Vinay Rajput

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Google Scholar: https://scholar.google.com/citations?user=YnIqsiAAAAAJ&hl=en

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PROFESSIONAL SUMMARY

Experienced Bioinformatics researcher specializing in NGS data analysis with over **6+ years** of expertise. Proficient in **Python and R**, with a solid background in **bioinformatics pipeline development** and the analysis of complex genomic datasets. Adept at collaborating with interdisciplinary teams and applying statistical models to derive impactful insights. Passionate about using cutting-edge technology to support precision medicine and personalized healthcare. **Aspiring machine learning practitioner**, eager to integrate ML techniques into bioinformatics for advanced predictive modeling and data-driven discoveries.

RESEARCH EXPERIENCE

- ❖ **Research experience: 6+ Years**

- ❖ **Bioinformatics Consultant: Pune Knowledge Cluster Private Limited** | October 2023 – Present

  Key Roles and Responsibilities: Provided bioinformatics consultancy for various NGS projects, focusing on SARS-CoV-2 surveillance, variant calling, Designing dashboards, metagenomics, genomics, and functional analysis

- ❖ **Senior Project Associate: National Collection of Industrial Microorganisms (CSIR-NCL)** | March 2023 – October 2023

  Key Roles and Responsibilities:

  - Conducted comprehensive **NGS data analysis** across diverse sequencing platforms, including **Illumina and Oxford Nanopore** technologies, for 16S/18S/ITS, shotgun metagenomes, and whole genome sequencing.

  - Managed end-to-end workflows, from sample collection and **DNA extraction** to **library preparation and sequencing**, for environmental sources such as rivers and glaciers.

  - Designed and implemented **custom bioinformatics pipelines** for **end-to-end analysis**, ensuring efficient data processing, visualization, and reporting.

  - Set up and maintained **Linux-based HPC infrastructure** for data analysis, while developing custom tools in **R, Python**, and **Bash** for specific project needs.

  - Provided technical guidance and **bioinformatics support** to PhD students, assisting them with **pipeline development and analysis** across various research projects.

- ❖ **Project Assistant I-III: National Collection of Industrial Microorganisms (CSIR-NCL)** | October

2018 – February 2023

Key Roles and Responsibilities: Conducted metagenomic analysis of environmental samples and microbial genomes, contributing to diverse environmental and microbial ecology projects.

❖ **Project Trainee: CSIR-Center for Cellular and Molecular Biology, Hyderabad** | September 2018 – October 2018

EDUCATION

❖ **Ph.D. in Bioinformatics**

CSIR - National Chemical Laboratory

August 2022 – Present

Pursuing a Ph.D. with a focus on bioinformatics and NGS data analysis.

❖ **Bachelor of Technology (B. Tech) in Bioinformatics**

SRM University, Delhi-NCR

2014 – 2018

C.G.P.A: 7.85/10 (78.5%)

Specialized in bioinformatics, covering computational biology, genomics, and systems biology.

❖ **Higher Secondary Education (12th Science)**

Government Boys Senior Secondary School, Alipur, Delhi

CBSE Board

2014

Percentage: 73.40%

❖ **Secondary Education (10th)**

Bhagatji Memorial Model Secondary School, Delhi

CBSE Board

2012

C.G.P.A: 7.2

CERTIFICATIONS

- **Full Stack Data Science Program (1-year)**
  iNeuron, Bengaluru
  Completed on November 21, 2022
  Comprehensive training in data science, covering full-stack data analysis and machine learning. Gained expertise in **Python** and its advanced topics, along with libraries such as **Pandas, NumPy, Matplotlib, Seaborn** etc. Also worked with databases including **MySQL**, **MongoDB**, **SQLite**, and **Cassandra**. Continuing to expand knowledge in **machine learning**, **predictive modeling**, and **advanced analytical techniques**.
- **Python Online Certification**
  Completed April 2020
  Course: *"Learn to Code in Python 3: Programming from Beginner to Advanced"*
  Gained advanced proficiency in Python programming.

