JAMES SACCO

They/Them/Theirs

Bioinformatics Scientist
Doudna Lab
Howard Hughes Medical Institute, University of California, Berkeley
Berkeley, CA, 94720

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 | 2022

Bioinformatics Scientist

hhmi Howard Hughes Medical Institute, University of California, Berkeley

Berkeley, CA

- Design and implement **bioinformatic pipelines to handle NGS data** from both prokaryotic and eukaryotic samples.
- Analyze and present both **genomic (DNA-seq) and transcriptomic (RNA-seq)** datasets using R.
- Perform **differential gene expression** analyses on RNA-seq data.
- Map genome deletions/insertions/mutations to chromosomal locations.

2022 | 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**.

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 **statistical, 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, IGV, Galaxy, BEDtools, SAMtools, **DESeq**, **edgeR,** Hail)

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.

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 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.

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 **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.

PROGRAMMING SKILLS

R

Python

Linux

Git

GitHub

Markdown

C++

MATLAB

LANGUAGES

English: Native

Spanish: Bilingual Proficiency

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.

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**

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.

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.

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

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