

BRIEF BIO-DATA OF DR. VISHAL ACHARYA

- Present Post:** Principal Scientist, Artificial Intelligence for Computational Biology Lab (AICoB), Biotechnology Division, CSIR-Institute of Himalayan Bioresource Technology (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 Mahavidyalaya (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.
- 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 Five Phd students** through Academy of Scientific and Innovation Research (AcSIR) research program and one DBT-Research Associate (RA)
 - ii) Presently, guiding 6 Phd** students through AcSIR, New Delhi
- Computational Experience** Perl, Python, Awk, Linux Server Administrator, R Package, GNU, Matlab, Bioconductor, PHP
- Professional Memberships** 1. Life Member of the Indian Science Congress Association (ISCA)

2. Joint Secretary of Bioclues Organization affiliated with International Society for Computational Biology and Asia-Pacific Bioinformatics Network

Countries Visited: Germany; France

Educational Qualifications

Examination	School/College	Year of Passing	Percentage/Remarks
PhD (Bioinformatics)	Center for DNA Fingerprinting & Diagnostics (CDFD), Hyderabad	2005- 2011	PhD Degree Awarded
M.Sc. (Biotechnology)	Madurai Kamaraj University, Madurai (T.N)	2003-2005	75.4%

Scientific Contributions:

Dr. Vishal Acharya's research work focuses on development of pipeline by means of the Artificial intelligence (AI) and deep learning algorithms on big/complex datasets of plant genomes. Dr. Vishal Acharya has published 38 papers of international repute with many of them in high impact factors like Free radical biology and medicine, Journal of Cheminformatics, iScience, Trends in Plant Sciences, Medicinal Research Reviews etc. He has also conceived and developed 10 software which is available to the interested researchers. Following his significant contributions can be summarized to AI on Plant & Human Sciences as below:

AI ON PLANT SCIENCES

- He conceived and developed the deep learning network algorithm (DLNet) using genomics data for the first time to understand the plant network architecture in response to pathogens (<https://gitlab.com/ravisaroch/dlnet-host-pathogen-interaction>) (**iScience, 2022; IF =6.1**).
- Basic protocol of his developed DLNet algorithm can be applied to any kind of plant-pathogen interactions and open to plant researchers (<https://gitlab.com/ravisaroch/star-protocols>) (**Star Protocols, 2023**).
- Discovered novel **domain** (animal-like defense regulator NACHT-NTPase) that was reported for the **first time** in early green plants (**PloS One, 2016; Molecular Genetics and Genomics, 2017**)
- The **stringent Hidden Markov model-based approach developed by him for prediction of disease-resistance** in *Malus x domestica* (apple) genome (**Plos One, 2014**) was being successfully applied in many **other plant sequenced genomes** supported by **≥ 100 publications**.
- He conceived and developed **AI-based logistic regression modeling** method suggested plant derived molecules from Himalayas as anti-oral cancer agents (**Molecular Omics, 2015**).
- He conceived and developed the **computational pipeline on prediction and identification of transcription factors** regulating secondary metabolite in medicinal plants (https://github.com/ShivalikaP/R_serpentina_transcriptome_annotation) **Plant Molecular biology reporter, 2015**) and abiotic stress (NAC) in potato (**DNA Research, 2013 (8th most read article)**) cited in **≥ 160 publications**.
- He conceived and developed pipeline on molecular adaptational analysis (<https://github.com/fgcsl/Molecular-adaptational-analysis-cold>) can easily be applied to any sequenced genomes even by non-bioinformatics researchers (**Genomics, 2020, IF=4.3**).

AI ON HUMAN HEALTH & DRUG DISCOVERY

- He conceived and developed pipeline <https://gitlab.com/neeraj-24/A-HIOT> on advanced Virtual Screening framework-**automated hit identification and optimization tool (A-HIOT)**-comprises chemical space-driven stacked ensemble for identification and protein space-driven deep learning architectures for optimization of an array of specific hits for fixed protein receptors (**Journal of Cheminformatics, 2022, IF =8.48**)
- Developed **artificial intelligence based software** (Support vector Machine) named “*Hansa*” (<http://www.cdfd.org.in/HANSA/>) for discrimination of pathogenic from nonpathogenic missense mutations with 10% more accurate than best known methods (**Human Mutation, 2012; 2013**).
- He conceived and developed pipeline on clustering of protein molecule 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 (**Computers in Biology & Medicine, 2023, IF=6.698**)

