Abhinav Mishra

Nationality: Indian **Date of birth:** 17/08/1994 **Place of birth:** Allahabad, India

Phone number: (+49) 15252431035 **Email address:** mishraabhinav36@gmail.com

LinkedIn: bibymaths

GitHub: bibymaths

Home: c/o Claudia Texeira de Sousa Soldiner Str. 67 , 13359 Berlin (Germany)

ABOUT ME

Bioinformatics professional motivated by mathematics and programming to tackle biological challenges.

EDUCATION AND TRAINING

Masters of Science in Bioinformatics

Freie Universität Berlin [01/11/2020 – 12/03/2025]

Address: Kaiserswerther Str. 16-18 , 14195 Berlin (Germany) | **Website:** https://www.fu-berlin.de/ | **Field(s) of study:** Natural sciences, mathematics and statistics: ● Inter-disciplinary programmes and qualifications involving natural sciences, mathematics and statistics ; Health and welfare: ● Inter-disciplinary programmes and qualifications involving health and welfare | **Final grade:** 2.4 | **Level in EQF:** EQF level 7 | **NQF Level:** 7 | **Type of credits:** ECTS | **Number of credits:** 120 | **Thesis:** Mathematical Optimization of Signalling Networks in Triple Negative Breast Cancer Cell Lines

Link: https://www.mi.fu-berlin.de/en/bioinf/stud/master/index.html

- Advanced Computational & Data Science Skills – Specialized in machine learning, statistical modeling, and algorithm development for bioinformatics applications, with a focus on data science in life sciences and computational cancer research.
- Interdisciplinary Bioinformatics Expertise – Integrated biomedical data analysis, complex systems modeling, and clinical trial methodology, applying computational techniques to biological and medical research.
- Practical & Research Experience – Conducted bioinformatics research internships, explored genomics, proteomics, and biometrics, and worked on current topics in medical genomics and human evolution.
- Occupational Skills – Developed biological network inference, pathway analysis, AI-driven bioinformatics, statistical programming, and computational modeling for biomedical applications.

Bachelor of Technology in Bioinformatics

Jaypee University of Information Technology (H.P.) [01/06/2013 – 12/07/2017]

Address: P.O. Waknaghat, Teh Kandaghat Distt. Solan , 173234 Waknaghat (India) | **Website:** https://www.juit.ac.in/ | **Field(s) of study:** Natural sciences, mathematics and statistics: ● Inter-disciplinary programmes and qualifications involving natural sciences, mathematics and statistics ; Health and welfare: ● Inter-disciplinary programmes and qualifications involving health and welfare | **Final grade:** 6.6 | **Level in EQF:** EQF level 6 | **NQF Level:** 6 | **Type of credits:** ECTS | **Number of credits:** 306 | **Thesis:** Identification of Potent Biomarkers for Prostate Cancer Through AR, MAPK, and mTOR Signaling Pathway Mining

Links: https://www.youracclaim.com/badges/6ce15459-9f86-44e5-9090-1a38e6d0858d/linked_in_profile | https://www.juit.ac.in/department/bio/Course_Curriculum_B.Tech_Bioinformatics.pdf

- Interdisciplinary Foundation – Integrated biology, computer science, and mathematics, covering molecular biology, genomics, structural biology, and computational modeling.
- Computational & Analytical Skills – Gained expertise in data structures, algorithms, machine learning, biostatistics, and biological databases for bioinformatics applications.
- Practical & Technical Training – Hands-on experience in Linux programming, molecular modeling, computational drug discovery, and systems biology.
- Occupational Skills – Developed data analysis, biological network modeling, algorithm development, and AI-driven bioinformatics techniques.
- Research & Industry Exposure – Engaged in laboratory work, software tool implementation, and bioinformatics-focused internships, preparing for roles in computational biology and AI-driven biomedical research.

