MICHAEL LAFFERTY

Bioinformatics | Human Genomics

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

R | Python | Bash | Java | C++

SKILLS

Sequence analysis
Dimensionality reduction
Linear modeling
Data normalization
Gene ontology analysis
Gene set enrichment analysis
Colocalization analysis
Enrichment analysis

TOOLS

PLINK | Seurat | STAR | Bowtie
Salmon | Picard | Granges
DESeq2 | matrixEQTL
EMMAX | Gviz

PROFILE

I am a PhD in Bioinformatics and Computational Biology with over 12 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

BIOINFORMATICIAN, Apr 2023 – Present
WATERSHED BIO, Cambridge, MA
- Developed 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, WGS, GWAS)
- Interpret and distill public databases to enable customized data analysis (UK Biobank, ChEMBL, OpenTargets, GTEx)

POSTDOCTORAL RESEARCH ASSOCIATE, May2022 – Mar2023
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:
  - Next generation sequencing (RNA-seq, ATAC-seq)
  - Gene expression data (microarrays, differential gene expression)
  - 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 and quantification
  - Immunocytochemistry and image analysis

PROCESS DEVELOPMENT ASSOCIATE, Jun 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