RESUME

Contact Information

Ashok Kumar Sharma

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Education

PhD in Computational Biology **Jan 2013 - May 2018**

IISER Bhopal, Madhya Pradesh, India

- Advisor: Dr. Vineet Kumar Sharma
- **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

- Advisor: Prof. Prasad V. Bharatam
- **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 research experience in multi-omics data analysis/integration, machine learning, predictive modeling, and biomarker identification. Proficient in managing and processing complex biological datasets using advanced computational techniques. Highly skilled in studying host-microbiome interactions and uncovering how the gut microbiome impacts host physiology, with a focus on gastrointestinal systems and health.

Research Experience

Bioinformatics Scientist **Sep 2024 - Present**

Digestive and Liver Diseases
Inflammatory Bowel and Immunobiology Research Institute
Cedars-Sinai Medical Center

As a Lead Bioinformatician at Cedars-Sinai, I provide computational support for diverse data analysis needs to advance translational research and clinical insights.

- **Develop and optimize pipelines** for analyzing large multi-modal datasets, ensuring accuracy and efficiency in high-throughput data processing.
- Support **power analysis and experimental design**, enabling robust study planning and interpretation for various research initiatives.

Scientist II, Computational Biology **Feb 2023 - Aug 2024**

Drug Safety Research Evaluation (DSRE)
Takeda

As a lead computational biologist at DSRE, I drive safety risk assessment through predictive modeling and large-scale transcriptomic (bulk, single, and spatial) data analysis, while spearheading pipeline development to enhance efficiency and consistency in drug discovery research.

- Leveraged **AI/ML-based models** for predictive modeling and biomarker discovery across diverse projects, facilitating informed decision-making for project representatives.
- **Developed off-target identification strategies** including a splicing analysis pipeline for oligonucleotide projects, enhancing the identification of safer oligo candidates.

- Developed a transcriptomic dataanalysis workflow and updated the CellMap visualization dashboard to **check gene expression across cell lines**, improving project efficiency and resource utilization.
- **Represented Takeda in an industry consortium** collaborating on the development of Hepatocarcinoma gene signatures and contributing to downstream network/pathway 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 was involved in the analysis and integration of multi-omics datasets aimed at identifying pathogenic factors in Inflammatory Bowel Disease (IBD). Here is a summary of the specific projects I worked on during that time:

- **Multi-omics data analysis** to uncover microbial regulation of immune responses within creeping fat in Crohn's disease.
- Quantified **bacterial growth rates from metagenomic datasets** to identify activities associated with Crohn's disease progression.
- Investigated **cell-specific gene expression** alterations in the host epithelium of Ulcerative Colitis (UC) patients post-IPAA surgery.

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 was responsible for managing and establishing computational pipelines on a high-performance computing facility at UMN. Furthermore, I played a crucial role in advancing various mutli-omics projects, detailed as follows:

- Analyzed **amplicon, metagenomic, and transcriptomic** datasets to comprehend the impact of diet and lifestyle on gut microbial taxonomic and functional compositions across traditional human and nonhuman primate populations.
- Identified gastrointestinal gene expression patterns in response to functional alterations in the gut microbiome, leveraging **meta-transcriptomic data analysis** techniques.
- Involved in developing innovative and advanced computational models for **meta-analysis of diverse microbiome datasets**, aimed at exploring microbiome-host interactions.

Senior Research Fellow (SRF) **June 2015 - March 2018**
MetaBioSys Lab, IISER Bhopal
Mentor: Dr. Vineet Kumar Sharma

- Developed **machine learning-based computational methods** for the analysis of complex genomic and metagenomic datasets.
- Conducted high-throughput predictions of gut microbial-mediated drug metabolism and toxicity using **chemical structure-centric approaches**.
- Identified taxonomic, functional, and metabolic **markers associated with colorectal cancer** patients in India.

PUBLICATIONS

1. Cohen, J.D., You, D., **Sharma, A.K.**, Takai, T., Hara, H., Sales, V.T., Yukawa, T. and Cai, B., **2024**. In Vitro Human Ion Channel Assays Predictive of Drug Induced Seizure. **Toxicological Sciences**, p.kfae148.
2. Sarode, G.V., Mazi, T.A., Neier, K., Shibata, N.M., Jospin, G., Harder, N.H., Caceres, A., Heffern, M.C., **Sharma, A.K.**, More, S.K. and Dave, M., **2023**. The role of

intestine in metabolic dysregulation in murine Wilson disease. **Hepatology Comm**, 7(10).