WORK EXPERIENCE

Research Intern

Dr. Matthias König [07/01/2025 – 28/02/2025]

Address: Philippstraße 13 Institute for Biology, Humboldt Universität zu Berlin, 10115 Berlin (Germany) | **Website:** https://livermetabolism.com/ | **Email address:** koenigmx@hu-berlin.de | **Name of unit or department:** Institute for Theoretical Biology - **Business or sector:** Professional, scientific and technical activities

- Developed a Physiologically-Based Pharmacokinetic (PBPK) model for Tirzepatide to characterize its absorption, distribution, metabolism, and excretion (ADME).
- Conducted a systematic literature review to identify and curate pharmacokinetic data from clinical studies.
- Implemented parameter optimization strategies to enhance the predictive accuracy of the PBPK model.
- Performed numerical simulations to evaluate Tirzepatide's pharmacokinetics across different patient populations, focusing on renal and hepatic impairments.
- Investigated dose dependency, body weight effects, and physiological variability to support personalized treatment strategies.
- Wrote and structured the research report detailing methodology, model validation, and key findings.

Repository: https://github.com/matthiaskoenig/tirzepatide-model
Publication: https://doi.org/10.5281/zenodo.14984688

Master Thesis Student

Prof. Dr. Dr. h.c. Edda Klipp [01/05/2024 – 02/01/2025]

Address: Invalidenstraße 42 Theoretical Biophysics, Institute of Biology, Humboldt-Universität zu Berlin , 10115 Berlin (Germany) | **Website:** https://www.klipp-linding.science/ | **Email address:** edda.klipp@rz.hu-berlin.de | **Name of unit or department:** Institute of Biology - **Business or sector:** Professional, scientific and technical activities

- Developed a dynamic mathematical model for estimating phosphorylation-based kinase activity in triple-negative breast cancer using mass spectrometry time-series data.
- Implemented a Python pipeline with Just-In-Time (JIT) compilation for efficient parameter estimation in large-scale optimization problems.
- Reconstructed signaling networks by integrating kinase-substrate interaction predictions and phosphorylation time-series data.
- Optimized kinase signaling networks using differential evolution (DE) and sequential least squares programming (SLSQP) to enhance model accuracy.
- Performed large-scale numerical simulations to identify key phosphorylation events and their role in cancer progression and therapeutic resistance.
- Applied advanced optimization techniques, including Karush-Kuhn-Tucker (KKT) conditions and residual profiling, to refine the model's predictive power.
- Visualized kinase-substrate interactions using network analysis tools to map key regulatory nodes.

Mathematics Tuition Teacher

Self-Employed [01/04/2019 – 30/09/2019]

City: Allahabad | **Country:** India | **Business or sector:** Education

- Provided mathematics tutoring for high school students, enhancing their conceptual understanding and problem-solving skills.
- Topics: Number Systems, Algebra, Coordinate Geometry, Geometry, Trigonometry, Mensuration, Statistics and Probability
- Helped students develop analytical thinking skills, preparing them for competitive exams and coursework challenges.

Bachelor Thesis Student

Prof. Dr. Tiratha Raj Singh [01/02/2016 – 31/03/2017]

Address: P.O. Waknaghat, Teh. Kandaghat, Department of Biotechnology and Bioinformatics, Jaypee University Of Information and Technology, 173234 Waknaghat (India) | **Website:** https://www.bioinfoindia.org/raj/ | **Email address:** tiratharaj.singh@juit.

ac.in | **Name of unit or department:** Department of Biotechnology and Bioinformatics - **Business or sector:** Professional, scientific and technical activities

Link: https://www.bioinfoindia.org/raj/people.php

- Identified potent biomarkers for prostate cancer through comprehensive AR, MAPK, and m-TOR signaling pathway mining, aiding in targeted therapeutic strategies.
- Developed a bioinformatics pipeline integrating multiple tools for differential gene expression analysis to detect prostate cancer-specific genetic signatures.
- Performed large-scale transcriptomic data analysis using microarray gene expression datasets from GEO (Gene Expression Omnibus) to identify key regulatory genes.
- Implemented statistical and computational techniques for gene selection, utilizing tools such as GEO2R, MeV (TM4), and WB-DEGS to ensure accurate detection of differentially expressed genes.
- Utilized R, Shiny, and STRING to conduct pathway enrichment analysis and visualize gene interactions in prostate cancer.
- Mapped inter-pathway and intra-pathway interactions of significant genes across AR, MAPK, and m-TOR signaling pathways using STRING and GeneMANIA databases.
- Applied clustering techniques and network-based analytics to classify biomarker candidates and improve predictive modeling for prostate cancer progression.
- Designed interactive visualizations of functional protein-protein interactions and pathway relationships for data-driven decision-making in cancer research.

