

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
|
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)

Data Curator

Genentech
(Contract)

South
San
Francisco,
CA

2019

-
2018

- 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.

Data Curator, Bioinformatics Analyst

BiOMARIN

BioMarin Pharmaceutical (Contract)

San Rafael, CA

2018 - 2017

- 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.

Research Associate



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

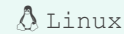
Miami, FL

2017 - 2016

- 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





EDUCATION

Rowan University, Graduate School of Biomedical Sciences

Master of Biomedical Science (Distinction)

Stratford, NJ

N/A

"Hippocampal long-term potentiation in neurodegenerative disorders"

Florida International University, The Honors College

BSc, Biological Sciences

Miami, FL



PROFESSIONAL DEVELOPMENT

Bulk and Single Cell Transcriptomics Training Program

Pine Biotech, Tauber Bioinformatics Research Center

Online

2022

Python for Data Science: Fundamentals Part I Course

Dataquest.io

Online

2022

Introduction to Genomic Technologies

Johns Hopkins University

Online

2021

Statistics for Genomic Data Science

Johns Hopkins University

Online

2021

Software Carpentry for R and UNIX

University of Miami

Miami, FL

2016

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

LANGUAGES

English: Native

Spanish: Bilingual Proficiency



PUBLICATIONS

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.

N/A

2016

Rao S.N., Pearse D.D. **Manuscript Editor**



CONFERENCE PAPERS

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

2020

Trinidad M., Hong X., **Sacco J.**, Nguyen H.P., Clark W.T., Froelich S., LeBowitz J.H., Gelb M.H.

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

2018

Sacco J., Clark W.T., Yu K., Wu K., LeBowitz J.H.



RESEARCH PROJECTS

Characterization of glycan substrates accumulating in GM1 gangliosidosis

Molecular Genetics and Metabolism Reports. 2019. 21, p.100524.

N/A

2019

Lawrence R., et al.

Utilizing ExAC to assess the hidden contribution of variants of unknown significance to Sanfilippo Type B incidence

PLoS One. 2018. 13(7):e0200008.

N/A

2018

Clark W.T., et al.

Phosphodiesterase Inhibitors as a Therapeutic Approach to Neuroprotection and Repair

International Journal of Molecular Sciences. 2017. 18(4): 696.

N/A

2017

Knott E.P., et al.



PRESENTATIONS

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

2022

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

Peer-Led Team Learning

Florida International University

Miami, FL

2009

General Biology II facilitator for two concurrent PLTL courses

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.

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