3. Guse, K., **Sharma, A.K.**, Weyenberg, E., Davison, S., Ma, Y., Choi, Y., Johnson, A.J., Chen, C. and Gomez, A., **2023**. Regular consumption of lacto-fermented vegetables has greater effects on the gut metabolome compared with the microbiome. **Gut Microbiome** , 4, p.e11.

4. Dina G. Moussa, **Sharma, A.K.**, Tamer Mansour, Bruce Witthuhn; Jorge Perdigao; Joel D. Rudney; Conrado Aparicio; Andres Gomez, **2022**. Functional Biomarkers of Ex-vivo Dental Caries Onset. **Journal of oral microbiology**, 14(1), p.2123624.

5. Rosa, F., **Sharma, A.K.**, Gurung, M., Casero, D., Matazel, K., Bode, L., Simecka, C., Elolimy, A.A., Tripp, P., Randolph, C. and Hand, T.W., **2022**. Human Milk Oligosaccharides Impact Cellular and Inflammatory Gene Expression and Immune Response. **Frontiers in Immunology.** 13: 907529. doi: 10.3389/fimmu.

6. Saxena, R., Prasoodanan PK, V., Gupta, S., Gupta, S., Waiker, P., Samaiya, A., **Sharma, A.K.** and Sharma, V.K., **2022**. Assessing the effect of smokeless tobacco-consumption on oral microbiome in healthy and oral cancer patients. **Frontiers in Cellular and Infection Microbiology**, p.331.

7. Omontese, B.O., **Sharma, A.K.**, Davison, S., Jacobson, E., DiConstanzo, A., Webb, M.J. and Gomez, A., **2022**. Microbiome network traits in the rumen predict average daily gain in beef cattle under different backgrounding systems. **Animal Microbiome**, 4(1), pp.1-15.

8. **Sharma, A.K.**, & Sam Davison; Barbora Pafco; Jonathan B. Clayton, Jessica M. Rothman, Matthew R. McLennan, Marie Cibot, Terence Fuh, Roman Vodicka, Carolyn Jost Robinson, Klara Petrzelkova, and Andres Gomez, **2022**. The primate gut mycobiome bacteriome interface is impacted by environmental and subsistence factors. **npj Biofilms Microbiomes** 8(1), pp.1-11..

9. Vishnu Prasoodanan P K, & **Ashok K Sharma**, Shruti Mahajan, Darshan B Dhakan, Abhijit Maji, Joy Scaria, Vineet K Sharma, **2021**. Western and non-western gut microbiomes reveal new roles of Prevotella in carbohydrate metabolism and mouth-gut axis. **npj Biofilms Microbiomes**, Oct 7;7(1):77.

10. **Sharma, A.K.**, & Petrzelkova, K., Pafco, B., Robinson, C.A.J., Fuh, T., Wilson, B.A., Stumpf, R.M., Torralba, M.G., Blekhman, R., White, B. and Nelson, K.E., Leigh S.R., Gomez A, **2020**. Traditional human and nonhuman primate populations show parallel gut microbiome adaptations to analogous dietary conditions. **mSystems**, 5(6).

11. Gomez, A., **Sharma, A.K.**, Grev, A., Sheaffer, C. and Martinson, K., **2020**. The horse gut microbiome responds in a highly individualized manner to forage lignification. **Journal of Equine Veterinary Science**, 96, p.103306.

12. **Sharma, A.K.**, & Debusk, W.T., Stepanov, I., Gomez, A. and Khariwala, S.S, **2020**. Oral microbiome profiling in smokers with and without head and neck cancer reveals variations between health and disease. **Cancer Prevention Research**, 13(5), pp.463-474.

13. Gupta, A., Dhakan, D.B., Maji, A., Saxena, R., PK, V.P., Mahajan, S., Pulikkan, J., Kurian, J., Gomez, A.M., Scaria, J. and Amato, K.R., **Sharma, A.K.** and Sharma V.K, **2019**, Association of Flavonifractor plautii, a flavonoid degrading bacterium, with the gut microbiome of colorectal cancer patients in India. **mSystems**, 4(6).

14. Gomez, A.*, **Sharma, A.K.***, Mallott, E.K., Petrzelkova, K.J., Robinson, C.A.J., Yeoman, C.J., Carbonero, F., Pafco, B., Rothman, J.M., Ulanov, A. and Vlckova, K, **2019**. Plasticity in the human gut microbiome defies evolutionary constraints. **mSphere**, 4(4), pp.e00271-19.