PROFESSIONAL SKILLS

Bioinformatics & NGS Analysis:

- **NGS Data Analysis:** DNA-seq, RNA-seq, ChIP-seq, Metagenomics, Whole Exome Sequencing (WES), Whole Genome Sequencing (WGS)

- **Gene Expression Analysis:** Microarray, Differential Gene Expression Analysis (DESeq2, EdgeR)

- **Single-Cell Analysis:** Processing and interpretation of single-cell sequencing data

- **Pipeline Development:** Automation and optimization of bioinformatics workflows (Snakemake, Nextflow)

- **Tools & Software:** BLAST, GATK, ClustalW, Muscle, FASTA, DIAMOND, QIIME, MOTHUR, MG-RAST, DeepARG, Kaiju, SPADES, miniasm, Flye, PATRIC, Prokka, RAST, MEGAN, DeepARG, ResFinder, iVar, Samtools, Bamtools, BWA etc.

- **Docking and Interaction Analysis:** Proficient in molecular docking and protein-protein interaction analysis using tools like AutoDock, PyDock, PyMOL, Chimera.

Computer Skills:

- **Operating Systems:** Proficient in Linux (any distribution) and Windows (any version).

Programming Languages:

- **Advanced:** Python, R, Linux Shell Scripting.
- **Basic:** C, C++, JavaScript, PHP, HTML, Perl.
- **Data Processing:** High proficiency in data retrieval and manipulation using tools like `awk`, `sed`, and `grep`.
- **Data Visualization:** Skilled in creating visualizations using Matplotlib, Seaborn, and other Python libraries.
- **Software Proficiency:** Proficient with the Microsoft Office Suite (Word, Excel, PowerPoint).

Wet Lab Techniques:

- **Molecular Biology:** DNA extraction, PCR, library preparation

- **Sequencing Platforms:** Oxford Nanopore, Illumina (MiSeq/HiSeq)

KEY INTERESTS

Bioinformatics pipelines development, Metagenomics, Cancer Genomics, Variant calling, Microbial Genomics, Single-cell Genomics, Oxford Nanopore Sequencing, Machine Learning.

PUBLICATIONS

[1] M. Kaari, R. Manikkam, J. Joseph, S. Krishnan, K.K. Annamalai, A. Khan, **V. Rajput**, Integrated genomic and functional analysis of Streptomyces sp. UP1A-1 for bacterial wilt control and solanaceae yield increase, Gene Reports 37 (2024) 102012. https://doi.org/10.1016/j.genrep.2024.102012.

[2] S. Zambre, P. Katarmal, S. Pawar, S. Dawkhar, P. Iyer, **V. Rajput**, Wastewater surveillance of severe acute respiratory syndrome coronavirus-2 in open drains of two Indian megacities captures evolutionary lineage transitions: a zonation approach, Environmental Science and Pollution Research 31 (2024) 49670–49681. https://doi.org/10.1007/s11356-024-34448-7.

[3] **V. Rajput**, R. Das, R. Pramanik, Early detection of KP.2 SARS-CoV-2 variant using wastewater-based genomic surveillance in Pune, Maharashtra, India, Journal of Travel Medicine (2024). https://doi.org/10.1093/jtm/taae097.

[4] H.V. Dhondge, V.T. Barvkar, S.G. Dastager, M.S. Dharne, **V. Rajput**, Genome sequencing and protein modeling unraveled the 2AP biosynthesis in Bacillus cereus DB25, International Journal of Food Microbiology 413 (2024) 110600. https://doi.org/10.1016/j.ijfoodmicro.2024.110600.

[5] **V. Rajput**, R. Pramanik, Genomic surveillance reveals early detection and transition of delta to omicron lineages of SARS-CoV-2 variants in wastewater treatment plants of Pune, India, Environmental Science and Pollution Research 30 (2023) 118976–118988. https://doi.org/10.1007/s11356-023-30709-z.

[6] P.G. Nair, E. Joseph, R. Yadav, **V. Rajput**, Production of poly-gamma-glutamic acid (γ-PGA) from sucrose by an osmotolerant Bacillus paralicheniformis NCIM 5769 and genome-based predictive biosynthetic pathway, Biomass Conversion and Biorefinery (2023). https://doi.org/10.1007/s13399-023-04522-0.

