

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 (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
|
2022

Bioinformatics Programmer III

 **Laboratory for Genomics Research**, University of California, San Francisco

 San Francisco, CA

- Led investigation of computational rules for **CRISPRi guide design** using open-source machine learning algorithms.
- Optimized of genome-wide **CRISPRi/a** transcriptional regulation in cancer cell lines, using epigenomic and genomic data analysis.
- **Computational lead** on CRISPR screen focused on lysosomal storage and mitochondrial dysfunction in Niemann-Pick Type C Disease.
- Integrated **single-cell epigenetic and transcriptomic data** to identify **gene regulatory networks** driving cell differentiation.
- Mentored junior programmers joining computational biology team.

2022
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2021

Bioinformatics Scientist




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

 jsacco001@gmail.com

 jsacco1.github.io

 github.com

 [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**

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
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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 ★★★★★

🗄️ SQL ★★★☆☆

🔗 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
- Microbiology
- 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: Limited Working 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

- 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 BMC 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
- 2022 • [Changes in chromatin accessibility are not concordant with transcriptional changes for single-factor perturbations](#)
 **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.

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: 2023-03-24. The most recent version of this resume is [available here](#).