# Abhinay Mishra

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## EDUCATION

Freie Universität Berlin, Germany

M.Sc. in Bioinformatics, Grade: 2.4 2020 - 2025

Jaypee University of Information Technology (JUIT)

Waknaghat, India B.Tech. in Bioinformatics, Grade: 6.6 2013-2017

EXPERIENCE

Internship

Systems Medicine of the Liver, Humboldt-Universität zu Berlin

Berlin, Germany Jan 2025–Feb 2025

- Created a physiologically based pharmacokinetic model for Tirzepatide using curated clinical data and parameter optimization. [5] **?** 

Theoretical Biophysics, Humboldt-Universität zu Berlin

Berlin, Germany May 2024–Jan 2025

- Built & validated an optimization framework to reconstruct triple-negative breast cancer phosphorylation networks from LC-MS and kinase-substrate data using Differential Evolution and Sequential Least Squares Programming. [4] 🔾

**Mathematics Tuition Teacher** 

Allahabad, India

Self-Employed

Master Thesis

Apr 2019-Sep 2019

Graduate Aptitude Test in Engineering (GATE)

Bioinformatics and Systems Biology, JUIT

Allahabad, India Aug 2017-Feb 2018

Biotechnology, All India Rank 681

Solan, India

Bachelor Thesis

Feb 2016-March 2017

- Built a pipeline using GEO2R, MeV, WB-DEGS, and R/Shiny to identify and validate prostate cancer biomarkers. [6] •

Computer Aided Drug Design, JUIT

Solan, India

Project

Aug 2015-Mar 2016

- Developed a docking workflow in Discovery Studio, Maestro, and Glide XP to screen FDA-approved drugs against the Dopamine D3 receptor and analyze protein-ligand interactions in PyMol & VMD. •

PROJECTS

**PhosKinTime** May 2024–May 2025

- Optimization driven ODE-based modeling package for analyzing cell-signaling dynamics over time. [4] 🖸 🗏

CodonAnalyzer  $\mathrm{Jan}\ 2025\mathrm{-May}\ 2025$ 

 Snakemake workflow for analyzing codon usage, extracting ORFs, translating sequences to protein, and computing hydropathy profiles. [1] 🞧 🗏

Jan 2025–Present Illumina2Lineage

- Nextflow pipeline for SARS-CoV-2 genome assembly and analysis from Illumina reads. [3]  $\mathbf{Q} \equiv$ 

Jan 2025-Present GRmap

— Snakemake pipeline for matching sequencing reads to a reference genome and annotating genomic features. [2] 🖸 🗏

### SKILLS

<b>?</b> Python	git Git	<b>snake</b> make
<b>♀</b> R	I≱T <sub>E</sub> X	Z Scientific Programming
<b>&gt;_</b> Bash	julià	Q Data Mining
<b>&gt;</b> Perl	Algorithms	<b>T</b> Project Development
nextflow		Data Analysis

# LANGUAGES

English: Native, Hindi: Native

### Conferences

• MATH+ Day 2024 with General Assembly and Poster Session	Oct 2024
• National Symposium on Computational Systems Biology (NSCSB)	Mar 2016
• R&D Expo, IEEE-JUIT	May 2016
• RECOMB 2020	June 2020

#### Publications

- [1] A. Mishra, Codonanalyzer: V1.0.2, version v1.0.2, May 2025. DOI: 10.5281/zenodo.15384943.
- [2] A. Mishra, Grmap: V0.2, version v0.2, May 2025. DOI: 10.5281/zenodo.15390191.
- [3] A. Mishra, Nf-illumina2lineage: V0.9.0, version v0.9.0, May 2025. DOI: 10.5281/zenodo.15376065.
- [4] A. Mishra, *Phoskintime: V0.4.0*, version v0.4.0, May 2025. DOI: 10.5281/zenodo.15351017.
- [5] A. Mishra and M. König, *Physiologically based pharmacokinetic (pbpk) model of tirzepatide*, version 0.9.3, Mar. 2025. DOI: 10.5281/zenodo.14984688.
- [6] N. Asati, A. **Mishra**, A. Shukla, and T. R. Singh, "Gene expression studies to identify significant genes in ar, mtor, mapk pathways and their overlapping regulatory role in prostate cancer", *Journal of Integrative Bioinformatics*, vol. 16, no. 3, p. 20180080, 2019. DOI: 10.1515/jib-2018-0080.