

JAMES SACCO

Laboratory for Genomics Research, University of California, San Francisco, San Francisco, CA 94158, USA

Self-motivated **computational biologist** with **seven years of both academic and industry experience** in: functional genomics, population genetics, and workflow automation.

An analytical thinker and quick learner, with broad understanding of **statistical and machine learning methods**, **gene regulatory network inference**, and **multi-omic single cell data analysis**. Published author of in the association of curated genotype and phenotype data to model **disease prevalence, and subtypes of Mendelian disorders**. Extensive experience in **AI and biomarker data analysis** to advance **cancer immunotherapy in clinical trials**. Advocate for diversity and inclusion 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**
UCSF Laboratory for Genomics Research, University of California, San Francisco
San Francisco, CA
 - Led investigation of computational rules for **CRISPR interference (CRISPRi) guide RNA design** optimization, using **Python machine learning modules**.
 - Improved whole-genome targeting of promoter regions in a **genome-wide CRISPRi dual-guide library** in K562 cancer cell lines.
 - **Identified over 100 putative therapeutic targets**, as computational lead on a CRISPRi screen focused on cellular dysfunction in Niemann-Pick Type C Disease.
 - Integrated **single-cell epigenetic and transcriptomic data** to computationally reconstruct **gene regulatory networks** for seventy-six transcription factors in iPSC-derived cells.
 - Mentored two junior programmers on the computational biology team.
 - Co-authored a manuscript officially intended for publication, on in-house experimental findings.

CONTACT INFO

✉ jsacco001@gmail.com

🔗 jsacco1.github.io

🌐 github.com

in [linkedin.com](https://www.linkedin.com)

📞 +1 (786)-473-9993

For more information, please contact me via email.

Work authorization: US Citizen

KEY SKILLS

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

Proficiency with **single cell gene expression, gene regulation, and epigenetic data analyses**, genomic data repositories, **machine learning**, experimental design, and CRISPR screening tools.

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

2022
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2021

Bioinformatics Scientist



ASC Therapeutics

📍 Milpitas, CA

- Quantified and characterized **CRISPR gene modifications** in a sickle-cell disease model, with both in-house 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 error detection methods**.
- Streamlined high-performance analyses for bench scientists via **custom data pipelines** and **user interfaces**, enabling round-the-clock analyses.

2020
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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.

2019
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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 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.
- Provided AI and genomic analytic insights in collaboration with Roche-wide data curators and integrators network, to establish F.A.I.R. data management strategies for legacy, current, and next-generation datasets
- Tested data querying capabilities of newly-acquired AWS-based tech stack.
- Scoped design of in-house proteomics assay data ingestion and storage

PROGRAMMING SKILLS

🐍 Python ★★★★★

📊 R ★★★★★☆

🐧 Linux ★★★★★☆

🔑 Git ★★★★★

📄 Markdown ★★★★★

📁 C++ ★★★★★☆

📐 MATLAB ★★★★★☆

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 **R statistical and data visualization packages** 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.

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

"Mechanisms of synaptic signaling dysfunction in hippocampal long-term potentiation"

Related coursework:

- Biochemistry
- Molecular Biology
- Cell Biology
- Mechanisms of Disease
- Pharmacology

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 Proficiency

Spanish: Native Proficiency

Dutch: Intermediate Proficiency

- Florida International University, The Honors College
BSc, Biological Sciences  Miami, FL



PROFESSIONAL DEVELOPMENT

- 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







PUBLICATIONS

- 2023 ● Predicting disease severity in metachromatic leukodystrophy using protein activity and a patient phenotype matrix.
Genome Biology. 2023 Jul 24:172.
Trinidad M., Hong X., Froelich S., Daiker J., **Sacco J.**, Phuc Nguyen H., Campagna M., Suhr D., Suhr T., LeBowitz J.H., Gelb M.H., Clark W.T.
- 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**



CONFERENCES

- 2023 ● Single Cell Analyses
 *Cold Spring Harbor Laboratory Single Cell Analyses Meeting.*
 Cold Spring Harbor, New York
- 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]  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** *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.
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
hhmi 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
- 2022 • Changes in chromatin accessibility are not concordant with transcriptional changes for single-factor perturbations
UCSF Laboratory for Genomics Research & Department Biochemistry & Biophysics, University of California, San Francisco
📍 San Francisco, CA
- Presented now-published preprint in contrast with established research at internal Journal Club to inform future experimental design in epigenetic editing.

HOBBIES

Stonewall Sports kickball. San Francisco, CA. 2023 – Present.

Ultimate frisbee player. San Francisco, CA. 2018 – Present.

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



TEACHING

2009



[Peer-Led Team Learning](#)

Florida International University

📍 Miami, FL

General Biology II facilitator for two concurrent PLTL courses

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Last update: 2023-11-13. The most recent version of this resume is [available here](#).