RAVI KUMAR

Academy of Scientific and Innovative Research (AcSIR)
Council of Scientific and Industrial Research-Institute of Himalayan Bioresource Technology (CSIR-IHBT),
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SUMMARY

PhD (Submitted) in Biological Sciences with specialization in Computational Biology, Bioinformatics, Machine Learning, Systems Biology, and host-microbe Interactions. Well-versed in analyzing and integrating high-throughput sequencing data, developing computational pipelines, applying machine learning approaches, and performing advanced statistical analyses. Experienced in working with complex biological datasets to uncover novel insights into molecular and systems-level processes. Seeking a postdoctoral or scientist-level position in bioinformatics or data science to apply my expertise in computational analysis, modeling, and data-driven discovery to address fundamental biological questions and advance translational research.

RESEARCH INTERESTS

Systems Biology/Network approaches to understand the network behavior of the host in response to the environment

- Immune Response
- High-throughput sequencing data analysis to understand the host-environment interactions
- Machine Learning application to predict the defense-related genes of host and effector proteins of pathogens
- Understanding the host response to different pathogens using computational approaches

EDUCATION

- **Ph.D. in Biological Science (Jan 2021-July 2025, Submitted):** AcSIR, CSIR-IHBT, Palampur, India
  Thesis title: Intersecting Machine Learning and Deep Learning Approaches to Unravel Complexities of Plant-Pathogen Interactions
  Supervisor: Dr. Vishal Acharya

- **M.Sc. in Computational Biology and Bioinformatics:** Centre for Computational Biology and Bioinformatics, School of Life Sciences, Central University of Himachal Pradesh, Dharamshala, India
  Dissertation title: Modelling Cell Cycle Regulation and Synchronized Oscillation in NF-kB Signaling
  Supervisor: Dr. Vikram Singh

- **B.Sc. in Basic Science:** Himachal Pradesh University, Shimla, India

RESEARCH EXPERIENCE

- **Project Associate-I** (October 03, 2023 – April 21, 2024 at CSIR- Institute of Himalayan Bioresource Technology)
  Project title: Himalayan Centre for high-throughput Computational Biology (HiCHiCoB)-BIC
  Achievements/Task: To develop a deep learning algorithm to predict the effector proteins using sequence, structural, and evolutionary information. It is an essential scientific tool that improves effector protein prediction accuracy and makes it possible to analyze fungal effectors to spur innovation.

- **Project Associate-I** (November 18, 2021 – March 31, 2023 at CSIR- Institute of Himalayan Bioresource Technology)
  Project title: Investigating mechanism underlying transgenerational heat stress adaptation in plants.
  Achievements/Task: Analysis of *Arabidopsis thaliana* transcriptome data (short reads-illumina) collected under different heat stress conditions to understand the plant's high-temperature sensing and signaling networks. Reference-based assembly and downstream analysis of next-generation sequencing data from susceptible and resistant potato varieties to understand the molecular mechanisms underlying high-temperature responses in potatoes, emphasizing the tuberization process.

- **Project Assistant-II** (January 21, 2019 – March 31, 2020, at CSIR-Institute of Himalayan Bioresource Technology)
  Project title: Development of a high-throughput genotyping platform for next-generation plant breeding in tea
  Achievements/Task: To develop a deep-learning-based method to construct a gene network and identify genes involved in the biotic/abiotic defense response. It involves pre-processing interaction pairs and expression profiles of plant treatment/control, using the DLNet algorithm to rank genes based on their contribution to data classification, and subjecting top-ranked genes to module and enrichment analysis.

- **Studentship** (November 2018 – January 18, 2019, CSIR- Institute of Himalayan Bioresource Technology)
  Project title: Establishment of Bioinformatics Infrastructure Facility for Biology Teaching through Bioinformatics
  Achievements/Task: Next Generation Sequencing (NGS) dataset analysis and conducted in-depth research using Illumina dataset treated with different abiotic stresses to develop next-generation abiotic stress-tolerant varieties.

- **Project Assistant-II** (July 03, 2015 – March 31, 2017, CSIR-Institute of Genomics and Integrative Biology, Delhi)
  Project title: Genomics and Informatics Solution for Integrating Biology (GENESIS)
  Achievements/Task: Developed and applied computational approaches to explore the bacterial genomes to develop biomarkers for identification. The proposed strategy is likely to prove helpful in properly detecting pathogens like *Vibrio*, *Streptococcus*, *Staphylococcus*, etc., for their rapid identification.