15. **Sharma, A.K.**, Pafčo, B., Vlčková, K., Červená, B., Kreisinger, J., Davison, S., Beeri, K., Fuh, T., Leigh, S.R., Burns, M.B. and Blekhman, R., Gomez, A, **2019**. Mapping gastrointestinal gene expression patterns in wild primates and humans via fecal RNA-seq. **BMC genomics**, 20(1), p.493.

16. Pafčo, B., **Sharma, A.K.**, Petrželková, K.J., Vlčková, K., Todd, A., Yeoman, C.J., Wilson, B.A., Stumpf, R., White, B.A., Nelson, K.E. and Leigh, S., 2019. Gut microbiome composition of wild western lowland gorillas is associated with individual age and sex factors. **American journal of physical anthropology**, 169(3), pp.575-585.

17. Dhakan, D.B., Maji, A., **Sharma, A.K.**, A.K., Saxena, R., Pulikkan, J., Grace, T., Gomez, A., Scaria, J., Amato, K.R. and Sharma, V.K, **2019**. The unique composition of Indian gut microbiome, gene catalogue, and associated fecal metabolome deciphered using multi-omics approaches. **GigaScience**, 8(3), p.giz004.

18. Kumar, K., Dhoke, G.V., **Sharma, A.K.**, Jaiswal, S.K. and Sharma, V.K., **2019**. Mechanistic elucidation of amphetamine metabolism by tyramine oxidase from human gut microbiota using molecular dynamics simulations. **Journal of cellular biochemistry**, 120(7), pp.11206-11215.

19. Kumar, K., Jaiswal, S.K., Dhoke, G.V., Srivastava, G.N., **Sharma, A.K.** and Sharma, V.K., **2018**. Mechanistic and structural insight into promiscuity based metabolism of cardiac drug digoxin by gut microbial enzyme. **Journal of cellular biochemistry**, 119(7), pp.5287-5296.

20. **Sharma, A.K.**, Jaiswal, S.K., Chaudhary, N. and Sharma, V.K., **2017**. A novel approach for the prediction of species-specific biotransformation of xenobiotic/drug molecules by the human gut microbiota. **Scientific reports**, 7(1), pp.1-13.

21. **Sharma, A.K.**, Srivastava, G.N., Roy, A. and Sharma, V.K., **2017**. ToxiM: A toxicity prediction tool for small molecules developed using machine learning and chemoinformatics approaches. **Frontiers in pharmacology**, 8, p.880.

22. Gupta, S., **Sharma, A.K.***, Shastri, V., Madhu, M.K. and Sharma, V.K., **2017**. Prediction of anti-inflammatory proteins/peptides: an insilico approach. **Journal of translational medicine**, 15(1), pp.1-11.

23. Gupta, A., Kumar, S., Prasoodanan, V.P., Harish, K., **Sharma, A.K.** and Sharma, V.K., **2016**. Reconstruction of bacterial and viral genomes from multiple metagenomes. **Frontiers in microbiology**, 7, p.469.

24. Gupta, S., **Sharma, A.K.***, Jaiswal, S.K. and Sharma, V.K., **2016**. Prediction of biofilm inhibiting peptides: an in silico approach. **Frontiers in microbiology**, 7, p.949.

25. Chaudhary, N., **Sharma, A.K.***, Agarwal, P., Gupta, A. and Sharma, V.K., **2015**. 16S classifier: a tool for fast and accurate taxonomic classification of 16S rRNA hypervariable regions in metagenomic datasets. **PLOS One**, 10(2), p.e0116106.

Conference publications

1. **Sharma, A.K.**, Martin, A., Moskowitz, J.E., Bora, S., Legree, K., Dorrestein, P., Underhill, D., Knight, R., Chen, P. and Devkota, S., 2022. 1166: In-patient antibiotic exposure promotes sars-cov-2 persistence in the gi tract in covid-19 admitted patients. **Gastroenterology, 162(7), pp.S-279**].
2. Lahcene, N.L., Moskowitz, J.E., **Sharma, A.K.**, Martin, A., Merchant, A., Fleshner, P. and Devkota, S., 2022. 1059: Spatial characterization of immune cells and bacterial co-localization in crohn's disease's creeping fat. **Gastroenterology, 162(7), pp.S-241**].

Book chapter

1. **Sharma, A.K.** and Dubey, V.S., **2021**. Metagenome Assembly for Gut Microbial Functional Diversity Associated with Xenobiotic Degradation. In Metagenomics and Microbial Ecology (pp. 79-87). **CRC Press**.

