

# Michael Lafferty

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## Education

**University of North Carolina**, Chapel Hill, NC, May 2022  
**School of Medicine**  
**PhD, Bioinformatics and Computational Biology**  
Jason Stein Laboratory  
Department of Genetics and Neuroscience Center

**University of Michigan**, Ann Arbor, MI, May 2010  
**College of Engineering**  
**B.S.E. Chemical Engineering**  
Concentration in Life Sciences  
Minor in Biochemistry

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## Professional/Research Experience

**Watershed Informatics**, Cambridge, MA, Apr 2023 – Present  
**Bioinformatician**

- Develop bioinformatics solutions for biologists and bioinformaticians across multiple fields to accelerate research and discovery of novel diagnostics and therapeutics
- Create data analysis workflows and pipelines using python, R, and the Watershed Platform
- Provide consultation and advice on multi-omic data analysis (RNA-seq, Single-Cell RNA-seq, Whole Genome Sequencing, Genome-wide Association Studies)
- Interpret and distill public databases to enable customized data analysis (UK Biobank, ChEMBL, OpenTargets, GTEx)

**University of North Carolina Medical School**, Chapel Hill, NC, May 2017 – Mar 2023  
**Postdoctoral Research Associate**, May 2022 – Mar 2023

**Graduate Research Assistant**, May 2017 – May 2022

Dept. of Genetics and Neuroscience Center, Dr. Jason Stein Laboratory

- Dissertation work investigating the role of genetic variation on gene expression in the developing human neocortex (mRNA/miRNA eQTLs)
- Implicate genes and genetic regulatory elements as possible mechanisms for developmental neuropsychiatric disorders via GWAS colocalizations
- Develop data analysis pipelines for:
  - Next generation sequencing data (RNA-seq, ATAC-seq)
  - Gene expression data (microarrays, differential gene expression)
  - Genotyping and imputation analysis (1000 Genomes/TOPMed)
- Investigate the biological pathways associated with neuronal proliferation and differentiation in human neural progenitor cells:
  - Primary cell culture (lentivirus generation/transduction)
  - RNA extraction and quantification (qPCR, RNA-seq, microarray)
  - Immunocytochemistry and image analysis (high-content imaging, CellProfiler)

## Professional/Research Experience (cont.)

**University of North Carolina Medical School**, Chapel Hill, NC, Jan 2016 – Aug 2016  
**Research Technician**, Dept. of Biochemistry and Biophysics, Dr. Saskia Neher Laboratory

- Developed molecular models of structural homologous proteins using the Rosetta molecular modeling suite of software (collaboration with Brian Kuhlman lab, UNC Chapel Hill)
- Studied enzyme inhibition kinetics of mutated and chimeric lipases using fluorometric assays
- Designed and purified proteins using e. coli and mammalian tissue culture techniques

**KBI Biopharma**, Research Triangle Park, NC, Jun 2015 – Jan 2016  
**Process Development Associate**, Downstream Process Development

- Developed unit operations for purification of novel biopharmaceuticals including monoclonal antibodies and therapeutic enzymes
- Scaled development purification processes for transfer to manufacturing
- Ran pilot plant unit operations for sizing studies and material generation

**Cytonet LLC**, Durham, NC, Jan 2014 – Jun 2015  
**Development Scientist**, Process and Product Development

- Optimized a cGMP liver cell isolation process in order to improve product quality and yield
- Developed a counter-flow centrifugal elutriation purification strategy to increase yield and reduce processing time
- Designed and implemented primary hepatocyte viability and functionality assays
- Authored SOPs for technology transfer between R&D and manufacturing departments
- Designed and executed experiments using DOE principles

**University of North Carolina Medical School**, Chapel Hill, NC, May 2011 – Dec 2013  
**Research Technician**, Dept. of Biochemistry and Biophysics, Dr. Saskia Neher Laboratory

- Computationally modeled protein structures using distributed computing resources
- Studied protein-protein interactions using molecular docking simulations
- Purified recombinant protein constructs using liquid chromatography, precipitation, and diafiltration
- Designed and optimized protein purification protocols for maximum purity and yield
- Developed enzyme activity assays using fluorescence and absorbance spectroscopy
- Probed protein-protein interactions using chemical cross linking, SDS-PAGE, western blotting, and enzyme kinetics
- Modeled inhibition kinetics data using Mathematica and Matlab software
- Investigated protein structure using macromolecular crystallography and atomic force microscopy

