

# JAMES SACCO

Pronouns: they/them/theirs

**Bioinformatics Scientist**  
**Department of Gene and Cell Therapy**  
**ASC Therapeutics**  
**Milpitas, CA, 95035**


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  
|  
2021

### Bioinformatics Scientist



ASC Therapeutics

 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.
- Spearhead implementation of version control, and programming best practices.

2020  
|  
2019

### Biomarker Data Analyst II



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.

## KEY SKILLS

Extensive experience with **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, BEDtools, SAMtools, **DESeq**, **edgeR**, Hail)

2019  
|  
2018

## Data Curator



### 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 machine learning and R/Bioconductor 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 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 R statistical and visualization 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 HPC 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.

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.

## PROGRAMMING SKILLS



## LANGUAGES

**English:** Native

**Spanish:** Proficient/Native

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recent version of this resume is  
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## 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**



## 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.

I am an active member of Biostars



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.



## 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