# RESUME

CONTACT INFORMATION

**Ashok Kumar Sharma**
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EDUCATION

*PhD in Computational Biology*                    **Jan 2013 - Feb 2018**
**IISER Bhopal**, Madhya Pradesh, India

- **Thesis**: Computational Modeling of Microbial Metabolic Potential Using Genome Assembly, Comparative Genomics, Multi-Omics Integration, and Predictive Modeling.

*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

PROFESSIONAL SUMMARY

Experienced Computational Biologist with 6+ years of expertise in multi-omics data integration, machine learning, and translational research. Proven track record in developing predictive models, discovering biomarkers, and analyzing complex biological datasets—including microbiome, transcriptomics (bulk, single-cell, spatial), and metabolomics—to study host-microbe interactions, microbial-mediated metabolism, and disease mechanisms. Adept at building scalable pipelines, applying AI/ML to biological problems, and driving innovation across academia and industry.

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.

- **Leading 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.
- **Designing and optimizing scalable, reproducible pipelines** for multi-modal data integration, enabling biomarker discovery and supporting collaborative, multidisciplinary research initiatives.
- **Providing statistical and computational guidance** for study design, including power analysis, and contribute to grant writing and manuscript preparation to drive research innovation.

**Scientist II, Computational Biology**                    **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 (for liver and neurotoxicity) 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: <u>Dr. David Casero</u>**, *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: <u>Dr. Andres Gomez</u>**
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, function, and genome-wide adaptations in human and nonhuman primate populations.
- **Identified** host gene expression patterns in response to gut microbiome alterations using meta-transcriptomic data and integrated multi-omics approaches, including comparative genomics and metabolic pathway analysis.
- Developed computational models for meta-analysis of microbiome datasets to explore microbiome-host interactions, incorporating **genome assembly, genome-scale metabolic models, and bacterial growth rate quantification** for functional characterization.

SELECTED SKILLS
- **Programming and Scripting:** Python (PyTorch, scikit-learn, pandas), R (tidyverse, Bioconductor), Unix/Linux, Git, Bash

- **Machine Learning and Statistical Modeling:** Predictive modeling, classification, regression, clustering, dimensionality reduction, survival analysis, biomarker discovery, mixed-effects modeling

- **Multi-Omics and Biological Data Analysis::** 6+ years: Genomics, metagenomics, metatranscriptomics, metabolomics and 2+ years: Single-cell RNA-seq, Spatial transcriptomics, Imaging Mass Cytometry (IMC)

- **Bioinformatics Pipelines and Workflow Automation:** Nextflow, Snakemake, Docker, API integration for scalable and reproducible analysis

- **Cloud Computing and Visualization:** AWS (EC2, S3, Batch), RShiny, Dash, Tableau, interactive dashboards for scientific storytelling

- **Genomic Databases and Tools::** GEO, GTEx, ENCODE, UCSC Genome Browser, UniProt, KEGG, MetaCyc, SILVA, dbSNP

- **Cross-Functional Collaboration and Project Leadership:** Experienced in leading bioinformatics initiatives in cross-disciplinary teams; skilled in communication of complex findings to technical and non-technical audiences

PROFESSIONAL CONTRIBUTIONS AND ACHIEVEMENTS

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