

JAMES SACCO

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.

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

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.

EXPERIENCE

Present
|
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**, **command line tools**, and **user interfaces**.
- Generate reproducible reports for publication-quality manuscripts.

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.

KEY SKILLS

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

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

Proficiency with *in silico* **CRISPR**
gene editing modules

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

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



Bioconductor (**DESeq2**,
edgeR)

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.

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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.

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.

PROGRAMMING SKILLS

R

Python

Linux

Git

GitHub

Markdown

Dash

C++

MATLAB

LANGUAGES

English: Native

Spanish: Bilingual Proficiency

Active member of Biostars



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



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

- 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 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 *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.

PRESENTATIONS

- 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

EXTRA-CURRICULAR


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.

TEACHING

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

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