BRIEF BIO-DATA OF DR. VISHAL ACHARYA

Present Post:	Principal Scientist, Artificial Intelligence for Computational Biology Lab (AICoB), Biotechnology Division, CSIR-Institute of Himalayan BioresourceTechnology (IHBT), Palampur-176061 (H.P.), India
Email-id	vishal@ihbt.res.in, acharya.vishalacharya@gmail.com
Awards	**i) Indian Science Congress Association (ISCA)** Young Scientist Award -2014 (New Biology) **ii) Young Scientist Award for Best Paper Presentation** (2014) by Society of Plant Biochemistry and Biotechnology, New Delhi **iii) Bioclues Innovation, Research and Development (BIRD) Award-2016** from International Society for Computational Biology and Asia-Pacific Bioinformatics Network under the age of 35. **iv) Awarded for 2nd Position** – Incentive Awards for Publications-2016 for publications in Year 2015, from BITSnet, Department of Biotechnology, Govt. of India (including my 5 out of total 8 papers). **v)** Elected as **"Associate" of National Academy of Agriculture Sciences (NAAS)** under Social Sciences (Bioinformatics)-**2021**
Honours	**i) Co-Chair of Bioclues organization** (an affiliate of International Society of Computational Biology (ISCB)) for the year 2017-2018. **ii) Chairperson and Invited speaker** for the "International Conference on Bioinformatics" held at Hans Raj Mahavidalaya (HMV), Jalandhar, 2019. **iii)** As a **Co-co-ordinator** for "Establishment of Bioinformatics infrastructure for biology through bioinformatics (BTBI) under BTISnet", Department of Biotechnology (DBT), Government of India. **iv)** Co-Investigator of DBT awarded project titled "**The Himalayan Centre for High-throughput Computational Biology (HiCHiCoB)-BIC"** for five (5) years (2022-2027)
Fellowships Merits	**i). ICAR's JRF** for MSc Programme-2003 **ii).DBT-Fellow (M.Sc), Gov. of India,** conducted by JNU-2003 **iii). JRF** (2005) for **PhD** granted by **DBT, Gov. of India** **iv).Travel fellowship** by European Science Foundation (Availed)
Supervisory Experience	i).Guided **Nine Phd students** through Academy of Scientific and Innovation Research (AcSIR) research program and one DBT-Research Associate (RA) ii) Presently, guiding **4 PhD** students through AcSIR, New Delhi

Software/Database Developed (12)

SI. No	Details of Software/Database*	Whether is a Developer, Co-developer or Associate
I.	**Software**: His conceived and novel approach on advanced Virtual Screening framework-**automated hit identification and optimization tool (A-HIOT)-** comprises chemical space-driven stacked ensemble from natural products for identification and protein space-driven deep learning architectures for optimization of an array of specific hits for fixed protein receptors https://gitlab.com/neeraj-24/A-HIOT **(Journal of Cheminformatics, 2022)**	Developer
II.	**Software:** His conceived and novel method on first ever implementation of deep learning network based named as DLNet using genomics data to understand the plant network architecture response to pathogens https://gitlab.com/ravisaroch/dlnet-host-pathogen-interaction/ **(iScience, 2022)**	Developer
III.	**Software**: His conceived method on any protein molecule derived from medicinal plants clustered into active/inactive targets (https://gitlab.com/neeraj-24/clustering-of-uncharacterised-data) by applying unsupervised machine learning using atom pair, fingerprints and similarity indices as features for drug discovery **(Computers in Biology & Medicine, 2023)**	Developer
IV.	**Software**: His conceived and novel protocol for network and expression integration to identify potential plant defense genes in host-pathogen interactions and can be extended and applied in any kind of plant-pathogen interactions. https://gitlab.com/ravisaroch/star-protocols (**Star Protocols, 2023)**	Developer
V.	**Database**: RicePathDLNet(https://fgcsl.ihbt.res.in/RicePathDLNet) repository was developed which will aid the rice-focused researchers in understanding the distinct network levels in pattern-triggered immunity (PTI)- and effector triggered immunity (ETI-based) models and within ETI-*Magnaporthe oryzae* and ETI-*Xanthomonas oryzae* models. (**iScience, 2022)**	Developer
VI.	**Software**: His conceived computational pipeline on prediction of transcription factors (https://github.com/ShivalikaP/R_serpentina_transcriptome_annotation) which led into the investigation and organization of secondary metabolites in *Rauvolfia serpentina* (**Plant Molecular biology reporter**, 2015)	Developer
VII.	**Software**: He conceived and developed pipeline on studying adaptive behavior of any genome (plant/microbes) adapting to cold conditions (https://github.com/fgcsl/Molecular-adaptational-analysis-cold) **(Genomics, 2020)**	Developer
VIII.	**Software: AI based-software** *"Hansa"* http://www.cdfd.org.in/HANSA/ (**Human Mutation,2012; 2013)** wherein novel biological-based features	Developer

