

## RESUME

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### CONTACT INFORMATION

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### EDUCATION

***PhD in Computational Biology***

**Jan 2013 - Feb 2018**

**IISER Bhopal**, Madhya Pradesh, India

- **Thesis:** Development of Computational Models and Algorithms for Designing of Novel Microbiome-based Therapeutics.

***Masters in Pharmacoinformatics***

**July 2010 - June 2012**

**NIPER Mohali**, Punjab, India

- **Thesis:** Modelling and Designing of Glycogen Synthase Kinase 3 Inhibitors.

***Bachelor of Pharmacy***

**Aug 2006 - June 2010**

**Dr. H. S. Gour University, Sagar**, Madhya Pradesh, India

### RESEARCH EXPERIENCE

**Bioinformatics Scientist**

**Sep 2024 - Present**

Digestive and Liver Diseases

Inflammatory Bowel and Immunobiology Research Institute

**Cedars-Sinai Medical Center**

As a Bioinformatician at Cedars-Sinai, I provide computational and analytical expertise to advance translational research and clinical insights through innovative data-driven solutions.

- **Lead computational analysis** of high-dimensional multi-omics datasets (genomics, transcriptomics, metabolomics) to uncover disease mechanisms and study host-microbiome interactions, with a focus on gastrointestinal health and inflammation.
- **Design and optimize scalable, reproducible pipelines** for multi-modal data integration, enabling biomarker discovery and supporting collaborative, multidisciplinary research initiatives.
- **Provide statistical and computational guidance** for study design, including power analysis, and contribute to grant writing and manuscript preparation to drive research innovation.

**Scientist II, Bioinformatics**

**Feb 2023 - Aug 2024**

Drug Safety Research Evaluation (DSRE)

**Takeda**

As a lead computational biologist, I spearheaded safety risk assessment and predictive modeling efforts, leveraging large-scale transcriptomic data (bulk, single-cell, and spatial) to enhance drug discovery pipelines.

- **Developed AI/ML-based models** for predictive analytics and biomarker discovery, enabling data-driven decision-making for project teams.
- **Engineered off-target identification strategies**, including a splicing analysis pipeline for oligonucleotide therapeutics, improving the identification of safer drug candidates.
- **Enhanced transcriptomic analysis workflows** and updated the CellMap visualization dashboard to streamline gene expression analysis across cell lines, optimizing resource utilization.
- **Represented Takeda** in an industry consortium focused on Hepatocarcinoma gene signature development and downstream network analysis.

## Postdoctoral Scientist

Feb 2021 - Jan 2023

### Casero Lab, Cedars-Sinai Medical Center

**Advisor:** Dr. David Casero, *Director, Translational Multiomics, Inflammatory Bowel Immunobiology Research Institute*

I conducted integrative multi-omics analyses to identify pathogenic factors in Inflammatory Bowel Disease (IBD), contributing to the following projects:

- **Multi-omics data integration** to investigate microbial regulation of immune responses in Crohn's disease-associated creeping fat.
- **Quantified bacterial growth rates** from metagenomic datasets to identify microbial activities linked to Crohn's disease progression.
- **Investigated host epithelial gene expression changes** in Ulcerative Colitis (UC) patients post-IPAA surgery using single-cell RNA-seq data.

## Postdoctoral Associate

March 2018 - Feb 2021

### Microbiomics Lab, University of Minnesota

**Mentor:** Dr. Andres Gomez

As the first computational team member in the department, I established and managed computational pipelines on a high-performance computing facility, advancing multi-omics research projects:

- **Analyzed amplicon, metagenomic, and transcriptomic datasets** to study the impact of diet and lifestyle on gut microbial composition and function in human and nonhuman primate populations.
- **Identified host gene expression patterns** in response to gut microbiome alterations using meta-transcriptomic data.
- **Developed computational models for meta-analysis** of microbiome datasets to explore microbiome-host interactions.

## SELECTED SKILLS

- **Programming and Scripting:** Proficient in Python and R for data analysis, algorithm development, and tool creation. Experienced in Unix/Linux environments and SQL for efficient data management and querying.
- **Multi-Omics Data Analysis:** 6+ years of experience in multi-omics data integration (genomics, metagenomics, metatranscriptomics, metabolomics). 2+ years of experience in single-cell RNA-seq and Imaging Mass Cytometry (IMC) data analysis.
- **Statistical Analysis and Machine Learning:** Expertise in multivariate statistics, linear/mixed-effects modeling, predictive analytics, and biomarker identification. Proficient in classification, regression, clustering, and survival analysis for biological datasets.
- **Genomic Data Resources:** Extensive experience with UCSC Genome Browser, Ensembl, ENCODE, NCBI SRA, GEO, GTEx, 1000 Genomes, dbSNP, UniProt, KEGG, MetaCyc, SILVA, Greengenes, and HMDB.
- **Collaboration and Project Management:** Experienced in collaborative development using version control systems (e.g., Git). Skilled in managing projects, timelines, and cross-functional teams.
- **Bioinformatics support:** Proficient in installation, maintenance, and development of bioinformatics tools and pipelines. Experienced in workflow management using Nextflow and Snakemake.
- **Cloud Computing and Data Visualization:** Experienced with AWS and creating interactive dashboards using RShiny and Tableau.

## PROFESSIONAL CONTRIBUTIONS AND ACHIEVEMENTS

**Peer reviewed publications:** 25+; Citations: 1000+, h-index=18, i10-index=24.  
For more details, [please visit Click](#)