Thesis: http://ir.juit.ac.in:8080/jspui/handle/123456789/6614
Publication: https://doi.org/10.1515/jib-2018-0080
Repository: https://github.com/bibymaths/bachelor_thesis

Project Researcher

Dr. Chittaranjan Rout (Deceased, 2019) [01/08/2015 – 31/03/2016]

Address: P.O. Waknaghat, Teh. Kandaghat Department of Biotechnology and Bioinformatics, Jaypee University Of Information and Technology, 173234 Waknaghat (India) | **Website:** https://scholar.google.com/citations?hl=en&user=IQnbW0sAAAAJ&view_op=list_works&sortby=pubdate | **Name of unit or department:** Department of Biotechnology and Bioinformatics - **Business or sector:** Professional, scientific and technical activities

- Secured 3rd prize in Poster Presentation at NSCSB, showcasing innovative research on molecular docking for schizophrenia drug discovery.
- Performed molecular docking simulations to identify potential drug candidates targeting the Dopamine D3 Receptor (DDR3), which is implicated in schizophrenia.
- Utilized Discovery Studio and Maestro for ligand-receptor docking, incorporating receptor and ligand flexibility to improve binding predictions.
- Analyzed docking results using computational tools, including PyMol, VMD, and Glide XP, to evaluate hydrogen bonding, polar interactions, and molecular alignments.
- Identified Misoprostol, Cisapride, Methotrexate, Carvedilol, and Terfenadine as potential lead molecules, demonstrating therapeutic relevance in schizophrenia.
- Developed a computational workflow integrating FDA-approved drug screening, protein-ligand binding affinity analysis, and receptor pharmacodynamics insights.
- Presented findings on novel drug interactions at scientific conferences and research forums, contributing to the field of computational psychiatry and drug repurposing.

Repository: https://github.com/bibymaths/poster_nscb16

PUBLICATIONS

[2025]

Physiologically based pharmacokinetic (PBPK) model of tirzepatide

Tirzepatide, a dual glucose-dependent insulinotropic polypeptide (GIP) and glucagon-like peptide-1 (GLP-1) receptor agonist, represents a novel approach for treating type 2 diabetes mellitus (T2DM) and obesity. By combining the actions of both incretins, it enhances insulin secretion, suppresses glucagon, and reduces appetite, leading to superior glycemic control and weight loss compared to traditional GLP-1 receptor agonists. Despite its efficacy, inter-individual variability in pharmacokinetics necessitates a mechanistic understanding for optimized therapeutic application. This study employs physiologically-based pharmacokinetic (PBPK) modeling to characterize tirzepatide’s absorption, distribution, metabolism, and excretion (ADME). The model integrates physiological parameters to assess dose proportionality, hepatic and renal impairment effects, and body weight dependency. By improving drug exposure predictions, this approach aids personalized treatment strategies and enhances clinical decision-making across diverse patient populations

Mishra, A., & König, M. (2025). Physiologically based pharmacokinetic (PBPK) model of tirzepatide (0.9.3). Zenodo.

Link: https://github.com/matthiaskoenig/tirzepatide-model

[2019]

Gene Expression Studies to Identify Significant Genes in AR, MTOR, MAPK Pathways and their Overlapping Regulatory Role in Prostate Cancer

