

JAMES SACCO

Bioinformatics Scientist
Department of Gene and Cell Therapy
ASC Therapeutics
Milpitas, CA 95035

Self-motivated **bioinformatics programming professional** with **six years** of experience in support of **rare disease and cancer therapies**. Areas of expertise include **transcriptomics**, **CRISPR gene editing**, development of robust, reproducible **data workflows** for scientific user interfaces.

An analytical thinker and quick learner, with a broad understanding of **statistical and machine learning methods**. Published author of research studies in the integration of genotype and phenotype data to **model disease progression and epidemiology**.

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

CONTACT INFO

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For more information, please
contact me via email

SELECTED 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**
and public genomic repositories

Proficiency with *in silico* **CRISPR**
gene editing analysis modules for
on/off-target characterization

Experience with **scRNA-Seq** data
analysis of **CRISPR screens**

Machine learning and applied
statistics

Data engineering & pipeline
development (AWS, Airflow,
PySpark)

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

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
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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.

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

Python ★★★★★

R ★★★★★

Linux ★★★★★

Git ★★★★★

GitHub ★★★★★

Markdown ★★★★★

SQL ★★★★★

Dash ★★★★★

C++ ★★★★★

MATLAB ★★★★★



EDUCATION

- Rowan University, Graduate School of Biomedical Sciences
 Master of Biomedical Science (Distinction) 📍 Stratford, NJ

 "Hippocampal long-term potentiation in neurodegenerative disorders"

 Related coursework:
 - Biochemistry
 - Molecular Biology
 - Cell Biology
 - Microbiology
 - Pharmacology
- Florida International University, The Honors College
 BSc, Biological Sciences 📍 Miami, FL



PROFESSIONAL DEVELOPMENT

- 2022 ● 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
- 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**

Active member of Biostars



Biostars
BIOINFORMATICS EXPLAINED

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

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.
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.

Avid supporter of the San Francisco Symphony and San Francisco Conservatory of Music



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.


ORAL COMMUNICATIONS

2022

- [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
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

2009

- [Peer-Led Team Learning](#)
Florida International University  Miami, FL
General Biology II facilitator for two concurrent PLTL courses

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