

# JAMES SACCO

## Bioinformatics Scientist

Doudna Lab

Howard Hughes Medical Institute, Department of Molecular and Cell Biology, University of California, Berkeley  
Berkeley, CA, 94720


Independent, self-motivated bioinformatics scientist, with **six years** of combined experience in cancer immunotherapy and **gene therapy**. Specialist in computational biology of **CRISPR gene editing**. An analytical thinker and quick learner, with experience in next-generation sequencing (**NGS**) methods, such as **RNA-Seq**, and development of **reproducible, robust pipelines**.

Integrated genotype-phenotype data to predict disease severity. Developed **machine learning** applications to analyze population-scale genomics and real-world patient data.

 [Download the PDF on Github.](#)


## CONTACT INFO

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For more information, please  
contact me via email.



## EXPERIENCE

Present  
|  
2022



### Bioinformatics Scientist



Howard Hughes Medical Institute, Department of Molecular and Cell Biology, University of California, Berkeley

 Berkeley, CA

- Design and implement **bioinformatic pipelines to handle NGS data** from both prokaryotic and eukaryotic samples.
- Analyze and present both **genomic (DNA-seq)** and **transcriptomic (RNA-seq)** datasets using R.
- Perform **differential gene expression** analyses on RNA-seq data.
- Map genome deletions/insertions/mutations to chromosomal locations.

2022  
|  
2021



### Bioinformatics Scientist



ASC Therapeutics (Contract)

 Milpitas, CA

- Quantify and characterize **CRISPR gene modifications**, with both custom and open-source tools for genomic data analysis.
- Query, retrieve, and integrate data from public genomics databases, to enhance on-target gene editing with sequence alignment protocols.
- Examine concordance and sensitivity of five open-source CRISPR off-target detection methods (**CALITAS**, **CHANGE-Seq**, **CRISPResso**, **GUIDE-Seq**, and **Cas-OFFinder**).
- Streamline high-performance analyses for bench scientists by constructing **custom data pipelines**.

## KEY SKILLS

Expert programming in **Python**, **R**,  
and **shell scripting**

Extensive experience with  
**statistical, NGS data analyses**  
(differential gene expression, gene  
set enrichment, variant annotation)  
and workflow development

Proficient in several *in silico*  
**CRISPR gene editing** modules

Familiar with public **genomic  
repositories** (NCBI, Ensembl);  
genomic data types and  
sequencing tools (Illumina, IGV,  
Galaxy, BEDtools, SAMtools,  
**DESeq**, **edgeR**, Hail)

2020  
|  
2019

## Biomarker Data Analyst II

Genentech

Genentech (Contract)

📍 South San Francisco, CA

- Established department-first **machine learning pipeline** to study effects of biomarker operations on quality of cancer immunotherapy assays.
- Upgraded **data operations** for six data streams, including flow cytometry, biomarker operations, and oncology data warehouses.
- Monitored and solved sample data quality issues for two cancer immunotherapy trial arms.

2019  
|  
2018

## Data Curator

Genentech

Genentech (Contract)

📍 South San Francisco, CA

- Collaborated with AI engineers to create an ETL pipeline for **multi-modal survival prediction and patient stratification**, by using Python ML and R to integrate **gene panel** and **RNA-Seq data**.
- Designed ETL data pipeline for integration of **real-world EHRs** into **deep learning** module, using Python, SQL, and Apache Spark.
- Organized and managed close coordination of Artificial Intelligence, data management, and DevOps functions, to bring **clinical machine learning** from prototype to production.

2018  
|  
2017

## Data Curator, Bioinformatics Analyst

BIOMARIN

BioMarin Pharmaceutical (Contract)

📍 San Rafael, CA

- Established an integrated genetic and curated literature workflow to predict incidence and prevalence rates of **over sixty rare, genetic disorders**, with **statistical and data visualization R packages (ggplot2)** and **MATLAB**.
- Upgraded and tested **RNA-Seq data pipeline (STAR2, SAMtools, Bioconductor)** to discern disease contribution of **rare variants** to neural disease.
- Spearheaded development of three relational databases derived from **Hail population genomics platform**, in collaboration with software engineer.
- Co-authored manuscript submitted to peer-reviewed publication, on **prediction of disease severity** in metachromatic leukodystrophy.
- Developed **allele-specific association models and GWAS analysis software** for two later published manuscripts.