Gene expression studies revealed a large degree of variability in gene expression patterns particularly in tissues even in genetically identical individuals. It helps to reveal the components majorly fluctuating during the disease condition. With the advent of gene expression studies many microarray studies have been conducted in prostate cancer, but the results have varied across different studies. To better understand the genetic and biological regulatory mechanisms of prostate cancer, we conducted a meta-analysis of three major pathways i.e. androgen receptor (AR), mechanistic target of rapamycin (mTOR) and Mitogen-Activated Protein Kinase (MAPK) on prostate cancer. Meta-analysis has been performed for the gene expression data for the human species that are exposed to prostate cancer. Twelve datasets comprising AR, mTOR, and MAPK pathways were taken for analysis, out of which thirteen potential biomarkers were identified through meta-analysis. These findings were compiled based upon the quantitative data analysis by using different tools. Also, various interconnections were found amongst the pathways in study. Our study suggests that the microarray analysis of the gene expression data and their pathway level connections allows detection of the potential predictors that can prove to be putative therapeutic targets with biological and functional significance in progression of prostate cancer.

Asati, Nimisha, Mishra, Abhinav, Shukla, Ankita and Singh, Tiratha Raj. Journal of Integrative Bioinformatics, vol. 16, no. 3, 2019, pp. 20180080

PROJECTS

[01/03/2025 – Current]

SequenceAligner

- Combining Single Instruction Multiple Data (SIMD) instructions with the Message Passing Interface (MPI) leverages both data-level and distributed parallelism, significantly accelerating sequence alignment computations.
- Implementing a recursive traceback across multiple data chunks ensures accurate alignment reconstruction in distributed computing environments, maintaining the integrity of the alignment process.
- Utilizing SIMD instructions to accelerate dynamic programming matrix calculations aligns with contemporary advancements in sequence alignment algorithms, allowing regions of the dynamic programming matrix to be computed more efficiently.
- Implementing overlapping regions between sequence chunks in MPI-based local alignment ensures continuity and accuracy, preventing potential misalignments at chunk boundaries.

Link: https://github.com/bibymaths/SequenceAligner

[23/01/2023 – Current]

GRMAP

Genomic Reads Mapping and Annotation Pipeline

- Utilizes Perl's fork and Parallel::ForkManager modules to distribute query processing across multiple CPU cores, enhancing performance.
- Implements real-time tracking of memory usage and execution time, providing insights into resource consumption during processing.
- Integrates multiple genomic features—such as genes, transcription start sites (TSS), CpG islands, and repeat regions—into the analysis pipeline for enriched annotation.
- Supports various input configurations, allowing users to select different read files and query sizes, thereby accommodating diverse experimental setups.
- Combines results from parallel processes into a unified output file, streamlining the workflow and ensuring comprehensive reporting.

Link: https://github.com/bibymaths/grmap

[27/09/2023 – 18/01/2025]

SARS Genome Assembly

- Utilizes a wide array of bioinformatics tools, including MultiQC, FastQC, fastp, Minimap2, SAMtools, BCFTools, IGV, Pangolin, PRESIDENT, BAMClipper, FreeBayes, VCFtools, VCFlib, MAFFT, BEDTools, IQ-TREE, Jalview, and Gnuplot, providing an all-in-one solution for SARS-CoV-2 genome assembly and analysis.
- Automates the workflow from raw data acquisition to final phylogenetic analysis, minimizing manual intervention and potential errors.
- Incorporating BAMClipper for primer sequence removal ensures accurate variant calling by eliminating primer-induced biases.
- Utilizing PRESIDENT to assess consensus sequences allows for the identification of nucleotide identity and ambiguous bases, ensuring the reliability of the assembled genomes.

Link: https://github.com/bibymaths/sars_genome_assembly

[10/06/2022 – 27/07/2022]

Machine Learning-Based Classification of Liver Hepatocellular Carcinoma Tissue Samples and Identification of Potential Epigenomic and Transcriptomic Biomarkers through Differential Gene Expression and Methylation Analyses

- The project integrates clinical, molecular, and genomic data, providing a holistic view of LIHC, which is crucial for understanding the disease's complexity.
- By utilizing notebook- or script-based pipelines, the project ensures that analyses are reproducible, facilitating validation and further research.

Link: https://github.com/bibymaths/liver_prediction

[01/08/2015 – 30/09/2015]

CodonAnalyzer

Perl-Based Bioinformatics Toolkit for Codon and GC Content Analysis

- Efficient codon usage analysis, GC content variation detection, and hydropathy plotting for DNA and protein sequences.
- It leverages sliding window algorithms, regex-based sequence scanning, and standardized input-output formats for high-speed and reproducible analysis.