	implemented (Gribskov's probability score) has been applied for **discrimination of disease causing mutations in proteins.**	
IX.	**Software:** He conceived and developed pipeline on studying adaptive behavior microbial genome adapting to cold conditions (Cold Adaptational tool) (https://github.com/fgcsl/Molecular-adaptational-analysis-cold)	Developer
X.	**Database:** Indian Himalayan metagenome database (IHM-DB) developed by him is a web-based database consisting of microbiome information on metagenomic datasets from various databases that are specifically reported from the Indian Himalayan Region (IHR) (https://fgcsl.ihbt.res.in/ihmdb)	Developer
XI.	**Software:** He developed an open-source 16S amplicon-based automated bioinformatics pipeline, AutoQii2, which will allow users to analyze the single-end and paired-end raw reads(https://github.com/fgcsl/autoqii2)	Developer
XII.	**Software:** He conceived and developed a computational pipeline, FunVFPred, providing a novel approach for predicting fungal virulence factors and advancing the study of fungal pathogenicity (https://github.com/ekjotkaurm/FunVFPred)	Developer

Technology Developed (One):

Deep-learning app for accurate detection of post-stroke using MRI data:

Developed and supervised a startup named Aamazing Brains specializing in AI-powered post-stroke detection using MRI data, offering rapid, high-accuracy analysis within minutes through a cloud-based platform (https://632b5225a3ef.ngrok-free.app/welcome).Designed for neurologists, radiologists, and researchers, it features a simple workflow — upload MRI scans, let the AI analyze them, and receive a clear visual report highlighting stroke indicators.

Selected Publications

1. Ruhika Sharma, **Vishal Acharya*** (2025) Lightweight Vision Transformer with Transfer Learning for Interpretable Alzheimer's Disease Severity Assessment *Scientific Reports* 15, Article number: 44028.
2. Nymphaea Arora, Anil Kumar Rana, Damanpreet Singh*, **Vishal Acharya*** (2025) Differential Roles of Neuro-Inflammatory Regulator, MAPK11 in Cortex and Hippocampus Following Post-Stroke Cognitive Impairments in Rats *Journal of Neuroimmune Pharmacology* 20, 93.
3. Neeraj Kumar, **Vishal Acharya***, (2024) Advances in machine intelligence-driven virtual screening approaches for big-data. *Medicinal Research Reviews,* 44:939-974 | doi: 10.1002/med.21995
4. Ravi Kumar, **Vishal Acharya*,** Effector protein structures: a tale of evolutionary relationship, *Trends in Plant Science,* 2023,ISSN 1360-1385.
5. Neeraj Kumar & **Vishal Acharya*** Machine intelligence-driven framework for optimized hit selection in virtual screening. *Journal of Cheminformatics* 2022 Jul 22;14(1):48. doi: 10.1186/s13321-022-00630-7. PMID: 35869511; PMCID: PMC9306080

   Software link: **https://gitlab.com/neeraj-24/A-HIOT**

6. Ravi Kumar, Abhishek Khatri & **Vishal Acharya*** Deep learning uncovers distinct behavior of rice network to pathogens response *iScience*, Volume 25, Issue 7, 104546

   Software link: https://gitlab.com/ravisaroch/dlnet-host-pathogen-interaction/ ;

   Database link:https://fgcsl.ihbt.res.in/RicePathDLNet

7. Meetal Sharma, Prince Anand, Yogender Padwad, Vivek Dogra, **Vishal Acharya*** DNA damage response proteins synergistically affect the cancer prognosis and resistance *Free Radical Biology & Medicine* 2021 Nov 27;S0891-5849 (21) 00831-5.
8. Neeraj Kumar, **Vishal Acharya*,** Machine intelligence-guided selection of optimized inhibitor for human immunodeficiency virus (HIV) from natural products*. Computers in Biology and Medicine* Volume 153, February 2023, 106525