Oral/Poster Presentations

- **Selected speaker, 2022** — 'In-Patient Antibiotic Exposure Promotes SARS-CoV-2 Persistence in the GI Tract in COVID-19 Admitted Patients' at *Digestive Disease Week (DDW) 2022*, at San Diego, CA.
- **Delivered a lecture, 2020** — 'Emergence of microbiome in therapeutics – Ongoing efforts, challenges, and future opportunities' at *Department of Pharmaceutical Sciences*, Dr. Hari Singh Gaur University Sagar, India.
- **Selected as one of the finalist's, 2019** in the Novartis – Academia Hackathon event held on event to be held August 12th – 23rd, 2019 on the Novartis Campus in Cambridge, MA, USA.
- **Selected speaker, 2018** — 'Mapping gastrointestinal gene expression patterns from fecal RNA-seq' at EpiQ (Quantitative Epidemiology) seminar series, UMN Seminar.
- **Selected speaker 2015** — 'Fast and Accurate Taxonomic Classification of 16S rRNA Hypervariable Regions in Metagenomic Datasets using 16S Classifier' *in The Human Microbiome conference, at EMBL, Heidelberg, Germany.*

Editor/Reviewer for journals

- **Associate Editor** for Frontiers in Microbiology - Systems Microbiology; **Guest Associate Editor** for Frontiers in Microbiology - Microbiome in Health and Disease; **Review Editor** for Frontiers in Microbiology - Gastrointestinal Microbes

Achievements

- **International Travel Grant, 2019** — Received $1000 grant to present my work at Keystone Symposium on "Microbiome: Therapeutic Implications (T1)" *in October 2019 at Ireland.*
- **PBC Postdoctoral Fellowship, 2018** — Received a Israel government fellowship for three years to pursue postdoctoral research *at Bar-Ilan University, Israel.*
- **DST Travel Award, 2017** — Received travel award from Department of Science and Technology, India to present my doctoral research *in Symposium: NextGen Immunology at Rehovot, Israel.*
- **EMBL Grant, 2015** — Received €1000 grant to present my work *in The Human Microbiome Conference" at EMBL Germany.*
- **GATE, 2012** — Secured 376 All India Rank in *Graduate Aptitude Test in Engineering for Life Sciences* conducted by IIT Delhi

TEACHING EXPERIENCE

- **BIOL 1961, Foundations of Biology Lab I for Biological Sciences Majors (BIOL):** — Teaching basics of microbiome to computational microbiology students (16 contact hours/week, from July 2018).
- **BIOL 3004, Foundations of Biology for Biological Sciences Majors, Part II Laboratory:** — Leading various groups of computational microbiology students for bioinformatics analysis of 16S rRNA data from published microbiome studies (16 contact hours/week, from July 2018).

SELECTED SKILLS

- **Programming and Scripting:** Proficient in R and Python; Unix/Linux environments; SQL programming for effective data management
- **Multi-modal data processing:** 6+ years of experience in multivariate analysis of NGS (genomics, metagenomics, metatranscriptomics), metabolomics and 1+ year of experience in analysis of single-cell RNAseq, and Imaging Mass Cytometry (IMC) data
- **Statistical Analysis and Machine Learning:** Data mining, multivariate statistics, linear/mixed-effects modeling, target/biomarker identification, predictive analytics, power analysis, classification, regression, clustering, and survival analysis.
- **Genomic Data Resources:** Experience working with UCSC Genome Browser, Ensembl, ENCODE, NCBI SRA, GEO, GTEx, 1000 Genomes, dbSNP, UniProt, KEGG, MetaCyc, SILVA, Greengenes, HMDB, etc.
- **Bioinformatics Libraries:** Bioconductor, Seurat, mixOmics, DESeq2, caret, limma, ggplot2, MetaboAnalystR, Pandas, NumPy, SciPy, Matplotlib, scikit-learn, Keras. Capable of adapting to incorporate additional libraries as required for comprehensive data analysis and interpretation.
- **Collaboration and Project Management:** Experience with collaborative development and version control systems (e.g., Git); ability to manage projects, and timelines.
- **Bioinformatics support:** Installation, maintenance, and development of bioinformatics tools/pipelines, including workflow management with Nextflow and Snakemake
- **Cloud Computing and Data Visualization:** Experienced working with AWS and creating data visualization dashboards using tools like RShiny and Tableau