

JAMES SACCO

Pronouns: they/them/theirs

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.

 [Download the PDF on Github.](#)

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

📍 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.
- Spearhead implementation of version control, and programming best practices.

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

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

Proficient in several ***in silico* CRISPR gene editing** modules

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

2019
|
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 machine learning and R/Bioconductor 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
|
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 visualization 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 HPC 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
|
2016

Research Associate



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

📍 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

LANGUAGES

English: Native

Spanish: Proficient/Native

This resume was built with using **R pagedown**.

Code available on [GitHub](#).

Last update: 2022-01-26. The most recent version of this resume is [available here](#).



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

- 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 Internal Research and Development Asilomar Conference. [Poster] Pacific Grove, CA
Sacco J., Clark W.T., Yu K., Wu K., LeBowitz J.H.

I am an active member of Biostars



I have participated in several 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

EXTRA-CURRICULAR

San Francisco chapter of *Big Gay Frisbee*. 2018 - Present.

Salsa dancing at *In Lak'ech Dance Academy*. 2019.

Seattle Quake rugby club. 2016 - 2017.



RESEARCH PROJECTS

2019



Characterization of glycan substrates accumulating in GM1 gangliosidosis

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

[doi:10.1016/j.ymgmr.2019.100524](https://doi.org/10.1016/j.ymgmr.2019.100524)

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.

[doi:10.1371/journal.pone.0200008](https://doi.org/10.1371/journal.pone.0200008)

Clark W.T., et al.



TEACHING

2009



Peer-Led Team Learning (PLTL)

Florida International University

📍 Miami, FL

General Biology II facilitator for two concurrent PLTL courses