

# GARIMA AYACHIT

Laval, QC, Canada

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## PROFESSIONAL SUMMARY

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Dynamic Bioinformatics scientist with over 8 years of comprehensive experience in NGS data analysis and AI/ML applications. Proficient in developing robust pipelines, conducting RNA-seq analysis, and applying advanced computational tools. Successfully engineered the ANNOTATOR-RNator pipeline and ML based genomic prediction pipeline miRDetect enhancing genomics and transcriptome analysis capabilities. Strong track record in mentoring and collaborating on complex projects. Adept at leveraging technical expertise to drive impactful research and innovation.

## CORE SKILLS & EXPERTISE

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- Bioinformatics & Genomics
  - NGS and Multi-omics (WGS, WES, RNA-seq, scRNA-seq, miRNA-seq, metagenomics)
  - Comparative genomics, transcriptomics, and biomarker discovery
  - Dual RNA-seq and host-pathogen interaction analysis
  - DNA barcoding and phylogenetics
- AI/ML, Programming & Data Science
  - Python (pipeline development, data processing, data analysis, biological resource mining and automation)
  - R (data visualization, statistical modeling, ggplot2, Tidyverse, DESeq2, normalization), Python (pandas, numpy, scikit-learn)
  - Machine learning approaches for spatio-temporal feature enhancement, classification and performance evaluation (SVM, Random Forest, kNN, cross-validation, ROC-AUC, feature importance and filtering and SHAP interpretability)
- High-Performance & Cloud Computing
  - HPC environments (SLURM, job scheduling, Singularity/apptainer containers), containerization
  - Compute Canada and Linux server administration
  - Cloud computing (AWS) for scalable bioinformatics workflows
- Tools & Pipelines
  - BWA, fastpGATK, STAR, HISAT2, DESeq2, Subread/FeatureCounts, Bedtools
  - Git/GitHub for version control and collaboration
  - Custom pipeline development (e.g., **ANNOTATOR-RNator**, **miRDetect**), command-line shell scripts
- Project Leadership & Collaboration
  - Mentoring and training graduate students and researchers
  - Cross-disciplinary collaborations with PhD scientists and clinicians
  - Research proposal drafting (national/state-level grants)
  - Strong written and oral communication skills

## PROFESSIONAL EXPERIENCE

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### Postdoctoral Fellow | INRS, Laval, QC | Feb 2022 – Oct 2023

- **Engineered** ANNOTATOR-RNator pipeline for pan-species transcriptome analysis integrating BLAST, BWA, Prokka, NetworkX, Get\_homologous, and FeatureCount
- **Executed** dual RNA-seq analysis of Neisseria-infected cell lines using DESeq2 to uncover host-pathogen interactions.
- **Leveraged** HPC (Compute Canada, SLURM) and Singularity for reproducible workflows and large scale analysis.
- **Advised** in analysis of bulk Metagenome data using various tools
- **Guided** a doctoral student in scRNAseq analysis using Seurat
- **Implemented** shell scripting and version control with GitHub for reproducible workflows.

### Research Bioinformatician | BaseSolve Informatics Pvt. Ltd | Oct 2020 – Feb 2021

- **Scrutinized** client NGS data (Eukaryotic WGS, Fungal genomics, amplicon sequence, RNAseq, exome)
- **Composed** detailed bioinformatics reports tailored to client research goals

- **Deployed** pipelines on SLURM clusters, Singularity containers, Linux environments, and AWS Cloud.

#### **Research Associate | Gujarat Biotechnology Research Centre, India | July 2016 – July 2019**

- **Led** team of junior research fellows for executing project on plant transcriptome analysis for upscaling of metabolites
- **Investigated** TCGA datasets to discover biomarkers for oral squamous cell carcinoma using differential expression analysis. Analyzed miRNA-seq data for different projects
- **Coordinated** and executed collaborative projects with IIT, India and trained students in Linux essentials
- **Drafted** research proposals for grant applications

#### **Senior Research fellow | Gujarat State Biotechnology Mission, India | June 2014 – June 2016**

- **Performed** whole-genome sequencing analysis of Asiatic lion (Schedule 1 species) to identify genetic variations.
- **Evaluated** WES and targeted cancer panels for rare disease research.
- **Characterized** saline desert microbiomes via shotgun metagenomic sequencing.
- **Generated** DNA barcodes for marine species biodiversity banking; deposited sequences in BOLD database.
- **Mentored** graduate students during Master's dissertation projects.

#### **Junior Research fellow | Gujarat State Biotechnology Mission, India | Aug 2012- June 2014**

- **Analyzed** whole-genome sequencing data of salt-tolerant desert bacteria.
- **Maintained** & customized PHP-MySQL grant management system for state research funding.

### **EDUCATIONAL CREDENTIALS**

2022	<b>PhD Bioinformatics</b> , Gujarat University, India
2015	<b>M. Phil. Biotechnology</b> , Hemchandracharya North Gujarat University, Patan, Gujarat, India
2011	<b>Master of Science</b> , Bioinformatics, G.H Patel Department of Computer Science and Technology, (GDCST), Sardar Patel University, India
2009	<b>Bachelor of Science</b> , Bioinformatics, N.V Patel College of Pure and Applied Sciences, Sardar Patel University, India

### **SELECTED PUBLICATIONS**

- Giraud-Gatineau, A., **Ayachit, G.**, Nieves, C., Dagbo, K.C., Bourhy, K., Pulido, F., Huete, S.G., Benaroudj, N., Picardeau, M. and Veyrier, F.J., 2024. Inter-species transcriptomic analysis reveals a constitutive adaptation against oxidative stress for the highly virulent *Leptospira* species. **Molecular Biology and Evolution**, 41(4), p.msae066.
- **Ayachit, G.**, Pandya, H. and Das, J., 2020. miRDetect: A combinatorial approach for automated detection of novel miRNA precursors from plant EST data using homology and Random Forest classification. **Genomics**.
- **Ayachit, G.**, Shaikh, Inayatullah., Pandya, H. and Das, J., 2020. Salient Features, Data and Algorithms for microRNA Screening from Plants: A Review on the Gains and Pitfalls of Machine Learning Techniques. **Current Bioinformatics**.
- **Ayachit, G.**, Shaikh, I., Sharma, P., Jani, B., Shukla, L., Sharma, P., Bhairappanavar, S.B., Joshi, C. and Das, J., 2019. De novo transcriptome of *Gymnema sylvestre* identified putative lncRNA and genes regulating terpenoid biosynthesis pathway. **Scientific Reports**, 9(1), pp.1-13.
- Shaikh, I., Ansari, A., **Ayachit, G.**, Gandhi, M., Sharma, P., Bhairappanavar, S., Joshi, C.G. and Das, J., 2019. Differential gene expression analysis of HNSCC tumors deciphered tobacco dependent and independent molecular signatures. **Oncotarget**, 10(58), pp.6168-6183.

### **GITHUB PROJECT LINKS**

- <https://github.com/BactSymEvol/Annotator-RNAtor>
- <https://github.com/Garima268/miRDetect>