



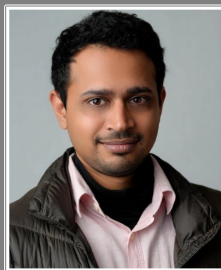
# Abhinav Sharma

## Academic Curriculum Vitae

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Indian

## EDUCATION

- **PhD Candidate (2023–current)** Stellenbosch University, Division of Molecular Biology and Human Genetics. Bioinformatics Research Unit. Supervisor: Prof. Gian van der Spuy.
- **Masters in Data Science (2020–2021).** Liverpool John Moores University, UK.
- **Post-graduate diploma in Data Science (2019–2020).** International Institute of Information Technology – Bengaluru.
- **Bachelors in Information Technology (2012–2016).** Delhi Technological University, India.

## GRANT AWARDS

1. NRF Scholarship for PhD, South Africa 2024-2026.
2. Oracle Research Cloud Credits, 2023-2026.
3. Google Cloud Research Credits 2024.
4. SAMRC registration bursary 2023.

## HUMAN LANGUAGES - PROFICIENCY

- English
- Hindi
- Portuguese

## MAIN SKILLS


- **Cloud Computing**
  - ✓ AWS
  - ✓ Azure
  - ✓ Google Cloud
  - ✓ Oracle Cloud
- **Programming Languages**
  - ✓ Nextflow
  - ✓ Python
  - ✓ R
  - ✓ Clojure(Script)
  - ✓ Powershell
  - ✓ Java
- **Databases**
  - ✓ MySQL
  - ✓ Sqlite3
  - ✓ DuckDB
  - ✓ Datomic
  - ✓ Oracle database
- **Project Management**
  - ✓ Clicks
  - ✓ RedCap

## EXPERIENCE


- **GENPATH Africa consortium (2024-current): Bioinformatician**
  - ✓ Performed Bioinformatic analysis, pipeline and SOPs implementation, data management, training development in Computer Science and Bioinformatics.
- **National Council for Scientific and Technological Development (CNPq), Brazil (2024-current) – REVIGET and GEMIBRA Consortiums: Bioinformatician and Capacity Building Mentor**
  - ✓ Performed Bioinformatic analysis, pipeline and SOPs implementation, data management, training development in Computer Science and Bioinformatics.
- **TORCH Consortium (2022-2024): Software Development (Nextflow pipeline)**
  - ✓ MAGMA Pipeline development and maintenance.
- **TELETHON KIDS INSTITUTE (2023-2024): Senior Data Scientist**
  - ✓ Facilitated the omics analysis for research groups at the institute for various clinical trials.
- **SEQERA LABS (2020 – 2022): Nextflow Specialist and Customer Success**
  - ✓ Helped top biopharma companies optimize their analysis environments (AWS /Azure) and debug their pipelines.
- **BIOSHARP OÜ (2020 -2023 ): Principal Data Scientist**
  - ✓ Provided data science and data engineering services to multiple clients.
  - ✓ Conducted multiple workshops across the globe for capacity building.
- **PXOXIMITY LABS (2020): Senior Full Stack Software Engineer**
  - ✓ Worked on the upgrade of the frontend into a performant progressive web app (PWA), with intuitive UX, performance and caching as the core concerns.
- **DEVNAGRI (2017-2019): Chief Technology Officer**
  - ✓ Lead a team of 15 software engineers to design and implement the digital platform.
  - ✓ Built an NLP engine to do initial translations, cross-platform CLI tool, web scrapers, data transformation services, etc.

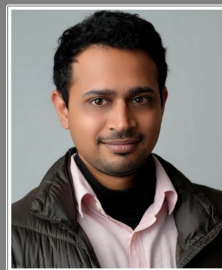
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## PUBLISHED/ACCEPTED PEER-REVIEWED ARTICLES

