James R Rose

412-445-8323
Jrrose5@emory.edu
307 Candler St NE
Atlanta GA, 30307

Computational biologist PhD, Former biotech/pharmaceutical bench scientist. Studying gene regulation and epigenetics of the immune system.

Looking for opportunities to apply my quantitative & computational analysis skills towards interesting biological questions in translational research

Skills

Data Analysis
- Next generation sequencing (NGS) analysis & pipeline development (QC, alignment, peak calling, single-cell RNAseq)
- Data visualization (ggplot, observable)
- Machine learning & gene regulatory network analysis
- Statistical modeling and inference

Programming
- R (tidyverse), python, bash & JavaScript
- Shiny App development
- DESeq2, BEDtools, PageRank, Homer, VCFtools
- Git, Docker, Rstudio server
- Remote server operations

Domain Knowledge
- Immunology (B & T cell)
- Epigenetics
- DNA methylation
- Translational research (autoimmunity, SLE)

Education

PhD Genetics & Molecular Biology, Emory University, 2019-2024 (expected)

Master's Biotechnology, Penn State University, 2011-2013

B.S. Biotechnology, Penn State University, 2008-2013

Research Experience

Graduate Research Assistant, Emory Genetics and Molecular Biology program
Emory University – *2019 to Present*
Advisor: Jeremy M Boss

- Applying computational biology tools to study gene regulation (RNAseq/scRNAseq) of immune cells (T cells & B cells) in the context of immune memory and autoimmune disease
- Thesis project focused on correlating clinical metrics (disease activity) with gene regulation and epigenetics (ATACseq) of immune cells in systemic lupus erythematosus (SLE). Collaboration with Dr. Ignacio Sanz MD of Emory University

Senior Associate Scientist, Janssen Research & Development, Biotherapeutics Development
Johnson & Johnson – *2016 to 2019*
- Implemented statistical process control technologies for monoclonal antibody manufacturing at international GMP facilities
- Authored sections of BLA and other regulatory filings

Engineer I, Cell Culture Technical Development
Biogen – *2013 to 2016*
- Mammalian cell culture process development role. Pilot plant and technology transfer operations
- Pioneered use of stochastic (Monte Carlo) simulation modeling for manufacturing facility fit analysis

Teaching

Guest Lecturer & TA, *Fall 2022*
IBS519: Statistical rigor, reproducibility, and experimental design
- Developed supporting materials for revamped course curriculum
- Lectured on data visualization principles and use of ggplot2 in R to incoming graduate students

Graduate Teaching Assistant, *Fall 2020 & 2021*
IBS500R: Intro to data analysis using R

Selected Publications

- Rose, J. R. *et al.* Distinct transcriptomic and epigenomic modalities underpin human memory T cell subsets and their activation potential. *Commun Biol* **6**, 363 (2023).
- Yusho Ishii, James Rose, *et al.* Distinct Transcriptomic and Epigenetic Profiles Mediated by Disease Activity in SLE. Poster, Arthritis & Rheumatology 74, 22-23, (2022).