CV – Abhinav Mishra

1. Personal Details

- **Surname**: Mishra
- **First Name**: Abhinav
- **Date of Birth**: 17-08-1994
- **Nationality**: Indian
- **Phone**: +49 15252431035
- **Email**: mishraabhinav36@gmail.com
- **Website**: https://bibymaths.github.io/
- **GitHub**: https://github.com/bibymaths
- **ORCID**: https://orcid.org/0009-0005-3179-7408

2. Language Skills: English (native), Hindi (native)

3. Degrees

- **2025**: *Master of Science in Bioinformatics*, Freie Universität Berlin, Germany
  Thesis: Mathematical Optimization of Signalling Networks in Triple Negative Breast Cancer Cell Lines
- **2017**: *Bachelor of Technology in Bioinformatics*, Jaypee University of Information Technology, India
  Thesis: Identification of Potent Biomarkers for Prostate Cancer Through AR, MAPK, and mTOR Signalling Pathway Mining

4. Previous Work Experience

- **Research Intern**, Institute for Biology, HU Berlin (Jan 2025–Feb 2025)
  Created a physiologically based pharmacokinetic model for Tirzepatide using curated clinical data and parameter optimization. [GitHub]
- **Master Thesis Student**, Theoretical Biophysics, HU Berlin (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. [GitHub]
- **Bachelor Thesis Student**, JUIT, India (Feb 2016–Mar 2017)
  Built a pipeline using GEO2R, MeV, WB-DEGS, and R/Shiny to identify and validate prostate cancer biomarkers. [GitHub]
- **Project Researcher**, JUIT, India (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 analyse protein–ligand interactions in PyMol & VMD. [GitHub]

5. Career Breaks

- **2018–2020**: Career break due to family reasons and illness (recurrent *pilonidal sinus*)
- **2012–2013**: Preparation for bachelor program entrance exams

6. Research Output

- **Publications**:
    - Mishra, A.and M. König. Physiologically Based Pharmacokinetic (PBPK) Model of Tirzepatide. 0.9.3, Zenodo, 7 Mar. 2025, doi:10.5281/zenodo.14984688.
    - Asati, N., Mishra, A., Shukla, A. & Singh, T. (2019). Gene Expression Studies to Identify Significant Genes in AR, MTOR, MAPK Pathways and their Overlapping Regulatory Role in Prostate Cancer. Journal of Integrative Bioinformatics, 16(3), 20180080. https://doi.org/10.1515/jib-2018-0080.
- **Software/Tools**:
    - *PhosKinTime*: An optimization driven ODE-based modeling pipeline for analyzing cell-signaling dynamics over time.
      [Publication] [GitHub] [Documentation]
    - *GRMAP*: A Snakemake pipeline for matching sequencing reads to a reference genome and annotating genomic features.
      [Publication] [GitHub] [Documentation]
    - *CodonAnalyzer*: A Snakemake workflow for analyzing codon usage, extracting ORFs, translating sequences to protein, and computing hydropathy profiles.
      [Publication] [GitHub] [Documentation]
    - *nf-Illumina2Lineage*: A Nextflow pipeline for SARS-CoV-2 genome assembly and analysis from Illumina reads—includes QC, mapping, variant calling, consensus generation, lineage annotation, and phylogenetics.
      [Publication] [GitHub] [Documentation]
    - *SequenceAligner*: A high-performance tool for global and local sequence alignment, accelerated with MPI, OpenMP, and SIMD for DNA and protein sequences.
      [Publication] [GitHub] [Documentation]

7. Awards and Honours

- 3rd Prize, Poster Presentation, NSCSB 2016, JUIT India
- GATE Qualified, AIR 681 (2018)

8. References

Signed recommendation letters from senior supervisors and professors are available upon request.