**University of Michigan Medical School**, Ann Arbor, MI, May 2010 – May 2011  
**Research Technician Associate**, Dept. of Radiation Oncology, Dr. Alnawaz Rehemtulla Lab

- Developed brain, pancreatic, and lung cancer mouse models for in vivo drug efficacy screening
  - Monitored tumor apoptosis in living mice using MRI and bioluminescence imaging
  - Studied protein-protein interactions by immunoprecipitations and immunohistochemistry
  - Oversaw laboratory safety, chemical hygiene, and hazardous waste management
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## Teaching

### **Biology 423L**, Spring 2020

Teaching assistant for Prof. Sarah Grant; senior level laboratory course in yeast genetics

### **How to Learn to Code**

Designed and taught course in introductory coding for graduate students and post-docs

**In R**, Summer 2018

**In Python**, Summer 2017

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## Committees

**Bioinformatics and Computational Biology Steering Committee**, Sep 2019 – May 2022

**Bioinformatics and Computational Biology Student Invited Speaker Committee**, Sep 2018 – Sep 2020

**Biological and Biomedical Science Program First Year Group Mentor**, Sep 2018 – Aug 2020

**Bioinformatics and Computational Biology Social Committee**, Sep 2017 – Sep 2018

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## Awards

**National Institute of General Medical Sciences T32 Bioinformatics and Computational Biology Training Grant** (5 T32 GM 67553-13), Aug 2017 – Aug 2018

**International Society of Psychiatric Genetics, Early Career Investigator Program, Poster Presentation Awardee**, Oct 2020

**UNC Bioinformatics and Computational Biology Research Retreat, Best Poster**, March 2019

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## Professional Development

**Molecular Psychiatry Association**, Mar 2022

Poster/Abstract: MicroRNA-eQTLs in developing human neocortex identify MIR4707 as a regulator of human brain size, Lahaina, Hawaii

**American Society of Human Genetics**, Oct 2021

Poster/Abstract: Genetic variants regulating microRNA expression in the developing human neocortex, Virtual

**World Congress of Psychiatric Genetics**, Oct 2020

Poster/Abstract: Genetic variants regulating microRNA expression in the developing human neocortex, Virtual

**UNC Bioinformatics and Computational Biology Research Retreat**, Sep 2019

Talk: The impact of common genetic variation on microRNAs associated with neurogenesis in the developing human neocortex, Wilmington, NC

**Leena Peltonen School of Human Genomics**, Aug 2019

Talk: The impact of common genetic variation on microRNAs associated with neurogenesis in the developing human neocortex, Les Diablerets, Switzerland

**UNC Computational Medicine Research in Progress Seminar Series**, May 2019

Talk: Novel microRNAs associated with neurogenesis in the developing human cerebral cortex, Chapel Hill, NC

**Neuroscience 2018 Presenter**, Nov 2018

Poster/Abstract: MicroRNAs associated with neurogenesis in the developing human cerebral cortex, San Diego, CA

**Advanced Genetic Epidemiology Statistical Workshop**, Oct 2017

Virginia Commonwealth University, Richmond, VA

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## Computational Skills and Classes

**Programming/Scripting Languages:** R, Python, Bash, Java, C++

**Bioinformatic Skills:** Sequence analysis, cluster and dimensionality reduction, exploratory data analysis, linear modeling, data normalization, gene ontology analysis, gene set enrichment analysis, differential gene expression analysis, colocalization analysis, enrichment analysis

**Bioinformatic Tools:** PLINK, STAR, Bowtie, Salmon, Picard tools, GRanges, DESeq2, Peer, matrixEQTL, EMMAX, Gviz

**Development Tools:** Rmarkdown, git, Github, Bitbucket, Slurm, LSF

**Classes:** Bio-algorithms, Programming Concepts, Data Structures, Applied Discrete Mathematics, C and Software Tools, Computer Organization and Assembly Language

