VINAY RAJPUT

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

Experienced bioinformatics Analyst specialized in NGS data analysis, proficient in Python and R, with a strong track record of delivering impactful insights from complex genomic datasets. Skilled in designing bioinformatics pipelines, applying statistical models, and collaborating with interdisciplinary teams to drive successful outcomes. Passionate about leveraging cutting-edge technologies to contribute to personalized medicine and precision healthcare.

RESEARCH EXPERIENCE

- **Research experience : 5+ Years**
- **Senior Project Associate** at National Collection of Industrial Microorganisms in **CSIR-National Chemical Laboratory**: working under the guidance of Dr. Mahesh Dharne from February 2023 to present.

➢ **Roles & Responsibilities :**

  - √ Carried out Data Analysis on multiple NGS sequences like 16s/18s/ITR amplicons, shotgun metagenomes, and whole genomes (bacteria/viruses) among others, sequenced using cutting edge technologies like Illumina (MiSeq/HiSeq) and Oxford Nanopore (MINion).
  - √ Sampling, sample preparation, DNA extraction, library preparation and sequencing of samples collected from environment sources like hot springs, rivers, hyper-saline lakesand glaciers.
  - √ Setup, maintenance and management of Linux based high performance computing infrastructure, setting up analysis pipelines, coding and programming in R/Bash/Python, maintenance of internal databases, and assisting in-house PhD students in analysis by providing insights on bioinformatics methods and creating custom tools and scripts to aidin their research.

- **Project Assistant-III** at National Collection of Industrial Microorganisms in **CSIR-National Chemical Laboratory**: worked under the guidance of Dr. Mahesh Dharne from October 2020 to February 2023.
- **Project Assistant-II** at National Collection of Industrial Microorganisms in **CSIR-National Chemical Laboratory**: worked under the guidance of Dr. Mahesh Dharne from October 2018 to October 2020.
- **Project Trainee** at **CSIR-Center for Cellular and Molecular Biology, Hyderabad** : worked under the guidance of Dr. Shrish Tiwari from September 2018 to October 2018.

EDUCATION

- **Full Stack Data Science Program**, Nov'2021 Batch at **iNeuron-Bengaluru**, Completed on 21st November 2022.
- **Python Online Certification Training**, Topic: "Learn to Code in Python3: Programming

beginner to advanced", Completed on April 2020.

- **Bachelor of Technology (B.Tech)** **specialization in Bioinformatics**, SRM University, Delhi-NCR, Duration of Course: 4 Years, From 2014 to 2018 (C.G.P.A 7.85/10, 78.5%).
- Higher Secondary Schooling (Science) – Government Boys Senior Secondary School, Alipur Delhi, CBSE Board (73.40%), Year of Passing: 2014.
- Secondary Schooling – Bhagatji Memorial Model Secondary School, Delhi. CBSE Board (CGPA – 7.2), Year of Passing: 2012.

RESEARCH PROJECTS

- Wastewater Surveillance of Covid-19 & other bacterial and viral patogens from Pune city under a mission of : One Health Approach. (Funding : Rockfeller foundationa,USA & CSIR)
- River Microbiome: Understanding the overall microbial ecology of the polluted urban rivers and also analyzing the impact of Mass gatherings events on the religiously important rivers of India.
- National Mission for Clean Ganga (NMCG) project: The project aims to understand the non-putrefying properties of Ganges river by employing Nanopore Sequencing technology.
- Lonar microbial ecology: The main aim is to delineate the microbial flora and associated functional potential in the extreme conditions of the unique Soda lake formed due to crater in Maharashtra, India.
- Whole Genome Sequencing: Genome assembly, gene prediction, functional annotation, phylogenetic analysis and pan-genomic study of Ochrobactrum species from clinical and environmental origins using long read based Oxford Nanopore Sequencing Technology.

PROFESSIONAL SKILLS

Dry Lab:

- Sequence and Structure retrieval and searching from any Database.
- Sequence Analysis tools: BLAST, clustalW, Muscle, FASTA, Diamond etc.
- Metagenomics tools: QIIME, MOTHUR, MG-RAST, MEGAN, DeepARG, Ressfinder, Kaiju etc.
- Pathway databases and tools: KEGG, MINT and BIND.
- Protein prediction tools: GeneMark, Glimmer, GenScan, etc.
- Genomic Annotation using tools and resources like: PATRIC, Prokka, RAST, etc.
- Assembly using tools like: SPADES, miniasm, flye, canu, Unicycler, wdbg2, velvet, etc.
- Extremely proficient in establishing analysis pipelines (snakemake and nextflow), format conversions, scripting of tools, etc.
- Interpretation of results and outputs of the above tools and database files.