## PROGRAMMING SKILLS

📊 R

🐍 Python

🐧 Linux

🔑 Git

🌐 GitHub

📄 Markdown

🔧 C++

📐 MATLAB

## LANGUAGES

English: Native

Spanish: Bilingual Proficiency

2017  
|  
2016

## Research Associate



University of Miami Miller School of Medicine, The Miami Project to Cure Paralysis, Pearse Lab

📍 Miami, FL

- Mentored research associates in developing bioinformatic skills, specifically in **multiple sequence alignment** and **standard molecular biological protocols** (restriction enzyme digestion, gel electrophoresis, spectrophotometry).
- Identified over forty putative **conserved vertebrate phosphodiesterase proteins**, by using multiple sequence alignment and genomic evidence.



## EDUCATION

### Rowan University, Graduate School of Biomedical Sciences

Master of Biomedical Science (Distinction)

📍 Stratford, NJ

"Hippocampal long-term potentiation in neurodegenerative disorders"

### Florida International University, The Honors College

BSc, Biological Sciences

📍 Miami, FL



## PROFESSIONAL DEVELOPMENT

2021

### Introduction to Genomic Technologies

Johns Hopkins University

📍 Online

2021

### Statistics for Genomic Data Science

Johns Hopkins University

📍 Online

2016

### Software Carpentry for R and UNIX

University of Miami

📍 Miami, FL



## PUBLICATIONS

2016

Regulating Axonal Responses to Injury: The Intersection between Signaling Pathways Involved in Axon Myelination and The Inhibition of Axon Regeneration.

*Frontiers in Molecular Neuroscience*. 2016 Jun 8;9:33.

Rao S.N., Pearse D.D. **Manuscript Editor**

I am an active member of Biostars



**Biostars**  
BIOINFORMATICS EXPLAINED

I have participated in several bioinformatics and software workshops and *Meetup.com* groups, in both Seattle, WA and San Francisco, CA, including:

*SF/Bay AI Developers Group*

*San Jose Data Science and AI/ML Meetup*

*Hacker Dojo*

*Seattle Sequencing*





### EXTRA-CURRICULAR

San Francisco chapter of *Big Gay Frisbee*. 2018 - Present.

Salsa dancing at *In Lak'ech Dance Academy*. 2019.

*Seattle Quake* rugby club. 2016 - 2017.


## CONFERENCE PAPERS


- 2020 • Prediction of disease severity in metachromatic leukodystrophy using measures of protein activity and a novel phenotype matrix.  
 *American Society of Human Genetics Virtual Meeting.*  
[Poster] [Forthcoming on bioRxiv.org]  
 Online  
Trinidad M., Hong X., **Sacco J.**, Nguyen H.P., Clark W.T., Froelich S., LeBowitz J.H., Gelb M.H.
- 2018 • Association of HGMD and gnomAD variants of unknown significance with prediction of disease incidence and prevalence.  
 *BioMarin Internal Research and Development Asilomar Conference.* [Poster]  
 Pacific Grove, CA  
**Sacco J.**, Clark W.T., Yu K., Wu K., LeBowitz J.H.

## RESEARCH PROJECTS

- 2019 • Characterization of glycan substrates accumulating in GM1 gangliosidosis  
*Molecular Genetics and Metabolism Reports.* 2019. 21, p.100524.  
[doi:10.1016/j.ymgmr.2019.100524](https://doi.org/10.1016/j.ymgmr.2019.100524)  
Lawrence R., et al.
- 2018 • Utilizing ExAC to assess the hidden contribution of variants of unknown significance to Sanfilippo Type B incidence.  
*PLoS One.* 2018. 13(7):e0200008.  
[doi:10.1371/journal.pone.0200008](https://doi.org/10.1371/journal.pone.0200008)  
Clark W.T., et al.

## TEACHING

- 2009 • Peer-Led Team Learning (PLTL)  
*Florida International University*  Miami, FL  
General Biology II facilitator for two concurrent PLTL courses

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