ASHOK KUMAR SHARMA

CONTACT INFORMATION

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Codes availability: https://github.com/ashoks773

EDUCATION

PhD in Bioinformatics **Dec 2012 - Jan 2018**
IISER Bhopal, Madhya Pradesh, India

- Advisor: Dr. Vineet Kumar Sharma
- **Thesis work**: Development and utilization of computational methods for the analyses of high-throughput multi-omics datasets.

Masters in Pharmacoinformatics **Dec 2010 - Jan 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

Postdoctoral Scientist
Casero Lab, Cedar Sinai Medical Hospital **Feb 2021 - Present**
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 is 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.
- Analysis of metagenomics, metatrascriptomics and Imaging Mass Cytometry (IMC) datasets to uncover microbial regulation of immune responses of creeping fat in Crohn's disease.

Postdoctoral Associate
Microbiomics Lab, University of Minnesota **March 2018 - Feb 2021**
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. I used system-wide multi-omics approaches to understand microbiome-host interactions in Animal and Human models under diverse physiological conditions. Broadly, I have contributed to the following projects:

- Multi-omics 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 alteration in the gut microbiome using meta-transcriptomic data analysis.

Junior/Senior Research Fellow (J/SRF)
MetaBioSys Lab, IISER Bhopal **Dec 2012 - Jan 2018**

Mentor: Dr. Vineet Kumar Sharma

As a graduate researcher, I was responsible for development and utilization of computational methods for the analysis of multi-omics datasets. I have contributed to the following projects:

- Development of machine learning-based computational pipelines for the analysis of large-scale 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.

Department of Pharmacoinformatics, NIPER Mohali **July 2010 - Jun 2012**
Research: *Computer Aided Drug Discovery*

Publications

1. Dina G. Moussa, **Sharma, A.K.**, Tamer Mansour, Bruce Witthuhn; Jorge Perdigao; Joel D. Rudney; Conrado Aparicio; Andres Gomez. Functional Biomarkers of Ex-vivo Dental Caries Onset. **eBioMedicine 2022** [**Under Review**].

2. 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.

3. **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.

4. 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.

5. **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).

6. **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.

7. 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).

8. 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.

9. **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.

10. 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.

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

12. 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.

Oral/Poster Presentations

- **Invited speaker, 2020** — 'Emergence of microbiome in therapeutics – Ongoing efforts, challenges, and future opportunities' at *Department of Pharmaceutical Sciences, Dr. H.S. Gour University, Sagar, M.P. India.*
- **Selected speaker, 2019** — 'Mapping gastrointestinal gene expression patterns from fecal RNA-seq' at *UMN Seminar, University of Minnesota Twin Cities, MN, USA.*
- **Selected speaker, 2016/2017** — 'Development of computational methods for large scale data analysis' *in 3rd and 4th Annual Biology meeting at IISER Bhopal, M.P., India.*
- **Invited speaker, 2015** — 'Basics of machine learning for high-throughput multi-omics data analysis' *in National Workshop at Barkatullah University Bhopal, India.*
- **Selected speaker 2015** — 'Computational methods for taxonomic and functional annotation using machine learning based approaches' *in The Human Microbiome conference, at EMBL, Heidelberg, Germany.*

Editor/Reviewer for journals

- Guest Associate Editor for Frontiers in Microbiology - Microbiome in Health and Disease
- Review Editor for Frontiers in Microbiology - Gastrointestinal Microbes.
- Review Editor for Frontiers in Microbiology - Systems Microbiology.
- Reviewer for Food Research International, British Journal of Nutrition, mSystems, Frontiers in Microbiology, Cell Reports, BMC Microbiology, and Molecular Biology and Evolution

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 - March 2021).
- **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 - March 2021).

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
- **Multi-omics data processing:** **6+ years** of experience in the statistical analysis of metagenomics, metatranscriptomics, and metabolomic datasets, and **recently started** analysis of single-cell RNA sequencing, and Imaging Mass Cytometry (IMC) data
- **Statistical analysis:** Multivariate statistics, linear mixed models, and machine learning for pattern identification from large-scale omics datasets
- **Tools and databases:** Experience in the installation/maintenance, development and implementation of bioinformatics pipelines at local and High-performance computing environment
- **Cloud platforms:** High-performance computing/AWS ecosystem, and Data management