Computer Skills:

- Operating systems: Linux (any distribution), Windows (any version).
- Programming languages:
  - √ Advanced:Python – NumPy, SciPy, Pandas, R, Linux Shell Scripting.
  - √ Basic: C,C++, Javascript, PHP,HTML,Perl,etc.
- Proficient with Microsoft office suite.

- Retrival of information from large data.
- High command on awk, sed, grep.
- Visualization of data using metplotlib, seaborn etc.

Wet Lab:

- Microbiological Techniques: Plating, Streaking, Staining, Microbial Culture requirements etc.
- Molecular Biology Techniques: DNA extraction, Purification, Amplification(PCR), Library Preparation etc.
- Instruments and Machine handling which includes: Microscopes, Sanger Sequencer, Oxford Nanopore Sequencer etc.
- Sampling and its intricacies (water and sediment).
- DNA sequencing : Oxford Nanopore.

AREA OF INTEREST

Programming, Metagenomics, Single cell genomics, epigenetics, cancer genomics, microbial genomcis, Bioinformatics pipelines development, Oxford Nanopore Sequencing.

PUBLICATIONS

1. Samson, R., **Rajput, V**., Yadav, R., Shah, M., Dastager, S., Khairnar, K., Dharne, M., 2023. 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, 162125. https://doi.org/10.1016/j.scitotenv.2023.162125

2. Malik, **V., Rajput**, V., Pramanik, R., Samson, R., Yadav, R. kumar, Kadam, P., Shah, N., Sawant, R., Bhalerao, U., Tupekar, M., Khan, S., Shah, P., Shashidhara, L., Kamble, S., Dastager, S., Karmodiya, K., Dharne, M., 2023. 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.

3. Yadav, R., **Rajput, V**., Dharne, M., 2023. Water Hyacinth microbiome: metagenomic cues from environment and functionality in urban aquatic bodies. Cold Spring Harbor Laboratory.

4. **Rajput, V**., Pramanik, R., Malik, V., Yadav, R., Kadam, P., Bhalerao, U., Tupekar, M., Deshpande, D., Shah, P., Shashidhara, L., Boargaonkar, R., Patil, D., Kale, S., Bhalerao, A., Jain, N., Kamble, S., Dastager, S., Karmodiya, K., Dharne, M., 2023. Genomic surveillance reveals early detection and transition of Delta to Omicron Lineages of SARS-CoV-2 Variants in wastewater treatment plants of Pune, India. Cold Spring Harbor Laboratory.

5. Prabhu, V.A., **Rajput, V**., n.d. Gut Microbiota Dysbiosis in Patients with Intracranial... : Annals of Indian Academy of Neurology [WWW Document]. LWW. URL https://journals.lww.com/annalsofian/Fulltext/2022/25050/Gut_Microbiota_Dysbiosis_in_Patients_with.56.aspx (accessed 5.29.23).

6. Rajput, V., Samson, R., Yadav, R., Dastager, S., Khairnar, K., Dharne, M., 2022. Metagenomic mining of Indian river confluence reveal functional microbial community with lignocelluloytic potential. 3 Biotech 12, 1–10. https://doi.org/10.1007/s13205-022-03190-7

7. Dharmadhikari, T., Rajput, V., Yadav, R., Boargaonkar, R., Patil, D., Kale, S., Kamble, S.P., Dastager, S.G., Dharne, M.S., 2022. High throughput sequencing based direct detection of SARS-CoV-2 fragments in wastewater of Pune, West India. Science of The Total Environment 807, 151038. https://doi.org/10.1016/j.scitotenv.2021.151038

8. High throughput sequencing based direct detection of SARS-CoV-2 fragments in wastewater of Pune, West India, T Dharmadhikari, **V Rajput**, R Yadav, R Boargaonkar, D Patil, S Kale,Science of The Total Environment 807, 151038

9. Metagenomic exploration reveals a differential patterning of antibiotic resistance genes in urban and peri-urban stretches of a riverine system, **V Rajput**, R Yadav, MS Dharne, Environmental Science and Pollution Research 28 (46), 66477-66484

10. Metagenomic analysis of a mega-city river network reveals microbial compositional heterogeneity among urban and peri-urban river stretch, R Yadav, **V Rajput**, M Dharne, Science of The Total Environment 783, 146960

11. Metagenomic analysis reveals genetic insights on biogeochemical cycling, xenobiotic degradation, and stress resistance in mudflat microbiome, M Mohapatra, R Yadav, **V Rajput**, MS Dharne, G Rastogi, Journal of Environmental Management 292, 112738

12. Spatio-temporal resolution of taxonomic and functional microbiome of Lonar soda lake of India reveals metabolic potential for bioremediation, J Chakraborty, **V Rajput**, V Sapkale, S Kamble, M Dharne, Chemosphere 264, 128574