[7] R. Samson, **V. Rajput**, Spatio-temporal variation of the microbiome and resistome repertoire along an anthropogenically dynamic segment of the Ganges River, India, Science of The Total Environment 872 (2023) 162125. https://doi.org/10.1016/j.scitotenv.2023.162125.

[8] R. Yadav, **V. Rajput**, M. Dharne, Water Hyacinth microbiome: metagenomic cues from environment and functionality in urban aquatic bodies, Cold Spring Harbor Laboratory, 2023. http://dx.doi.org/10.1101/2023.03.09.531941 (accessed October 7, 2024).

[9] V. Malik, **V. Rajput**, R. Pramanik., Campus Sewage Water Surveillance based dynamics and infection trends of SARS-CoV-2 variants during third wave of COVID-19 in Pune, India, Cold Spring Harbor Laboratory, 2023. http://dx.doi.org/10.1101/2023.03.02.23286683 (accessed October 7, 2024).

[10] V.A. Prabhu, **V. Rajput**, R. Yadav., Gut Microbiota Dysbiosis in Patients with Intracranial Sino-Venous Thrombosis and Acute Ischemic Stroke in the Young, Annals of Indian Academy of Neurology 25 (2022) 980–983. https://doi.org/10.4103/aian.aian_393_22.

[11] **V. Rajput**, R. Samson., Metagenomic mining of Indian river confluence reveal functional microbial community with lignocelluloytic potential, 3 Biotech 12 (2022). https://doi.org/10.1007/s13205-022-03190-7.

[12] T. Dharmadhikari, **V. Rajput**, R. Yadav, High throughput sequencing based direct detection of SARS-CoV-2 fragments in wastewater of Pune, West India, Science of The Total Environment 807 (2022) 151038. https://doi.org/10.1016/j.scitotenv.2021.151038.

[13] **V. Rajput**, R. Yadav, M.S. Dharne, Metagenomic exploration reveals a differential patterning of antibiotic resistance genes in urban and peri-urban stretches of a riverine system, Environmental Science and Pollution Research 28 (2021) 66477–66484. https://doi.org/10.1007/s11356-021-16910-y.

[14] R. Yadav, **V. Rajput**, M. Dharne, Metagenomic analysis of a mega-city river network reveals microbial compositional heterogeneity among urban and peri-urban river stretch, Science of The Total Environment 783 (2021) 146960. https://doi.org/10.1016/j.scitotenv.2021.146960.

[15] M. Mohapatra, R. Yadav, **V. Rajput**, M.S. Dharne, G. Rastogi, Metagenomic analysis reveals genetic insights on biogeochemical cycling, xenobiotic degradation, and stress resistance in mudflat microbiome, Journal of

Environmental Management 292 (2021) 112738. https://doi.org/10.1016/j.jenvman.2021.112738.

[16] J. Chakraborty, **V. Rajput**., Spatio-temporal resolution of taxonomic and functional microbiome of Lonar soda lake of India reveals metabolic potential for bioremediation, Chemosphere 264 (2021) 128574. https://doi.org/10.1016/j.chemosphere.2020.128574.

[17] R. Yadav, **V. Rajput**, M. Dharne, Functional metagenomic landscape of polluted river reveals potential genes involved in degradation of xenobiotic pollutants, Environmental Research 192 (2021) 110332. https://doi.org/10.1016/j.envres.2020.110332.

[18] R. Yadav, **V. Rajput**, K. Gohil, K. Khairnar, M. Dharne, Comprehensive metagenomic insights into a unique mass gathering and bathing event reveals transient influence on a riverine ecosystem, Ecotoxicology and Environmental Safety 202 (2020) 110938. https://doi.org/10.1016/j.ecoenv.2020.110938.

[19] K. Gohil, **V. Rajput**, M. Dharne, Pan-genomics of Ochrobactrum species from clinical and environmental origins reveals distinct populations and possible links, Genomics 112 (2020) 3003–3012. https://doi.org/10.1016/j.ygeno.2020.04.030.

