Ruhila S.

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RuhilaS
https://github.com/RuhilaS/

"Nothing exists for itself alone, but only in relation to other forms of life."
– Charles Darwin

Personal Data

Name	Ruhila S.
Date Of Birth	20.09.2001
Virudhunagar	Tamil Nadu, India

Education

2021–PRESENT **B.S-M.S. Biology (Major) Data Science (Minor)**, *Indian Institute of Science Education and Research (IISER)*, Mohali, *India*
8.3 CGPA

Experience

Internships

SUMMER 2021 **Dr. Lolitika Mandal**, *IISER Mohali*, Research Intern
Exploring Genetic Tools for working with Drosophila from a wet-lab perspective of data collection and analysis.

Summer 2022–present **Prof. Arnar Pálsson**, *University of Iceland*, Research Staff

Detailed analysis in a literate and reproducible manner for simulating a series of possible molecular evolutionary pathways for the *Salmolid* using phylogenetic trees. This involved the five steps on an HPC (High Performance Computer) with literate programming visualization in R:

- Data curation with NCBI databases
- Homology inference using similarity measures (BLAST)
- Multiple sequence alignment (MUSCLE5)
- Alignment trimming (G-BLOCK)
- Tree simulation with distance measures (BIONJ) and maximum likelihood approaches (RAXML-NG)

Project Report: Computational Primitives for Evolutionary Paths (≈ 147 pages)

Volunteer Work

2021–present **Biological Society**, *IISER Mohali*, Member

Enthusiastic participant and also arrange for independent peer-reviewed article readings.

2021–present **Dance Society**, *IISER Mohali*, Member

Active participant for choreography and performances.

Certifications

NPTEL Courses

Sep 2022 **Applications of machine learning techniques in biology using WEKA**, *IIT Madras*, Distinction, 93%

Technical Skills

Programming Languages

Experienced: R, Python (3.x), Shell (zsh,bash)

Familiar: C, Java

Bioinformatics Packages

Experienced: Randomized Axelerated Maximum Likelihood new generation (RAXML-NG), MUSCLE5 (multiple sequence alignment)

Familiar: WEKA, BEAST2 (Bayesian Evolutionary Analysis Sampling Trees) via babette, Snakemake

Tools

Experienced: Git (version control), ssh, Vim, Markdown

Familiar: Office-Suites (MS, OpenOffice, LibreOffice)

Experimental

Biological Handling flies (wild-type, w1118, tubby), Drosophila larva dissection (brain, salivary gland, proventriculus, imaginal discs, gastric caeca), Fixing, staining, mounting viewing tissues with Flourescent microscopes, Making PBS, PFA

Professional Time management, critical thinking, problem solving, communication

Research Topics

Experienced Phylogenetic Tree Construction (Distance, Maximum Likelihood, Bayesian), Evolutionary Biology, Population genetics, R reproducible literate programming, High performance open source software, Scientific Software Development for High Throughput calculations

Interested Biomolecular simulations, Genomics, Modeling genetic markers for disease

Affiliations

Memberships

2022–present **RSB (Royal Society of Biology)**, -Student Member

2022–present **IEEE EMBS (Engineering in Medicine and Biology Society)**, Student Member

2022–present **British Ecological Society**, Student Member