GARIMA AYACHIT

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PROFESSIONAL SUMMARY

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 including BLAST and DESeq2. Successfully engineered the ANNOTATOR-RNAtor pipeline, enhancing 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

- 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
- Programming & Data Science
  - Python (pipeline development, data processing, data analysis, biological resource mining and automation)
  - R (data visualization, statistical modeling, ggplot2, Tidyverse, DESeq2), Python (pandas, numpy, scikit-learn)
  - Machine learning approaches for sequence and expression analysis
- 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

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

Senior Research fellow | Gujarat State Biotechnology Mission, India | June 2014 – June 2016
- o **Performed** whole-genome sequencing analysis of Asiatic lion (Schedule 1 species) to identify genetic variations.
- o **Evaluated** WES and targeted cancer panels for rare disease research.
- o **Characterized** saline desert microbiomes via shotgun metagenomic sequencing.
- o **Generated** DNA barcodes for marine species biodiversity banking; deposited sequences in BOLD database.
- o **Mentored** graduate students during Master's dissertation projects.

Junior Research fellow | Gujarat State Biotechnology Mission, India | Aug 2012- June 2014
- o **Analyzed** whole-genome sequencing data of salt-tolerant desert bacteria.
- o **Maintained** & customized PHP–MySQL grant management system for state research funding.

EDUCATIONAL CREDENTIALS

2022	**PhD Bioinformatics**, Gujarat University, India
2015	**M. Phil. Biotechnology**, Hemchandracharya North Gujarat University, Patan, Gujarat, India
2011	**Master of Science**, Bioinformatics, G.H Patel Department of Computer Science and Technology, (GDCST), Sardar Patel University, India
2009	**Bachelor of Science**, 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