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## Publications

**Lafferty, M.J.**, Aygün, N., Patel, N.K., Krupa, O., Liang, D., Wolter, J.M., Geschwind, D.H., de la Torre-Ubieta, L., Stein, J.L., (2023). MicroRNA-eQTLs in the developing human neocortex link miR-4707-3p expression to brain size. [eLife](https://doi.org/10.7554/eLife.79488). doi.org/10.7554/eLife.79488

Wolter, J.M., Le, B.D., Matoba, N., **Lafferty, M.J.**, Aygun, N., Liang, D., Courtney, K., Piven, J., Zylka, M., Stein, J.L., (2022). Cellular genome wide association study identifies common genetic variation influencing lithium induced neural progenitor proliferation. [Biological Psychiatry](https://doi.org/10.1016/j.biopsych.2022.08.014). doi.org/10.1016/j.biopsych.2022.08.014

Aygün, N., Elwell, A. L., Liang, D., **Lafferty, M. J.**, Cheek, K. E., Courtney, K. P., Mory, J., Hadden-Ford, E., Krupa, O., de la Torre-Ubieta, L., Geschwind, D. H., Love, M. I., & Stein, J. L. (2021). Brain-trait-associated variants impact cell-type-specific gene regulation during neurogenesis. [American Journal of Human Genetics](https://doi.org/10.1016/j.ajhg.2021.07.011), 108(9), 1647–1668. doi.org/10.1016/j.ajhg.2021.07.011

Liang, D., Elwell, A. L., Aygün, N., Krupa, O., Wolter, J. M., Kyere, F. A., **Lafferty, M. J.**, Cheek, K. E., Courtney, K. P., Yusupova, M., Garrett, M. E., Ashley-Koch, A., Crawford, G. E., Love, M. I., de la Torre-Ubieta, L., Geschwind, D. H., & Stein, J. L. (2021). Cell-type-specific effects of genetic variation on chromatin accessibility during human neuronal differentiation. [Nature Neuroscience](https://doi.org/10.1038/s41593-021-00858-w), 24(7), 941–953. doi.org/10.1038/s41593-021-00858-w

Goldfarb, D., **Lafferty, M. J.**, Herring, L. E., Wang, W., & Major, M. B. (2018). Approximating Isotope Distributions of Biomolecule Fragments. [ACS Omega](https://doi.org/10.1021/acs.omega.8b01649), 3(9), 11383–11391. doi.org/10.1021/acs.omega.8b01649

Hayne, C. K., Yumerefendi, H., Cao, L., Gauer, J. W., **Lafferty, M. J.**, Kuhlman, B., Erie, D. A., & Neher, S. B. (2018). We FRET so You Don't Have To: New Models of the Lipoprotein Lipase Dimer. [Biochemistry](https://doi.org/10.1021/acs.biochem.7b01009), 57(2), 241–254. doi.org/10.1021/acs.biochem.7b01009

Hayne, C. K., **Lafferty, M. J.**, Eglinger, B. J., Kane, J. P., & Neher, S. B. (2017). Biochemical Analysis of the Lipoprotein Lipase Truncation Variant, LPLS447X, Reveals Increased Lipoprotein Uptake. *Biochemistry*, 56(3), 525–533. doi.org/10.1021/acs.biochem.6b00945

**Lafferty, M. J.**, Bradford, K. C., Erie, D. A., & Neher, S. B. (2013). Angiopoietin-like protein 4 inhibition of lipoprotein lipase: Evidence for reversible complex formation. *Journal of Biological Chemistry*, 288(40), 28524–28534. doi.org/10.1074/jbc.M113.497602

Galbán, S., Jeon, Y. H., Bowman, B. M., Stevenson, J., Sebolt, K. A., Sharkey, L. M., **Lafferty, M. J.**, Hoff, B. A., Butler, B. L., Wigdal, S. S., Binkowski, B. F., Otto, P., Zimmerman, K., Vidugiris, G., Encell, L. P., Fan, F., Wood, K. V., Galbán, C. J., Ross, B. D., & Rehemtulla, A. (2013). Imaging Proteolytic Activity in Live Cells and Animal Models. *PLoS ONE*, 8(6). doi.org/10.1371/journal.pone.0066248

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