

EDUCATION

Freie Universität

M.Sc. in Bioinformatics, *Grade: 2.4*

Berlin, Germany

2020–2025

Jaypee University of Information Technology (JUIT)

B.Tech. in Bioinformatics, *Grade: 6.6*

Waknaghat, India

2013–2017

EXPERIENCE

Systems Medicine of the Liver, Humboldt-Universität zu Berlin

Internship, Supervisor: *Dr. Matthias König*

Berlin, Germany

Jan 2025–Feb 2025

- Developed a Physiologically-Based Pharmacokinetic (PBPK) model for Tirzepatide by curating pharmacokinetic data from clinical literature and implementing parameter optimization to improve model accuracy. [2]
- Conducted simulations across varied patient populations (renal/hepatic impairment, weight classes) to explore dose dependency and physiological variability, supporting personalized therapy strategies. Documented methodology, validation, and results in a structured research report.

Theoretical Biophysics, Humboldt-Universität zu Berlin

Master Thesis, Supervisor: *Prof. Dr. Dr. h.c. Edda Klipp*

Berlin, Germany

May 2024–Jan 2025

- Developed an ODE-based optimization framework for reconstructing phosphorylation signaling networks in triple-negative breast cancer using time-series LC-MS data and kinase-substrate predictions. Focused on parameter estimation via DE and SLSQP, with biological constraint integration. [1]
- Complemented thesis with *phoskintime*: a modular toolkit for phosphorylation model optimization featuring flexible weighting schemes, sensitivity analysis, and constraint based optimization.

Mathematics Tuition Teacher

Self-Employed

Allahabad, India

Apr 2019–Sep 2019

Graduate Aptitude Test in Engineering (GATE)

Biotechnology, *All India Rank 681*

Allahabad, India

Aug 2017–Feb 2018

Bioinformatics and Systems Biology, JUIT

Bachelor Thesis, Supervisor: *Prof. Dr. Tiratha Raj Singh*

Solan, India

Feb 2016–March 2017

- Built a bioinformatics pipeline to identify key biomarkers for prostate cancer by integrating differential gene expression analysis with transcriptomic datasets from GEO, leveraging tools like GEO2R, MeV, WB-DEGS, and R/Shiny for statistical validation and visualization.[3]
- Conducted pathway enrichment and protein interaction analyses via STRING and GeneMANIA to map AR, MAPK, and m-TOR signaling networks, applying clustering and network-based methods to classify biomarkers and support targeted therapeutic strategies.

Computer Aided Drug Design, JUIT







Project, Supervisor: *Dr. Chittaranjan Rout* (Deceased, 2019)

Solan, India
















Aug 2015–Mar 2016

- 3rd prize in Poster Presentation, NSCSB
- Designed a molecular docking workflow using Discovery Studio, Maestro, and Glide XP to screen FDA-approved drugs against the Dopamine D3 Receptor for schizophrenia treatment. Integrated protein-ligand flexibility, pharmacodynamic insights, and interaction analysis using PyMol and VMD.
- Identified potential lead compounds including Misoprostol and Carvedilol, and presented results at scientific forums, advancing computational psychiatry and drug repurposing efforts.

PROJECTS

SequenceAligner <ul style="list-style-type: none">– Lightweight command-line tool for sequence alignment. 	Mar 2025–Present
GRMAP – Genomic Reads Mapping and Annotation Pipeline <ul style="list-style-type: none">– Modular pipeline for genomic read mapping and annotation. 	Jan 2023–Present
PhosKinTime <ul style="list-style-type: none">– Developed a Python toolkit for phosphorylation ODE modeling and optimization, featuring custom weighting schemes, sensitivity analysis, and constraint-based parameter estimation. 	May 2024–May 2025
SARS Genome Assembly <ul style="list-style-type: none">– Pipeline for genome assembly and annotation of SARS coronavirus strains. 	Sep 2023–Jan 2025
ML Classification of Liver HCC <ul style="list-style-type: none">– Built ML classifiers to distinguish liver cancer tissue using transcriptomic and epigenomic features. 	Jun 2022–Jul 2022
CodonAnalyzer <ul style="list-style-type: none">– Tool for codon usage bias analysis in DNA sequences. 	Aug 2015–Sep 2015

SKILLS

 Python	 Git	 Academic Writing
 R	 \LaTeX	 Scientific Programming
 Bash	 Data Analysis	 Data Mining
 Perl	 Algorithms	 Project Development
 Julia	 Modelling	 Machine Learning

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**, *Phoskintime: V0.4.0*, version v0.4.0, May 2025. DOI: 10.5281/zenodo.15351017.
- [2] A. **Mishra** and M. König, *Physiologically based pharmacokinetic (pbpk) model of tirzepatide*, version 0.9.3, Mar. 2025. DOI: 10.5281/zenodo.14984688.
- [3] 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.