

JAMES SACCO

Laboratory for Genomics Research, Department of Biochemistry & Biophysics, University of California, San Francisco, San Francisco, CA 94158, USA

Self-motivated **computational biologist** with **six years of both academic and industry experience** in: functional genomics (CRISPR-based screens), population genetics, and pipeline automation.


An analytical thinker and quick learner, with broad understanding of **statistical and machine learning methods**. Published author of research studies in the integration of genotype and phenotype data to **model disease prevalence, and sub-types**. Pre-clinical research experience in Mendelian disorders and immunology, specifically cancer immunotherapy. Advocate for diversity and inclusion of under-represented minorities in science.




View this CV online with links at
<https://jsacco1.github.io/cv/>

SELECTED EXPERIENCE

Present
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2022

- **Bioinformatics Programmer III**
 **Laboratory for Genomics Research & Department**
Biochemistry & Biophysics, University of California, San Francisco
San Francisco, CA
 - **Develops algorithms, computational tools, and statistical methods** to analyze and interpret biological data.
 - **Multi-omic data analysis** for optimization of genome-wide **CRISPRi/a** transcriptional regulation in generic cell lines.
 - **Computational lead** on CRISPR screen focused on lysosomal storage and mitochondrial dysfunction in Niemann-Pick Type C Disease.

2022
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2021

- **Bioinformatics Scientist**
 **ASC ASC Therapeutics (Contract)**
Milpitas, CA
 - Quantified and characterized **CRISPR gene modifications**, with both custom and open-source tools for genomic data analysis.
 - Queried, retrieved, and integrated data from public genomics databases, to enhance on-target gene editing with **sequence alignment** protocols.
 - Examined concordance and sensitivity of **five computational CRISPR off-target detection methods**.
 - Streamlined high-performance analyses for bench scientists via **custom data pipelines** and **user interfaces**.

CONTACT INFO

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For more information, please
contact me via email

Work authorization: US Citizen

KEY SKILLS

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

Experience with **multi-omic data**
analysis and integration

Proficiency with *in silico* analysis
modules for **single cell RNA-Seq**
& **CRISPR screening protocols**

Machine learning, applied
statistics, and experimental design

High scientific rigor & willingness
to teach and learn about new
computational methods and
biology

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
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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
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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

Python ★★★★★

R ★★★★★

Linux ★★★★★

Git ★★★★★

GitHub ★★★★★

Markdown ★★★★★

SQL ★★★★★

Dash ★★★★★

C++ ★★★★★

MATLAB ★★★★★

2017
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2016

Research Associate



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

📍 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"

Related coursework:

- Biochemistry
- Molecular Biology
- Cell Biology
- Microbiology
- Pharmacology

Florida International University, The Honors College

BSc, Biological Sciences

📍 Miami, FL



PROFESSIONAL DEVELOPMENT

2022

Bulk and Single Cell Transcriptomics Training Program

OmicsLogic

📍 Online

2022

Python for Data Science: Fundamentals Part I Course

Dataquest.io

📍 Online

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

Active member of Biostars



Biostars
BIOINFORMATICS EXPLAINED

I have participated in 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

LANGUAGES

English: Native

Spanish: Bilingual Proficiency



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 in Genome Biology]**

📍 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.

Avid supporter of the San Francisco Symphony and San Francisco Conservatory of Music

Ultimate frisbee at *Big Gay Frisbee*. San Francisco, CA. 2018 – Present.

Salsa dance at *In Lak'ech Dance Academy*. Oakland, CA. 2019.

Rugby at *Seattle Quake RFC*. Seattle, WA. 2016 – 2017.



RESEARCH PROJECTS

2019

- [Characterization of glycan substrates accumulating in GM1 gangliosidosis](#)
Molecular Genetics and Metabolism Reports. 2019. 21, p.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.
Clark W.T., et al.

2017

- [Phosphodiesterase Inhibitors as a Therapeutic Approach to Neuroprotection and Repair](#)
International Journal of Molecular Sciences. 2017. 18(4): 696.
Knott E.P., et al.

ORAL COMMUNICATIONS

2022

- [Data Visualization of RNA-Seq Differential Expression Analysis with DESeq2](#)



[Doudna Lab](#): Howard Hughes Medical Institute, Department of Molecular and Cell Biology, University of California, Berkeley

📍 Berkeley, CA

Topics: Introduction to RNA-Seq, Standard Workflows with DESeq2, Reference-Based Assembly, Exploratory Data Analysis, Statistical Analysis, Data Visualization, Gene Set Enrichment, Variant Annotation

- Presented publication-quality RNA-Seq data summaries and representations to post-doctoral associates

TEACHING

2009

- [Peer-Led Team Learning](#)

Florida International University

📍 Miami, FL

General Biology II facilitator for two concurrent PLTL courses

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