Link: https://github.com/bibymaths/codonanalyzer

CONFERENCES AND SEMINARS

[18/10/2024 – 18/10/2024] Urania Berlin, An der Urania 17, 10787 Berlin

MATH+ Day 2024 with General Assembly and Poster Session

Over 60 MATH+ research projects were presented in an extensive poster session. This session highlighted the diversity of research topics within MATH+, ranging from pain medication design and sustainable travel planning to battery research for solar cells and studies on the dynamics of networks.

Presentation on Insights

Internal Seminar

- Presented key ideas and research topics from the poster session.
- Discussed advancements in mathematical optimization, network dynamics, and applications group's active projects.
- Facilitated discussions on potential applications of these methodologies in our ongoing research.

Link: https://mathplus.de/events/math-day-2024-with-general-assembly-and-poster-session/

[10/05/2020 – 13/05/2020] Virtual

RECOMB 2020

The International Conference on Research in Computational Molecular Biology (RECOMB) is a prestigious annual meeting that brings together computational and experimental scientists in the field of molecular biology. The 2020 conference covered topics like computational genomics, systems biology, and network analysis.

Link: https://link.springer.com/book/10.1007/978-3-030-45257-5

[06/05/2017 – 07/05/2017] Jaypee University of Information Technology, Waknaghat, Himachal Pradesh, India

R&D Expo, IEEE-JUIT

Organized by the IEEE Student Branch at Jaypee University of Information Technology (JUIT), this expo showcased student research projects, fostering innovation and collaboration.

Link: https://events.vtools.ieee.org/m/159469

[18/03/2016 – 20/03/2016] Jaypee University of Information Technology, Waknaghat, Himachal Pradesh, India

National Symposium on Computational Systems Biology (NSCSB)

This symposium focused on advancements in computational systems biology, providing a platform for researchers to discuss the integration of computational methods with biological systems.

HONOURS AND AWARDS

Indian Institute of Technology, Guwahati

All India Rank 681 in GATE-2018

Qualified GATE (Graduate Aptitude Test in Engineering), a national-level exam for engineering and science proficiency in India,

Core Subjects: Engineering Mathematics, General Biology, Genetics, Cellular and Molecular Biology, Biological Engineering, Bioprocess Engineering, Plant, Animal and Microbial Biotechnology, Recombinant DNA Technology, Analytical and Computational Tools.

Link: https://drive.google.com/file/d/1A88smWrSrvz5uss-tlXfYJt5aGPGwhc7/view?usp=sharing

[20/03/2016] Jaypee University of Information Technology

Poster Presentation Prize

Awarded 3rd prize in a poster presentation titled **Identification of potential lead molecule for Schizophrenia through docking based approach** at the National Symposium for Computational Systems Biology 2016, JUIT, Waknaghat, India.

Link: https://drive.google.com/file/d/14okli8trEvPuDtolYyXkIV8FOtcrJ0HI/view?usp=sharing

NETWORKS AND MEMBERSHIPS

[01/09/2020 – Current] BioBaes

Administrator

A non-profit bioinformatics community dedicated to fostering open and equal opportunities for learning and networking. Managed community engagement, facilitated knowledge-sharing platforms, and contributed to an interactive learning ecosystem. Supported members in accessing tailored information to help them make informed career and academic decisions in bioinformatics.

Link: https://www.linkedin.com/company/biobaes

[01/06/2020 – 31/05/2021] International Society for Computational Biology

Professional Member

Held a one-year professional membership at the International Society for Computational Biology (ISCB), gaining access to global bioinformatics research, conferences, and professional networking opportunities. Engaged with cutting-edge advancements in computational biology and interdisciplinary collaborations

Link: https://www.iscb.org/

VOLUNTEERING

[2010] Allahabad, India

High-School Project in Biotechnology

I had the privilege of representing my school at the state-level National Children's Science Congress (NCSC) held in Allahabad, Uttar Pradesh. The NCSC is an annual event organized by the Department of Science and Technology, Government of India, aiming to nurture scientific temper among young minds by encouraging them to address local issues through scientific research. Participating in this congress allowed me to develop a competitive scientific mindset and contribute to addressing challenges related to land resource management.

