# James R Rose

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*Computational biologist PhD, former biotech/pharmaceutical bench scientist. Expertise in multi-omic data analysis, translational research, and the immune system.*

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

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## Skills

*Data Analysis*

- Next generation sequencing (NGS) bioinformatics analysis & pipeline development (QC, alignment, peak calling, single-cell RNAseq, ATACseq)
- 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, 2019-2023 (expected Fall)

**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. *Advisor: Jeremy M Boss.*
Emory University, Atlanta GA – *Aug. 2019 to Present*

- Apply comp bio tools to study gene regulation of immune cells by generating hypothesis or biological insight from sequencing data
- Current project: correlating clinical metrics (disease activity) with gene regulation and epigenetics (ATACseq) of immune cells in systemic lupus erythematosus (SLE).
- Thesis focus: Integration of multi-omic sequencing datasets

***Senior Associate Scientist*****,** Janssen Research & Development, Biotherapeutics Development
Johnson & Johnson, Malvern PA – Aug. *2016 to Jun. 2019*

- Led a team of development researchers on process development, new technology implementation, and regulatory submissions for therapeutic product worth $6B in annual sales
- 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, Durham NC– Jun. *2013 to Aug. 2016*

- Developed mammalian cell culture processes for monoclonal antibody production at large-scale manufacturing
- Pioneered use of stochastic (Monte Carlo) simulation modeling for manufacturing facility fit analysis

## Teaching

**Course lecturer & TA,** *Fall 2022, 2023*
IBS519: Statistical rigor, reproducibility, and experimental design

- Developed teaching materials for revamped course curriculum
- Lecture 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, Ishii Y., et al. Clinically inactive SLE resting naïve B cells retain distinct transcriptomes and durable alterations to the epigenome. (*In preparation*)
- Rose, J. R., Akdogan-Ozdilek, B., *et al*. Distinct transcriptomic and epigenomic modalities underpin human memory T cell subsets and their activation potential. *Commun Biol* **6**, 363 (2023).

*Github:* https://github.com/jrose835 *Mastodon:* @jrose835@genomic.social