patterns associated with patient clinical outcome.

Graduate Student Research Associate Sept 2014 – December 2015
University of Connecticut, Storrs, CT
Performed various molecular biology techniques to quantify gene and protein expression levels of galectin receptors in the Hawaiian bobtail squid *Euprymna scolopes*. Operated a confocal microscope to characterize hemocyte cells in this organism.

Undergraduate Student Research Associate January 2013 – May 2014
Boston College, Chestnut Hill, MA
Responsible for culturing and maintaining ten different human intestinal cancer cell lines for use in various experiments carried out by postdoctoral and scientific research staff. Utilized western blot and ELISA to measure protein levels of innate immune (toll-like) system receptors before and after antigen stimulation.

RESEARCH SKILLS

- Proficient at working in LINUX/UNIX high-performance computing environments for bioinformatics analyses.
- Utilization of R, Python, Perl, and UNIX shell software for analysis of various types of next generation sequencing (NGS) data
- Skilled at creating software packages in integrated development environments (RStudio) and maintaining through Git version control
- Experience with developing web applications (R shiny) for sharable and interactive browsing, analysis, and visualization of large datasets

Programming languages:
- R (Fluent)
- Python (Intermediate)
- UNIX shell (Intermediate)
- Perl (Intermediate)
- JAVA (Beginner)
- HTML (Beginner)

Operating Systems:
- Mac OS X
- Windows
- Linux/UNIX

PUBLICATIONS

1. "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.* (*in review*).

2. "BiFET: Sequencing Bias-free Transcription Factor Footprint Enrichment Test" A. Youn, E. J. Marquez, **N. Lawlor**, M. L. Stitzel, and D. Ucar (*in review*).

3. "Robust detection of hidden variation in single cell transcriptomes using Iteratively Adjusted-SVA (IA-SVA)" D. Lee, A. Cheng, **N. Lawlor**, M. Bolisetty, and D. Ucar (*in review*).

4. "Type 2 Diabetes associated genetic variants regulate chromatin accessibility in human" S. Khetan, R. Kursawe, A. Jillette, A. Youn, **N. Lawlor**, E. J. Marquez, D. Ucar, and M. L. Stitzel (*in review*).

5. "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

6. "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]

7. "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

8. "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]

9. "multiClust: An R-package for Identifying Biologically Relevant Clusters in Cancer Transcriptome Profiles" **N. Lawlor*,** A. Fabbri*, P. Guan, J. George, and K. Karuturi. *Cancer Informatics.* 2016 Jun 12. https://www.ncbi.nlm.nih.gov/pubmed/27330269 [* equal contributor]

10. "Human Milk Components Modulate Toll-Like Receptor–Mediated Inflammation" Y. He*, **N. Lawlor***, D. S. Newburg. *Advances in Nutrition.* 2016 Jan 7. https://www.ncbi.nlm.nih.gov/pubmed/26773018

11. "The human milk oligosaccharide 2'-fucosyllactose modulates CD14 expression in human enterocytes, thereby attenuating LPS-induced inflammation" Y. He, S. Liu, D. E. Kling, S. Leone, **N. Lawlor**, Y. Huang, S. B. Feinberg, D. R. Hill, D. S. Newburg. *Gut*. 2014 Nov 27. https://www.ncbi.nlm.nih.gov/pubmed/25431457

ORAL PRESENTATIONS

1. University of Connecticut Molecular Cell Biology Professional/Career Development Seminar, Storrs, CT, April 13th, 2017.
2. The Jackson Laboratory for Genomic Medicine, Summer Student Symposium, Farmington, CT, August 14th, 2015.