Link: https://dst.gov.in/sites/default/files/18th_national_children.pdf

LANGUAGE SKILLS

Mother tongue(s): English | Hindi

DIGITAL SKILLS

Digital Skills - Test Results

Information and data literacy	**ADVANCED**	Level 5 / 6
Communication and collaboration	**ADVANCED**	Level 5 / 6
Digital content creation	**INTERMEDIATE**	Level 4 / 6
Safety	**INTERMEDIATE**	Level 4 / 6
Problem solving	**ADVANCED**	Level 5 / 6

Results from self-assessment based on The Digital Competence Framework 2.1

MANAGEMENT AND LEADERSHIP SKILLS

Financial Head, Synapse Bio-Club, JUIT (2013–2014)

- Managed budgets, secured funding, and oversaw accounts to facilitate various events organized by Synapse, the Biotechnology and Bioinformatics club at Jaypee University of Information Technology (JUIT).
- Successfully organized a skit addressing the wastage and mixing of chemicals in food, performed by Vasu Walia and his group, under the auspices of Synapse.
- One notable event during my tenure was a biomodelling competition for undergraduate and postgraduate students, supervised by Dr. Dipankar Sengupta and Dr. Gargi Dey. This competition provided students with practical experience in biomodelling, enhancing their understanding of complex biological systems.

My involvement in Synapse not only honed my financial management skills but also deepened my appreciation for collaborative scientific endeavors.

Links: https://www.juit.ac.in/synapse-students-club | https://www.juit.ac.in/attachments/juitReverie_Volume5_2013-14.pdf

COMMUNICATION AND INTERPERSONAL SKILLS

Effective Teamwork
Collaborated with diverse teams in research, administrative, and organizational roles, ensuring smooth workflow and productive outcomes.

Clear Presentation & Public Speaking
Presented research insights and innovative ideas to academic groups and at conferences, engaging audiences with structured and impactful discussions.

Link: https://drive.google.com/drive/folders/0B4ld_4Qp0OwmNTZUNlZqeXFHWWM?resourcekey=0-HjhZenmOXj8R3Fao9iMY7w&usp=sharing

Strong Writing & Documentation
Authored scientific reports, research reports, and administrative documentation with clarity and precision.

Adaptability & Flexibility
Successfully adapted to different work environments, international research labs in different countries while maintaining professionalism and efficiency.

Active Knowledge Sharing
Delivered internal presentations and discussions, translating complex mathematical and bioinformatics concepts into accessible information for varied audiences.

Collaborative Problem-Solving
Worked closely with colleagues and mentors to troubleshoot research challenges, propose solutions, and refine methodologies.

CREATIVE WORKS

[2013 – Current]

Photography & Visual Art

- Capturing and curating high-quality photographs for over a decade, showcasing a diverse portfolio of artistic and documentary-style images.
- Publicly hosted and shared work, engaging with the global photography community.
- Developed a keen eye for composition, lighting, and storytelling through visual media.

Link: https://500px.com/p/mishra36/galleries/untitled_1

HOBBIES AND INTERESTS

Reading
Philosophy, Psychology, Non-Fiction, Mathematical Theories, Research Papers

Cycling
I enjoy cool breeze on my face while going fast.

Cooking
I test the limits of my skillsnot only in career pursuits, but also in kitchen.