AWARDS & HONOURS

- **Best poster presentation** award at IPS North Zone Meet and National Symposium of Himalayan Phytopathological Society on "New Vistas in Plant Pathological Research."
  Organized by the Indian Phytopathological Society (NZ) at Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur, India, November 7-8, 2024

SKILLS

- **Computational modeling:** Machine learning and Network modeling to provide insights into biological systems
- **Genomics/Big Data Analysis:** Next Generation sequencing (NGS) data analysis, interpretation, and visualization.
- **Programming Languages:** Core analytics using R, Machine Learning using Python, Batch scripting using Shell.
- **Software/Tool:** for analysis, visualization, and interpretation of biological data.
- **Algorithm Development**

PUBLICATIONS

1. Mohapatra, S., Mishra, A., Godara, R., Twinkle, Bali, S., Kumar, A., **Kumar, R.,** Kumar, N., Kumar, P., Acharya, V., Dogra, V. (2025) Oxidative stress in chloroplasts activates polyphenol oxidase that triggers an inter organelle communication via oxidized flavonoids in *Camellia sinensis* (Under Review)

2. Jose-Santhi, J., Sheikh, F.R., Kalia, D., Sood, R., **Kumar, R.,** Acharya, V., Singh, R.K. (2024) Transcriptional dynamics in source-sink tissues identifies molecular factors regulating the corm development process in saffron (Crocus sativus L.). *Physiologia Plantarum*, 176:e14285. doi: 10.1111/ppl.14285

3. **Kumar, R.,** Acharya, V. (2023) Effector protein structures: a tale of evolutionary relationship. *Trends in Plant Science*, Cell Press 28:746-748 doi: 10.1016/j.tplants.2023.04.010

4. Mali, S., Datta, M., Goel, K., Raturi, V., Kundu, P., **Kumar, R.**, Gahlaut, V., Acharya, V., Gupta, V.K., Sood, S., Zinta, G. (2023) High-temperature trigger differential expression of JUMONJI C (JmjC) domain-containing histone demethylase genes in leaf and stolen tissue of potato (*Solanum tuberosum L.*) genotypes. *Journal of Plant Growth Regulation* 44:1500-1514 doi: 10.1007/s00344-023-11094-w

5. **Kumar, R.**, Acharya, V. (2023) Deep learning-based protocol to construct an immune-related gene network of host-pathogen interactions in plants. *STAR Protocols,* Cell Press 4:101934. doi: 10.1016/j.xpro.2022.101934

6. Kalia, D., Santhi, J.J., **Kumar, R.**, Singh, R.S. (2022) Analysis of PEBP Genes in Saffron Identifies a Flowering Locus T Homologue Involved in Flowering Regulation. *Journal of Plant Growth Regulation* 42: 2486–2505. doi: 10.1007/s00344-022-10721-2

7. **Kumar, R.**, Khatri, A., Acharya, V. (2022) Deep learning uncovers distinct behaviour of rice network to pathogens' response. *iScience*, Cell Press 25:104546. doi: 10.1016/j.isci.2022.104546

8. **Kumar, R.**, Koul, S., Kumar, P., Kalia, V.C. (2016) Searching biomarkers in the sequenced genomes of *Staphylococcus* for their rapid identification. *Indian J Microbio*l 56: 64-71. doi: 10.1007/s12088-016-0565-9

9. Kalia, V.C., **Kumar, R.**, Kumar, P., and Koul, S. (2016) A Genome-Wide profiling strategy as an aid for searching unique identification biomarkers for *streptococcus*. *Indian J Microbial* 56: 46-58. doi: 10.1007/s12088-015-0561-5

10. Kalia, V.C., Kumar, P., **Kumar, R.**, Mishra, A., and Koul, S. (2015) Genome-wide analysis for rapid Identification of *Vibrio* species. *Indian J Microbiol* 55: 375–383. doi: 10.1007/s12088-015-0553-5