[20] R. Samson, **V. Rajput**, M. Shah, R. Yadav, P. Sarode, S.G. Dastager, M.S. Dharne, K. Khairnar, Deciphering taxonomic and functional diversity of fungi as potential bioindicators within confluence stretch of Ganges and Yamuna Rivers, impacted by anthropogenic activities, Chemosphere 252 (2020) 126507. https://doi.org/10.1016/j.chemosphere.2020.126507.

[21] J. Chakraborty, V. Sapkale, **V. Rajput**, M. Shah, S. Kamble, M. Dharne, Shotgun metagenome guided exploration of anthropogenically driven resistomic hotspots within Lonar soda lake of India, Ecotoxicology and Environmental Safety 194 (2020) 110443. https://doi.org/10.1016/j.ecoenv.2020.110443.

[22] J. Chakraborty, V. Sapkale, M. Shah, **V. Rajput**., Metagenome sequencing to unveil microbial community composition and prevalence of antibiotic and metal resistance genes in hypersaline and hyperalkaline Lonar Lake, India, Ecological Indicators 110 (2020) 105827. https://doi.org/10.1016/j.ecolind.2019.105827.

[23] Zothanpuia, A.K. Passari, P. Deka, **V. Rajput**., Draft Genome Sequence of Freshwater-Derived Streptomyces sp. Strain BPSDS2, Isolated from Damte Stream, Northeast India, Microbiology Resource Announcements 8 (2019). https://doi.org/10.1128/mra.00874-19.

[24] R. Samson, M. Shah, R. Yadav, P. Sarode, **V. Rajput**, S.G. Dastager, M.S. Dharne, K. Khairnar, Metagenomic insights to understand transient influence of Yamuna River on taxonomic and functional aspects of bacterial and archaeal communities of River Ganges, Science of The Total Environment 674 (2019) 288–299. https://doi.org/10.1016/j.scitotenv.2019.04.166.

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TRAININGS

- **5-Day Industrial Training:** Attended training at the International Center for Genetic Engineering and Biotechnology (ICGEB), New Delhi, India.

- **2-Month Summer Training:** Completed summer training at CSIR-Center for Cellular and Molecular Biology (CCMB), Hyderabad, under the guidance of Dr. Shrish Tiwari, from 25th May 2017 to 25th July 2017.
- **6-Month Dissertation Project:** Conducted dissertation research at CSIR-Center for Cellular and Molecular Biology (CCMB), Hyderabad, under the supervision of Dr. Shrish Tiwari, from 4th January 2018 to 4th July 2018.
- **Skill Development Program:** Assisted in organizing the "Microbial Identification by Biochemical, Genetics and Genomic Techniques" program at CSIR-National Chemical Laboratory (NCL), Pune, from 18th June 2018 to 28th June 2018.

CONFERENCES

- **International Conference on Antimicrobial Resistance, Nobel Drug Discovery and Development:** Participated in the conference organized by SRM University, Delhi-NCR, in 2015.
- **International Conference on Integrative Biology & Applied Genetics (ICIBAG):** Attended the event held at Osmania University, Hyderabad, in March 2018.
- **9th International Conference on NextGen Genomics, Biology, Bioinformatics, and Technologies (2019-NGBT):** Participated in the conference from 30th September to 2nd October 2019, in Mumbai, India.

PERSONAL DETAILS

- **Name**: Vinay Rajput
- **Father's Name**: Anil Kumar
- **Mother's Name**: Suman Devi
- **Date of Birth**: 29th November 1996
- **Marital Status**: Single
- **Languages Known**: English, Hindi
- **Nationality**: Indian
- **Mobile Number**: +91-8447432515

REFERENCES

- **Dr. Shrish Tiwari** | Principal Scientist | CSIR-Center for Cellular and Molecular Biology (CCMB) Hyderabad, India | Email: shrish@ccmb.res.in | Phone: +91-40-27192777
- **Dr. Mahesh Dharne** | Principal Scientist and Head, National Collection of Industrial Microorganisms (NCIM) | CSIR-National Chemical Laboratory (NCL) | Pashan, Pune-411008, India | Email: ms.dharne@ncl.res.in | Phone: +91-20-25902456