13. Functional metagenomic landscape of polluted river reveals potential genes involved in degradation of xenobiotic pollutants, R Yadav, **V Rajput**, M Dharne, Environmental Research 192, 110332

14. Comprehensive metagenomic insights into a unique mass gathering and bathing event reveals transient influence on a riverine ecosystem, R Yadav, **V Rajput**, K Gohil, K Khairnar, M Dharne, Ecotoxicology and Environmental Safety 202, 110938

15. Pan-genomics of Ochrobactrum species from clinical and environmental origins reveals distinct populations and possible links, K Gohil, **V Rajput**, M Dharne, Genomics 112 (5), 3003-3012

16. Deciphering taxonomic and functional diversity of fungi as potential bioindicators within confluence stretch of Ganges and Yamuna Rivers, impacted by anthropogenic activities, R Samson, **V Rajput**, M Shah, R Yadav, P Sarode, SG Dastager, Chemosphere 252, 126507

17. Shotgun metagenome guided exploration of anthropogenically driven resistomic hotspots within Lonar soda lake of India, J Chakraborty, V Sapkale, **V Rajput**, M Shah, S Kamble, M Dharne, Ecotoxicology and Environmental Safety 194, 110443

18. Metagenome sequencing to unveil microbial community composition and prevalence of antibiotic and metal resistance genes in hypersaline and hyperalkaline Lonar Lake, India, J Chakraborty, V Sapkale, M Shah, **V Rajput**, G Mehetre, S Agawane, Ecological Indicators 110, 105827

19. Draft Genome Sequence of Freshwater-Derived *Streptomyces* sp. Strain BPSDS2, Isolated from Damte Stream, Northeast India, Zothanpuia, AK Passari, P Deka, **V Rajput**, LPM Priya, M Dharne, Microbiology Resource Announcements 8 (43), e00874-19

20. Metagenomic insights to understand transient influence of Yamuna River on taxonomic and functional aspects of bacterial and archaeal communities of River Ganges, R Samson, M Shah, R Yadav, P Sarode, **V Rajput**, SG Dastager, Science of the Total Environment 674, 288-299

21. Draft Genome Sequence of Streptomyces thermocarboxydus BPSAC147, a Potentially Plant Growth-Promoting Endophytic Bacterium, AK Passari, **V Rajput**, Zothanpuia, LPM Priya, M Dharne, S Dastager,
Microbiology Resource Announcements 8 (23), e00363-19

22. Draft Genome Sequence of Plant Growth-Promoting Endophytic *Microbacterium hydrothermale* BPSAC84, Isolated from the Medicinal Plant *Mirabilis jalapa*, AK Passari, **V Rajput**, Zothanpuia, LPM Priya, M Dharne, S Dastager, Microbiology Resource Announcements 8 (22), e00406-19

TRAININGS & CONFERENCES

- 5-Days Industrial training at International Center for Genetic Engineering and Biotechnology (ICGEB), New-Delhi, India.
- Completed 2-Months Summer training at CSIR-Center for Cellular and Molecular Biology, Hyderabad under the guidance of Dr. Shrish Tiwari. From 25th May 2017 to 25th July2017.
- Dissertation project training for 6-Months at CSIR- Center for Cellular and Molecular Biology, under the guidance of Dr. Shrish Tiwari. From 4th Jan 2018 to 4th July 2018.
- Participated in International conference on Antimicrobial Resistance, Nobel Drug Discovery and Development: Challenges and Opportunities, organized by SRM University, Delhi- NCR. Year: 2015.
- Participated in International conference on ‶Integrative Biology & Applied Genetics″- ICIBAG: 2018, organized by Osmania University, Hyderabad. Year: March-2018.
- Participated in 9th International Conference on ‶NextGen Genomics, Biology, Bioinformatics and Technologies (2019-NGBT)″. Date: 30th Sep – 2nd Oct 2019, Mumbai, India.
- Participated in organizing Skill Development Program conducted at CSIR-National Chemical Laboratory, Pune. Title: Microbial Identification by Biochemical, Genetics and Genomic Techniques. From : 18th June 2018 to 28th June 2018

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.
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REFERENCES

- **Dr. Shrish Tiwari |** Principal Scientist |CSIR-Center For Cellular and Molecular Biology, Hyderabad-India | Email:- shrish@ccmb.res.in | Phone:- 040-27192777
- **Dr. Mahesh Dharne** | Principal Scientist and Head, | National Collection of Industrial Micro- Organisms (NCIM) | CSIR-National Chemical Laboratory | Pashan, Pune-411008, India.| Email : ms.dharne@ncl.res.in | Contact : +91-20-25902456