RECOMMENDATIONS

Name: **Prof. Dr. Katja Nowick** | Professor
I am pleased to write this letter in support of Abhinav Mishra, who participated in my Human Evolution course at the Freie Universität Berlin. While I did not have the opportunity to work with him extensively, I was able to observe his strong analytical abilities and enthusiasm for science and computational prob- lem-solving. During the course, Abhinav demonstrated a notable aptitude for data analysis and scripting, excelling in Python and R-based applications. His ability to interpret complex biological data and apply bioinformat- ics tools such as samtools and GATK was particularly impressive. These technical skills, combined with his mathematical proficiency and experience in handling multi-omics data, reflect a strong foundation in computational biology. Beyond technical expertise, Abhinav exhibits intellectual curiosity, independence, and a proactive ap- proach to learning. His engagement with research—ranging from his Master's thesis on mathematical modeling of breast cancer cell signaling to an internship in systems medicine and PBPK modeling— demonstrates his ability to design experiments, generate hypotheses, and tackle complex scientific problems. His publication in the Journal of Integrative Bioinformatics and presentations at computational biology symposia further attest to his research potential. Additionally, he possesses excellent communication skills and a collaborative spirit. Whether presenting his work or engaging in discussions, he conveys ideas clearly and confidently. His contributions to teaching, leadership roles, and interdisciplinary teamwork highlight his ability to thrive in dynamic re- search environments. I am confident that Abhinav will be a valuable asset in any research team, whether in academia or indus- try. I strongly recommend him for admission to a PhD program or a research-focused position in industry.
Email: katja.nowick@fu-berlin.de | **Phone number:** (+49) 3083863761

Links: https://www.bcp.fu-berlin.de/en/biologie/arbeitsgruppen/zoologie/ag_nowick/index.html | http://www.nowick-lab.info/?author=1

Name: **Dr. Matthias König** | Internship Supervisor
I am pleased to provide my strong recommendation for Abhinav Mishra. As Abhinav's supervisor during his Masters Internship at the Humboldt University of Berlin (01/2025-02/2025), I was able to observe his impressive research skills and professional growth. Abhinav's internship focused on the development of an advanced physiologically based pharmacokinetic (PBPK) model for the GIP and GLP-1 agonist tirzapetide, integrating bioinformatics, systems medicine, and pharmacokinetic data science. His major contributions include the meticulous compilation of an extensive database of tirzapetide pharmacokinetic data. In addition, he has successfully constructed detailed computational models that have improved our understanding of how hepatic and renal impairment, as well as body weight, affect tirzapetide clearance. Abhinav's work stands out among his peers for its rigor, accuracy and clear practical implications for diabetes treatment and weight loss management. Throughout our collaboration, Abhinav has consistently demonstrated reliability and initiative. He quickly mastered standardized computational workflows and PBPK modeling, areas in which he initially had limited experience. His rapid skill acquisition and consistent dedication enabled him to deliver high quality, reproducible models that significantly enhanced our lab's capabilities. In addition to his technical expertise, Abhinav's interpersonal and teamwork skills are outstanding. He has fostered a positive and productive environment through effective collaboration and clear, insightful communication during his presentations. His ability to convey complex scientific information with precision and clarity makes him an invaluable member of any research team. Given Abhinav's remarkable blend of scientific skills, collaborative spirit, and strong motivation, I am confident that he will excel in his future academic and professional pursuits. Please feel free to contact me for more information on Abhinav's qualification.
Email: koenigmx@hu-berlin.de | **Phone number:** (+49) 30209398435

Link: https://livermetabolism.com

Name: **Prof. Dr. Rajinder Singh Chauhan** | Professor & Dean
It is my pleasure to write this letter on behalf of Mr. Abhinav Mishra, who completed his Bachelor of Technology in Bioinformatics at Jaypee University of Information Technology (JUIT), Solan, India. As the Head of the Department and his professor for courses such as Genetics and Molecular Biology, I had the privilege of closely observing Abhinav's academic and personal growth over the

