

Michael Lafferty

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[Website](#) | [LinkedIn](#) | [GitHub](#)

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

Professional/Research Experience

Datapol Solutions, Boston, MA, Remote, Aug 2024 – Present

Senior Bioinformatics Scientist

- Support early-stage biotech startups with bioinformatic strategies for drug discovery and development

Watershed Bio, Cambridge, MA, Apr 2023 – July 2024

Bioinformatician

- Developed bioinformatics solutions for biologists and bioinformaticians across multiple fields to accelerate research and discovery of novel diagnostics and therapeutics
- Created data analysis workflows and pipelines using python, R, and distributed computing environments
- Provided consultation and advice on multi-omic data analysis (RNA-seq, Single-Cell RNA-seq, Whole Genome Sequencing, Genome-wide Association Studies)
- Integrated public databases to enable customized target identification (CCLE, TCGA, 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)
- Implicated genes and genetic regulatory elements as possible mechanisms for developmental neuropsychiatric disorders via GWAS colocalizations
- Developed data analysis pipelines for next generation sequencing data (RNA-seq, ATAC-seq), gene expression data (microarrays, differential gene expression), and genotyping and imputation analysis (1000 Genomes/TOPMed)
- Investigated the biological pathways associated with neuronal proliferation and differentiation in human neural progenitor cell culture (lentivirus generation/transduction, qPCR, RNA-seq, ICC/IHC)

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

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

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

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

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

Publications

Glass, M.R., Waxman, E.A., Yamashita, S., **Lafferty, M.J.**, Beltran, A., Farah, T., Patel, N.K., Matoba, N., Ahmed, S., Srivastava, M., Drake, E., Davis, L.T., Yeturi, M., Sun, K., Love, M.I., Hashimoto-Torii, K., French, D.L., Stein, J.L., (2024). Cross-site reproducibility of human cortical organoids reveals consistent cell type composition and architecture. *Stem Cell Reports* (accepted). doi.org/10.1101/2023.07.28.550873

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*. 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*. 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*, 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*, 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*, 3(9), 11383–11391. doi.org/10.1021/acsomega.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*, 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