Technology/Software Developed

Sl. No	Details of Product/Technology/Software* (Also write in one bullet point its impact in terms of adoption, commercialization and revenue generated)	List according to category (I,II,III,IV or V) as given in 2 of the guidelines for evaluation	Whether Nominee is a Developer, Co-developer or Associate
1.	Software: He conceived the novel method on first ever implementation of deep learning network algorithm named DLNet using genomics data to understand the plant network architecture in response to pathogens https://gitlab.com/ravisaroch/dlnet-host-pathogen-interaction/	I (Methodologies developed)	Developer
2.	Software: He conceived and developed the novel method on any protein molecule derived from medicinal plants clustered into active/inactive targets by applying unsupervised machine learning using atom pair, fingerprints and similarity indices as features for drug discovery https://gitlab.com/neeraj-24/clustering-of-uncharacterised-data	I (Methodologies developed)	Developer
3.	Software: He conceived and developed the novel approach on advanced Virtual Screening framework- automated hit identification and optimization tool (A-HIOT) -comprising 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	I (Methodologies developed)	Developer

4.	<p>Software: He developed the novel machine learning protocol for integration of network and expression profiling to identify potential host defense genes in all kind host-pathogen interaction datasets. https://gitlab.com/ravisaroch/star-protocols</p>	I (Methodologies developed)	Developer
5.	<p>Software: He conceived and developed the computational pipeline on prediction and identification of transcription factors regulating secondary metabolite in medicinal plants with <i>Rauvolfia serpentina</i> as a case study https://github.com/ShivalikaP/R_serpentina_trascriptome_annotation</p>	I (Methodologies developed)	Developer
6.	<p>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</p>	I (Methodologies developed)	Developer
7.	<p>Software: He developed AI based-software “Hansa” wherein novel biological-based features implemented (Gribskov’s probability score) has been applied for future prediction of disease-resistance genes on the basis of SNPs http://www.cdfd.org.in/HANSA/</p>	I (Methodologies developed)	Developer
8.	<p>Software: RicePathDLNet, online repository developed by him will aid the rice-focused researchers in understanding the distinct network levels in pattern-triggered immunity (PTI)- and effector triggered immunity (ETI)-based models of <i>Xanthomonas oryzae</i> and <i>Magnaporthe oryzae</i> https://fgcsl.ihbt.res.in/RicePathDLNet/</p>	I (Methodologies developed)	Developer
9.	<p>Software: 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</p>	I (Methodologies developed)	Developer

10.	Software: He conceived and 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)	I (Methodologies developed)	Developer
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Selected Publications

1. 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 <https://onlinelibrary.wiley.com/doi/full/10.1002/med.21995> (IF=13.3)
2. Ravi Kumar, **Vishal Acharya***, Effector protein structures: a tale of evolutionary relationship, *Trends in Plant Science*, 2023,ISSN 1360-1385, <https://doi.org/10.1016/j.tplants.2023.04.010> (IF =22.01)
3. 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 (IF=6.698)
Software link: <https://gitlab.com/neeraj-24/clustering-of-uncharacterised-data>
4. 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 (IF =8.48)
Software link: <https://gitlab.com/neeraj-24/A-HIOT>
5. Ravi Kumar, Abhishek Khatri & **Vishal Acharya*** Deep learning uncovers distinct behavior of rice network to pathogens response **iScience**, Volume 25, Issue 7, 104546 (IF =6.1)
Software link: <https://gitlab.com/ravisaroch/dlnet-host-pathogen-interaction/>
Database link: <https://fgcsl.ihbt.res.in/RicePathDLNet>
6. 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. doi:10.1016/j.freeradbiomed.2021.11.033 (IF=8.1)

Details of Publications is provided at the link: https://fgcsl.ihbt.res.in/fgcsl_lab/publication.php

Books Authored:

1. VijayKumar Muley & **Vishal Acharya** (2013) Genome-Wide Prediction and Analysis of Protein-Protein Functional Linkages in Bacteria, **Springer Briefs in Systems Biology** Volume 2,1-2, https://doi.org/10.1007/978-1-4614-4705-4_1 Online ISBN 978-1-4614-4705-4

Book Chapters:

1. Neeraj Kumar & **Vishal Acharya*** Metabolomics Resources: An Introduction of Databases and Their Future Prospective (2018) **Recent Trends and Techniques in Plant Metabolic Engineering** Springer DOI (Editors: Sudesh Kumar Yadav, Vinay Kumar, Sudhir P Singh) DOI: <https://doi.org/10.1007/978-981-13-2251-8> Online ISBN 978-981-13-2251-8

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