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.

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-performace 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.

Download the PDF on Github.

CONTACT INFO

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For more information, please contact me via email.

KEY SKILLS

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

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 (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 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

C++

CSS

HTML

MATLAB

LANGUAGES

English: Native

Spanish: Bilingual Proficiency

*This resume was made with ♥ using R **pagedown**.*

Last update: 2022-01-27.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.
ASHG *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.

I am an active member of Biostars
Biostars BIOINFORMATICS EXPLAINED

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
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
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