JAMES SACCO

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

Independent, self-motivated bioinformatics scientist, with five years of experience in cancer immunotherapy and gene therapy for rare diseases. Specialist in computational biology of CRISPR gene editing. An analytical thinker and quick learner, with experience in next-generation sequencing (NGS) methods, especially RNA-Seq, and construction of reproducible and robust analysis pipelines. Integrated genotype phenotype data to predict disease severity. Developed machine learning applications to analyze population-scale genomic and real-world patient data. Experienced with cross-functional teams of diverse cultural and technical backgrounds.

EMPLOYMENT

Present | 2021

Bioinformatics Scientist

ASC Therapeutics — Milpitas, CA

- Support NGS experiments to quantify and characterize on/off-targets of gene modifications by performing data wrangling and analysis, using open-source methods (e.g., CALITAS, CHANGE-Seq, CRISPResso2, GUIDE-Seq, Cas-OFFinder) and custom scripts.
- Query, retrieve, and integrate data from public genomics databases, to characterize alignments between CRISPR target sequences and guide RNAs.
- Compare concordance and sensitivity of five CRISPR off-target detection methods.
- Spearhead implementation of reproducible, robust bioinformatics data practices

2020 | 2019

Biomarker Data Analyst

Genentech — South San Francisco, CA

- Established department-first machine learning pipeline to study effects of biomarker operations on quality of cancer immunotherapy assays.
- Generated over ten percent annual operation cost reduction via analysis of vendor performance over twenty clinical sites.
- 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 clinical trial arms.

CONTACT INFO

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For more information, please contact me via email.

SKILLS

Extensive experience with NGS data analysis and workflow development

Hands-on experience in sequencing pipelines and tools, such as: Illumina, BEDtools, SAMtools, DESeq, edgeR

Proficient in several *in silico* CRISPR gene editing and RNA-Seq analysis tools and methods

Programming Skills

- R
- Python
- Linux
- Git
- GitHub

2019 | 2018

Data Curator
Genentech — 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.

● Tested and refined a textual entity and geolocation matching pipeline for clinical trial site management, resulting in over 90% accuracy.

● 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 gRED Artificial Intelligence, data management, and DevOps functions, to bring clinical machine learning from prototype to production.

2018 | 2017

Data Curator, Bioinformatics Analyst
BioMarin Pharmaceutical — 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.

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 — Stratford, NJ

Florida International University, The Honors College
BSc, Biological Sciences — Miami, FL

PUBLICATIONS & POSTERS

2020

Prediction of disease severity in metachromatic leukodystrophy using measures of protein activity and a novel phenotype matrix.
American Society of Human Genetics. **[Forthcoming on bioRxiv.org; pending acceptance in PLoS Genetics]**
M. Trinidad, X. Hong, **J. Sacco**, H.P. Nguyen, W.T. Clark, S. Froelich, J.H. LeBowitz, M.H. Gelb.

2018

Association of HGMD and gnomAD variants of unknown significance with prediction of disease incidence and prevalence.
Annual BioMarin Research Conference. **[Poster]**
J. Sacco, W.T. Clark, K. Yu, K. Wu, J.H. LeBowitz.

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. **Acknowledgement**

LANGUAGES

English: Native

Spanish: Native