1. Heupinkin\*, Verboven\*, Sharma\* et al. The MAGMA pipeline for comprehensive genomic analyses of clinical *Mycobacterium tuberculosis* samples (**\*1<sup>st</sup> author**) - <https://doi.org/10.1371/journal.pcbi.1011648>.
2. Sharma\* et al. Tuberculosis drug resistance profiling based on machine learning: A literature review – (**\*1<sup>st</sup> author**) <https://doi.org/10.1016/j.bjid.2022.102332>.
3. (**ACCEPTED**) A Near-complete Genome of the Uncultured Staphylococcus aureus Phage COMBAT-CF\_PAR1, Isolated from the Lungs of an Infant with Cystic Fibrosis.
4. A Genome-Focused Investigation Reveals the Emergence of a *Mycobacterium tuberculosis* Strain Related to Multidrug-Resistant Tuberculosis in the Amazon Region of Brazil - <https://doi.org/10.3390/microorganisms12091817>.
5. Description of new species of *Mycobacterium terrae* complex isolated from sewage at the São Paulo zoological park foundation in Brazil - <https://doi.org/10.3389/fmicb.2024.1335985>.
6. Whole-Genome Sequencing of *Alcaligenes faecalis* HZ01, with Potential to Inhibit Nontuberculous Mycobacterial Growth - <https://doi.org/10.1128/mra.00521-21>.
7. Molecular epidemiology of *Mycobacterium tuberculosis* in Brazil before the whole genome sequencing era: A literature review - <https://doi.org/10.1590/0074-0276020517>.
8. Genomic Diversity of the Rarely Observed Genotype of the *Mycobacterium tuberculosis* Central Asian (CAS) Lineage 3 from North Brazil - <https://doi.org/10.3390/microorganisms11010132>.
9. Analysis of potential household transmission events of tuberculosis in the city of Belem, Brazil – <https://doi.org/10.1016/j.tube.2018.09.011>.
10. Characterization of *Mycobacterium tuberculosis* var. *africanum* isolated from a patient with pulmonary tuberculosis in Brazil - <https://doi.org/10.1016/j.meegid.2020.104550>.
11. Evaluation of drug susceptibility profile of *Mycobacterium tuberculosis* Lineage 1 from Brazil based on whole genome sequencing and phenotypic methods – <https://doi.org/10.1590/0074-02760200520>.

## ARTICLES UNDER PEER-REVIEW

1. Marcon\*, Sharma\* et al. Genomic surveillance reveals transmission profiles of the first extensively drug-resistant tuberculosis cases in Pará, Brazil (**\*1<sup>st</sup> author**) – **Frontiers in Microbiology, Oct, 2024.**
2. Virome Assembly Reveals Draft Genomes of Native Pseudomonas Phages isolated from a Paediatric Bronchoalveolar Lavage Sample – **Microbiology Resource Announcements, Sep, 2024.**

## ARTICLES IN-SUBMISSION

1. Sharma\* et al. MTBseq-nf: Enabling Scalable Tuberculosis Genomics “Big Data” Analysis through a User-Friendly Nextflow Wrapper for MTBseq pipeline (**\*1<sup>st</sup> author**). **Intended journal: PEERJ.**
2. Sharma\* et al. CholeraSeq: a comprehensive genomic automated pipeline for cholera surveillance and near real-time outbreak investigation. (**\*1<sup>st</sup> author**). **Intended journal: Oxford Bioinformatics.**
3. Sharma# et al. Ten simple rules to build sustainable bioinformatics capacity using Nextflow and nf-core with a focus on early-mid career researchers: The Kids Institute case report. (**#Senior author**). **Intended journal: PLOS One Bioinformatics.**
4. Leveraging the State of Whole Genome Sequencing for Precision Public Health in a High-Burden Tuberculosis Setting using the GEMIBRA Platform. **Intended journal: Discovery Public Health.**

## INTERNATIONAL COLLABORATION NETWORK

1. **SOUTH AFRICA:** Stellenbosch University Research Groups (TB Genomics – Rob Warren, CERI – Tulio de Oliveira, Host Genetics – Marlo Moller, Africa Microbiome Institute - Kristine Nel van Zyl), University of the Western Cape (UWC) - Alan Christoffels', University of Limpopo - Ivy Rukasha, and DIPLOMICS - Mhlekezi Molatoli.
2. **BRAZIL:** Instituto Evandro Chagas (Karla Lima), Fiocruz-IOC (Philip Suffys), Fiocruz-INI (Cristina Lourenço), UNIFESP (Cristina Viana), UNIPEX (Patricia Reis), USP (Ana Marcia Guimaraes), UFC (Cristiane Frota).
3. **ZAMBIA:** Tropical Disease Research Center (TDRC), Ndola (Kabengele Keith).
4. **BELGIUM:** Antwerp University (Annelies van Rie) and University Hospital Ghent (Tom Sante).
5. **AUSTRALIA:** The Kids Institute and University of Western Australia (Patricia Agudelo-Romero).
6. **SPAIN:** nf-core and Nextflow communities (Seqera Labs) - Ambassador.
7. **UNITED KINGDOM:** LSHTM (Jody Phelan).