

# Ruhila S.

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🌐 <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  
Birthplace 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  
2020 **Intermediate (AISSCE)**, *Velammal Vidyalaya, Ayanabakkam, Chennai, India*  
83.8% Central Board of Secondary Education (CBSE)  
2017 **High School (AISSE)**, *Velammal Vidyalaya, Ayanabakkam, Chennai, India*  
10.0 Cumulative Grade Point Average (CGPA) in Central Board of Secondary Education (CBSE)

## Experience

### Internships

WINTER 2022 **Dr. Nagma Parveen, IIT Kanpur**, Research Intern  
I shall be working on wet-lab methods for studying the mechanisms of viral action under varying external stimuli.

SUMMER	<b>Prof. Arnar Pálsson</b> , <i>University of Iceland</i> , Research Staff
2022–PRESENT	<p>Detailed analysis in a literate and reproducible manner for simulating a series of possible molecular evolutionary pathways for the <i>Salmolid</i> using phylogenetic trees. This involved the five steps on an HPC (High Performance Computer) with literate programming visualization in R:</p> <ul style="list-style-type: none"> <li>○ Data curation with NCBI databases</li> <li>○ Homology inference using similarity measures (BLAST)</li> <li>○ Multiple sequence alignment (MUSCLE5)</li> <li>○ Alignment trimming (G-BLOCK)</li> <li>○ Tree simulation with distance measures (BIONJ) and maximum likelihood approaches (RAXML-NG)</li> </ul> <p>PROJECT REPORT: Computational Primitives for Evolutionary Paths (<math>\approx</math> 147 pages)</p>
SUMMER 2021	<p><b>Dr. Lolitika Mandal</b>, <i>IISER Mohali</i>, Research Intern</p> <p>Exploring Genetic Tools for working with <i>Drosophila</i> from a wet-lab perspective of data collection and analysis.</p> <p><b>Volunteer Work</b></p>
2022–PRESENT	<p><b>IEEE P3173</b>, <i>IEEE Standards Committee</i>, Secretary</p> <p>Am supporting the drafting the IEEE Standard for Endocrine Disrupting Chemical Hazard Labeling</p>
2021–PRESENT	<p><b>Biological Society</b>, <i>IISER Mohali</i>, Member</p> <p>Enthusiastic participant and also am responsible for arranging independent peer-reviewed article readings.</p>
2021–PRESENT	<p><b>Dance Society</b>, <i>IISER Mohali</i>, Member</p> <p>Active participant for choreography and performances.</p>

## Certifications

### NPTEL Courses

SEP 2022	<b>Applications of machine learning techniques in biology using WEKA</b> , <i>IIT Madras</i> , Distinction, 93%
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### Other Courses

NOV 2022	<b>Practical Python for beginners: a biochemist's guide</b> , <i>Biochemical Society</i> , U.K.
NOV 2022	<b>The future of HPC programming - a Modern Fortran workshop</b> , <i>Swedish National Infrastructure for Computing</i> , Online

## Technical Skills

### Programming Languages

EXPERIENCED	R, Python (3.x), Shell (zsh,bash)	FAMILIAR	C, Java
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## Bioinformatics Packages

EXPERIENCED	Randomized Axelerated Maximum Likelihood new generation (RAXML-NG), MUSCLE5 (multiple sequence alignment)	FAMILIAR	WEKA, BEAST2 (Bayesian Evolutionary Analysis Sampling Trees) via babbette, Snakemake
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## Tools

EXPERIENCED	Git (version control), ssh, Vim, Markdown	FAMILIAR	Office-Suites (MS, OpenOffice, LibreOffice)
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## Experimental

BIOLOGICAL	Handling flies (wild-type, w <sup>1118</sup> , tubby), Drosophila larva dissection (brain, salivary gland, proventriculus, imaginal discs, gastric caeca), Fixing, staining, mounting viewing tissues with Fluorescent microscopes, Making PBS, PFA	PROFESSIONAL	Time management, critical thinking, problem solving, communication
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## 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, Oncology and stem cells, Human genetics
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## Affiliations

### Memberships

2022–PRESENT	<b>RSB (Royal Society of Biology)</b> , Student Member
2022–PRESENT	<b>British Ecological Society</b> , Student Member
2022–PRESENT	<b>Biochemical Society, UK</b> , Undergraduate Member
2022–PRESENT	<b>Genetics Society, UK</b> , Undergraduate Member

2022–PRESENT **Genetics Society of America**, Undergraduate Member

2022–PRESENT **Royal Microscopical Society, UK**, Undergraduate Member

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

2022–PRESENT **Federation of European Biochemical Societies (FEBS)**, Member

2022–PRESENT **European Microscopy Society**, Member

2022–PRESENT **ACM (Association for Computing Machinery)**, Student Member

## Publications

### CONFERENCE PROCEEDINGS

Rohit Goswami, Ruhila S, Amrita Goswami, Sonaly Goswami, and Debabrata Goswami. “Reproducible High Performance Computing Without Redundancy with Nix (accepted).” In: *2022 Seventh International Conference on Parallel, Distributed and Grid Computing (PDGC)*. 2023.

Rohit Goswami and Ruhila S. “High Throughput Reproducible Literate Phylogenetic Analysis (accepted).” In: *2022 Seventh International Conference on Parallel, Distributed and Grid Computing (PDGC)*. 2023.

## Conference Records

### Posters

NOVEMBER 2022 **Tracing Lineages of *Salmo Salar* through Histone sequence data**, *BES Annual Meeting 2022*, Ruhila S., Accepted

### Oral Presentations

NOVEMBER 2022 **High Throughput Reproducible Literate Phylogenetic Analysis**, *IEEE PDGC-2022*, R. Goswami, Ruhila S., Accepted

NOVEMBER 2022 **Reproducible High Performance Computing Without Redundancy with Nix**, *IEEE PDGC-2022*, R. Goswami, Ruhila S., A. Goswami, S. Goswami and D. Goswami, Accepted

NOVEMBER 2022 **Reproducible Literate Programming Workflows for Censored Data**, *IOP Machine Learning for Healthcare*, R. Goswami, R. S.