course of his undergraduate studies. Abhinav consistently distinguished himself through his intellectual curiosity, sharp analytical skills, and the ability to articulate complex scientific concepts with clarity. His exceptional performance in Genetics and Molecular Biology was matched by his capacity to engage with challenging material in a thoughtful and insightful manner. From the outset, I was impressed by his ability to ask meaningful questions, his engagement in class discussions, and his dedication to continuous improvement, reflected by his consistent academic progress throughout his time at JUIT. His passion for research became particularly evident during his bachelor thesis, where he explored potent biomarkers for prostate cancer through AR, MAPK, and m-TOR signaling pathway mining—a project that culminated in a published paper in the Journal of Integrative Bioinformatics. This accomplishment highlighted not only his technical skills but also his ability to independently pursue complex research questions. In addition to his academic strengths, Abhinav possesses strong programming skills in Python, R, and Perl, alongside a solid foundation in mathematics and data analysis. His interdisciplinary research experiences, including work on mathematical modeling and simulations, further underscore his versatility as a researcher and problem-solver. Abhinav also demonstrated excellent leadership and organizational skills through his role as Financial Head at Synapse Bio-Club, where he effectively managed budgets and contributed to organizing departmental activities. His ability to balance academic rigor with extracurricular responsibilities speaks to his discipline, time management, and collaborative spirit. His achievements—such as securing an All India Rank of 681 in the Graduate Aptitude Test in Engineering (Biotechnology)—attest to his strong conceptual understanding and commitment to excellence. I am confident that Abhinav's intellectual drive, problem-solving abilities, and collaborative nature will make him a valuable asset to any academic, research, or professional setting. I offer him my highest recommendation for any opportunity he chooses to pursue and am available to provide any further information if needed.

Email: rajinder.chauhan@mahindrauniversity.edu.in | **Phone number:** (+91) 9418405536

Link: https://www.mahindrauniversity.edu.in/faculty/rajinder-singh-chauhan/

Name: **Prof. Dr. Tiratha Raj Singh** | Professor & Faculty In-charge, Media Relations

I am pleased to write this letter of recommendation for Abhinav Mishra, a highly capable and motivated individual who has demonstrated exceptional proficiency in bioinformatics and computational biology. Having closely observed Abhinav's academic and research journey, I am confident in his potential to contribute significantly to the doctoral program in your esteemed university. Abhinav has excelled in his coursework, particularly in the Advanced Algorithms in Bioinformatics & Computational Systems Biology module, where he demonstrated deep analytical skills and problem-solving abilities. His Master's thesis, which resulted in a publication, reflects his ability to engage in meaningful research, explore complex biological systems, and contribute novel insights to the field. His academic background, an M.Sc. in Bioinformatics from Freie Universität Berlin (focused on Data Science) and a B.Tech. in Bioinformatics from Jaypee University of Information Technology, India, has provided him with a strong foundation in both theoretical and applied bioinformatics. Technically, Abhinav possesses an impressive skill set, including proficiency in Python, R, Julia, and Bash, along with experience in samtools, GATK, and various bioinformatics pipelines. His high mathematical aptitude allows him to efficiently handle multi-omics data, computational modeling, and machine learning applications in biological research. His internship in Systems Medicine of the Liver (PBPK modeling) and current research on mathematical modeling of breast cancer cell-line signaling further highlight his ability to integrate computational approaches with biological questions. Beyond technical skills, Abhinav exhibits strong research potential and independence. His ability to design experiments, formulate hypotheses, and tackle intricate research problems is commendable. He has successfully presented his findings at the National Symposium on Computational Systems Biology and has a publication in the Journal of Integrative Bioinformatics on prostate cancer pathways, reinforcing his capacity to contribute meaningful research to the field. Abhinav is also an excellent collaborator and communicator. His willingness to engage in teamwork, mentor peers, and contribute to an inclusive research environment sets him apart. His experience as a tuition teacher and leadership roles in Synapse Bio-club and the BioBaes community illustrate his ability to guide and inspire others. His strong written and verbal communication skills ensure that he can effectively present complex scientific concepts with clarity. Moreover, Abhinav's motivation and enthusiasm for learning are truly remarkable. His eagerness to explore new methodologies, such as his upcoming flow cytometry course and his readiness to undertake another internship in plant metabolomics (focused on time-series analysis) demonstrate his continuous drive for professional growth. I strongly endorse Abhinav Mishra's candidacy for doctoral-level research position. His technical expertise, research acumen, and collaborative spirit make him an outstanding candidate. I am confident that he will excel in any competitive program and contribute meaningfully to any research team.

Email: tiratharaj.singh@juit.ac.in | **Phone number:** (+91) 9816954695

Link: https://www.juit.ac.in/public/faculty.php?id=108&dep=bio&page=0