BOOK CHAPTERS

- **Kumar, R.**, Koul, S., Kalia, V.C. (2017) Exploiting bacterial genomes to develop biomarkers for identification (pp. 357- 370). In "Drug Resistance in Bacteria, Fungi, Malaria and Cancer". Editors: Arora, G., Sajid, A., Kalia, V.C. Springer Switzerland. ISBN 978-3-319-48682-6 doi: 10.1007/978-3-319-48683-3_16

- Kalia, V.C., **Kumar, R.**, Koul, S. (2017). In silico analytical tools for phylogenetic and functional bacterial genomics (pp. 339-355). In "Drug Resistance in Bacteria, Fungi, Malaria and Cancer". Editors: Arora, G., Sajid, A., Kalia, V.C. Springer Switzerland. ISBN 978-3-319-48682-6 doi: 10.1007/978-3-31948683-3_15

DATABASES AND SOFTWARE/TOOLS

- Protocol for network and expression integration to identify potential defense genes in host-pathogen interactions https://gitlab.com/ravisaroch/star-protocols (2023)
- RicePathDLNet: Visualization of Rice Pathogen Deep Learning Network https://fgcsl.ihbt.res.in/RicePathDLNet (2022)
- Pipeline for deep learning network construction of host-pathogen interaction (DLNet-HPI) https://gitlab.com/ravisaroch/dlnet-host-pathogen-interaction (2022)
- EffectorFold: A machine learning based tool for prediction of effector proteins from fungi (under construction) (2025)

CONFERENCES/WORKSHOPS/WEBINARS

Oral: Leveraging machine learning approaches to unravel the plant immune system and enhance effector protein prediction. **Kumar, R., & Acharya, V.**
National Symposium on Molecular Intricacies of Plant-Associated Microorganisms 2025 (MIPAM 2025) at Indian Institute of Technology, Mandi, India, March 7-8, 2025

Oral: Deep learning architecture for exploring network properties of rice in response to multiple pathogens. **Kumar, R., Khatri, A., & Acharya, V.**
6th Annual Crops in Silico Symposium & Hackathon at the University of Illinois, Urbana-Champaign, USA, May 11-13, 2022 (Virtual)

Poster: Investigating the host-pathogen interactions through machine learning approaches for enhancing treatment strategies. **Kumar, R., & Acharya, V.**
IPS North Zone Meet and National Symposium of Himalayan Phytopathological Society on "New Vistas in Plant Pathological Research" at Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur, India, November 7-8, 2024

Poster: Network-based deep learning approach to uncover the plant immune system in response to biotic stresses. **Kumar, R., & Acharya, V.**
17th Annual International Biocuration Conference at Indian Biological Data Centre (IBDC), Regional Centre for Biotechnology (RCB), Faridabad, India, March 5-8, 2024

Resource Person: Deep Bioinformatics Boot Camp 2" at CSIR-Institute of Himalayan Bioresource Technology (CSIR-IHBT), Palampur, Himachal Pradesh, and DBT-India, February 18-21, 2025

Resource Person: Deep Bioinformatics Boot Camp" at CSIR-Institute of Himalayan Bioresource Technology (CSIR-IHBT), Palampur, Himachal Pradesh, and DBT-India, August 28-30, 2023

Resource Person: Bioinformatics Tools and its Application in Agriculture workshop by CSK Himachal Pradesh Agriculture University, Palampur, Himachal Pradesh, and DBT-India, February 24, 2019

Participated in the "NSM HPC Systems& AI: From Theory to Practice" training program at CSIR-Fourth Paradigm Institute (CSIR-4PI), Bengaluru, and C-DAC Bengaluru, Karnataka, India, July 04-05, 2024

Participated in the Workshop on "Trends in the Evolutionary Systems Biology and Computational Structural Dynamics" at CSIR-Institute of Himalayan Bioresource Technology (CSIR-IHBT), Palampur, Himachal Pradesh, India, March 23-24, 2015

PERSONAL DETAILS

- Date of birth: 25-12-1989
- Nationality: Indian
- Marital status: Married to Dr. Shudh Kirti Dolma
- Correspondence address: Ward No. 1 Lohna, Near Neugal Chowk, Nagar Nigam Palampur, PO Bandla Tea Estate, Tehsil Palampur, District Kangra, Himachal Pradesh, India,176061

REFEREES

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