

MICHAEL LAFFERTY

Bioinformatics | Multi-omic Data Analysis

CONTACT

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

Raleigh, NC

EDUCATION

PhD Bioinformatics and Computational Biology

University of North Carolina
Chapel Hill, NC, 2022

BSE Chemical Engineering

University of Michigan
Ann Arbor, MI, 2010

LANGUAGES

Python | R | Bash | Java | C++

SKILLS

Single-cell sequence analysis
Genome-wide association
Dimensionality reduction
Linear modeling
Data normalization
Gene ontology analysis
Gene set enrichment analysis
Colocalization analysis
Enrichment analysis

TOOLS

PLINK | Seurat | Scanpy
STAR | Bowtie | Salmon
Picard | Granges | DESeq2
matrixEQTL | EMMAX | GSEA

PROFILE

I am a PhD in Bioinformatics and Computational Biology with over 13 years of industry and academic experience working in both dry-lab and wet-lab settings. I have a track record of rigorous science, bioinformatic expertise, and clear and concise communication. I love working on complex problems in a fast-paced and collaborative environment.

EXPERIENCE

SENIOR BIOINFORMATICS SCIENTIST, Aug 2024 – Present
DATAPOL SOLUTIONS, Boston, MA - Remote

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

BIOINFORMATICIAN, Apr 2023 – July 2024
WATERSHED BIO, Cambridge, MA

- Developed data analysis workflows and pipelines using python, R, and distributed computing environments
- Provided consultation on multi-omic data analysis (RNA-seq, Single-Cell RNA-seq, WGS, GWAS)
- Integrated public databases to enable customized target identification (TCGA, UK Biobank, ChEMBL, OpenTargets, GTEx)

POSTDOCTORAL RESEARCH ASSOCIATE, May 2022 – Mar 2023
GRADUATE RESEARCH ASSISTANT, May 2017 – May 2022
UNIVERSITY OF NORTH CAROLINA, Chapel Hill, NC

- Investigated 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
- Assessed reproducibility of human cortical organoid differentiations using single-cell rna-sequencing
- Developed data analysis pipelines for:
 - o Next generation sequencing (RNA-seq, ATAC-seq)
 - o Gene expression data (differential expression, enrichment)
 - o Genotyping and imputation analyses (1000 Genomes/TOPMed)
- Investigated biological pathways associated with neuronal proliferation and differentiation using human primary neural progenitor cells (primary cell culture, rna extraction, ICC/IHC)

PROCESS DEVELOPMENT ASSOCIATE, June 2015 – Jan 2016
KBI BIOPHARMA, Research Triangle Park, NC

Developed unit operations for purification of novel biopharmaceuticals and scaled development purification processes for transfer to manufacturing