ASHOK KUMAR SHARMA

CONTACT INFORMATION

9344 National Blvd, Apt 14 — 651-424-9112
Los Angeles CA 90034 — ashoks773@gmail.com
Website: https://ashoks773.github.io/

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

RESEARCH EXPERIENCE

Scientist II, Toxicology **April 2023 - Present**
Drug Safety Research Evaluation (DSRE)
Takeda Pharmaceuticals

Bioinformatics Data Scientist **Dec 2022 - April 2023**
Senior Statistical Services 2, Data Intelligence Team
Land O'Lakes
As a Bioinformatics Data Scientist at Land O'Lakes, I am actively Driving the bioinformatics roadmap, vision, and strategy for Purina animal nutrition.

- Development of existing bioinformatics pipeline for managing, and statistical analysis of microbiome data.
- Development and implement data pipelines, and AI/ML algorithms to provide end-to-end bioinformatics solutions for researchers.

Postdoctoral Scientist **Feb 2021 - Dec 2022**
Casero Lab, Cedars-Sinai Medical Center
Advisor: Dr. David Casero, *Director, Translational Multiomics, Inflammatory Bowel Immunobiology Research Institute*
Co-Advisor: Dr. Suzanne Devkota, *Director of Microbiome Research at the F. Widjaja Foundation Inflammatory Bowel and Immunobiology Research Institute*
Broadly, I am involved in the analysis and integration of multi-omics datasets to identify pathogenic factors in IBD. Provided below are the list of my current projects.

- Quantification of bacterial growth rates from metagenomic datasets to identify bacterial activities associated with the progression of Crohn's disease.
- Alterations/reprogramming of cell-specific gene expression in the host epithelium of UC patients that undergo IPAA surgery and develop pouchitis.
- Analysis of multi-omics datasets to uncover microbial regulation of immune responses of creeping fat in Crohn's disease.

Postdoctoral Associate **March 2018 - Feb 2021**
Microbiomics Lab, University of Minnesota

Mentor: Dr. Andres Gomez
Being the first computational hire in the department, I was responsible for maintaining and setup computational pipelines on a high-performance computing facility at UMN. And, I have actively contributed to the following projects

- Whole genome sequencing data analysis to understand the effect of diet/lifestyle on gut microbial taxonomic and functional compositions in traditional human and nonhuman primate populations.
- Identification of gastrointestinal gene expression patterns in response to the functional alternation in the gut microbiome using meta-transcriptomic data analysis.

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

As a graduate researcher, I have contributed in the following projects:

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

PUBLICATIONS

1. 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.

2. 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.

3. 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.

4. 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.

5. **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..

6. 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.

7. **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).

8. 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.

9. **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.

10. 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).

11. 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.

12. **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.

13. 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.

14. 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.

15. 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.

16. 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.

17. **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.

18. **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.

19. 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.

20. 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.

21. 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.

22. **Sharma, A.K.**, Kumar, S., Harish, K., Dhakan, D.B. and Sharma, V.K., **2016**. Prediction of peptidoglycan hydrolases-a new class of antibacterial proteins. **BMC genomics**, 17(1), pp.1-12.

23. 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, 2016/2017** — 'Oral presentation on "Prediction of peptidoglycan hydrolases- a new class of antibacterial proteins" *in 3rd and 4th Annual Biology meeting at IISER Bhopal*, India.
- **Invited speaker, 2015** — 'Demonstration of R-software in data analysis' *in National Workshop at Barkatullah University Bhopal.*
- **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

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).

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.*
- **CSIR NET, 2013** — Qualified *CSIR-NET Lectureship Exam* conducted by Council for Scientific and Industrial Research (CSIR).
- **GATE, 2012** — Secured 376 All India Rank in *Graduate Aptitude Test in Engineering for Life Sciences* conducted by IIT Delhi
- **GAPT, 2010** — Secured 456 All India Rank in *Graduate Pharmacy Aptitude test* conducted by M.S. University Vadodara.

Selected skills

- **Programming:** Proficient in languages such as Perl, R and Python
- **Shell scripting:** Unix/Linux
- **Bioinformatics libraries:** Galaxy, Bioconductor, Ingenuity Pathways, Nextflow, Sankemake, SciPy, etc.
- **Multi-omics data processing:** **7+ years** of experience in the statistical analysis and integration of genomics (bulk and single-cell), metagenomics and metabolomics datasets, and **1+** analysis of proteomics, and Imaging Mass Cytometry (IMC) data
- **Statistical analysis:** Data mining, Multivariate statistics, linear mixed models, and machine learning/deep learning for pattern identification from large-scale biological data sets, predictive modeling, and target/biomarker identification
- **Tools and databases:** Experience in the installation/maintenance, development and implementation of bioinformatics tools, pipelines, and databases at local and High-performance computing environment
- **Cloud platforms:** High-performance computing/AWS ecosystem