

Faculty Details

Name: Dr. Pankaj Singh Dholaniya

Mail: pankaj@uohyd.ac.in

Contact: 040-2313-4591

Area Of Research: Theoretical and Data Biology

Bioinformatics Data Science, Neurological Disorders, Disease Biology

Faculty Details

Dr. Pankaj Singh is a computational biologist having expertise in the field of machine learning and data science.

EDUCATIONAL CREDENTIALS

Ph.D Biotechnology (2017)

Department of Biotechnology & Bioinformatics, University of Hyderabad, Hyderabad, Telangana.

M. Tech. Bioinformatics (2011)

University of Hyderabad, Hyderabad, Andhra Pradesh;

B. Tech. Biotechnology (2009)

SVBP University of Agri. & Tech., Meerut, U.P;

FELLOWSHIPS

German Academic Exchange Service (DAAD) fellowship under NPTI program 2012

CSIR-NET Lectureship 2010

DBT-JRF 2009 and 2010

GATE 2009

TEACHING COURSES AT UOH

Computers and Programming

Machine learning methods and Data analytics

Database design and development

(For M.Tech Bioinformatics and integrated M.Sc. Systems Biology students)

Notice Board

No Records Available

Students And Project Trainees

Students/Projects Trainees

Name	Joined As	Mail	Contact
------	-----------	------	---------

Baby Kumari	Ph.D.	baby059696@gmail.com	---
-------------	-------	----------------------	-----

Neha	Ph.D.	nehaskumar101@gmail.com	---
------	-------	-------------------------	-----

Ahmad	Ph.D.	ahmadmailbook@gmail.com	---
-------	-------	-------------------------	-----

MD Zainul Ali	Ph.D.	mdzainulali@gmail.com	---
---------------	-------	-----------------------	-----

Mallikarjun Ratnam	P.Project Student (M.Tech., Bioinformatics)	21lsmi11@uohyd.ac.in	
--------------------	---	----------------------	--

E. Sai Suvani	Project Student (M.Tech., Bioinformatics)	21lsmi12@uohyd.ac.in	---
---------------	---	----------------------	-----

Kata Krishna Prasad	Project Student (M.Tech., Bioinformatics)	21lsmi16@uohyd.ac.in	
---------------------	---	----------------------	--

Prashant Kumar	Project Student (M.Sc., Bioitechnology)		
----------------	---	--	--

pkprashantsingh5577@gmail.com	---
-------------------------------	-----

Former Students/Projects Trainees

Name	Joined As	Working
------	-----------	---------

Samreen	Project Student (M.Tech., Bioinformatics)	IT Engineer, Regeneron India
---------	---	------------------------------

Mukulika Mandal	Project Student (M.Tech., Bioinformatics)	Ph.D., University of Hyderabad
-----------------	---	--------------------------------

MD Zainul Ali	Project Student (M.Sc., Bioitechnology)	Continuing Ph.D. with same group
---------------	---	----------------------------------

Kushagra	Project Student (M.Tech., Bioinformatics)	Ph.D., CDRI Lucknow
----------	---	---------------------

Vikram Teja Naik	Project Student (M.Tech., Bioinformatics)	
------------------	---	--

Swarna Kundu	Project Student (M.Tech., Bioinformatics)	Healthcare Analyst, Apollo Health
--------------	---	-----------------------------------

Itishree Jali	Project Student (M.Tech., Bioinformatics)	Ph.D., NIAB, Hyderabad
---------------	---	------------------------

Aishwarya	Project Student (M.Sc., Bioitechnology)	Ph.D., CCMB, Hyderabad
-----------	---	------------------------

Manish	Project Student (I.M.S., Systems Biology)	
--------	---	--

Neha Project Student (M.Sc., Bioitechnology) Continuing Ph.D. with same group
 Sarthak Srivastava Project Student (M.Sc., Bioitechnology)
 Aishwarya Subramaniam Project Student (M.Tech., Bioinformatics) Software Engineer
 (ML in Healthcare), Tech Mahindra
 Mayur Saini Project Student (M.Tech., Bioinformatics)
 Sreenidhi Ramamoorthy Project Student (M.Tech., Bioinformatics) Research Engineer at
 TCS
 LOGA PRIYA R Project Student (M.Tech., Bioinformatics) Bioinformatics Analyst at
 MedGenome Labs, Bangalore
 Sourav Jana Project Student (M.Sc., Bioitechnology)
 Rittik Mandal Summer Intern
 Shashaank Varma Summer Intern

Publications

- 18 Gupta, Prateek., Dholaniya, Pankaj Singh., Kunnappady, Princy., Madhavan, Athira Sethu., Yellamaraju, Sreelakshmi., Sharma, Rameshwar., (2024) , Augmenting tomato functional genomics with a genome-wide induced genetic variation resource , Frontiers in Plant Science, Frontiers,14,, IF - 5.6.
- 17 Ali Zainul MD, Dholaniya, Pankaj Singh* (2022) , Oxidative phosphorylation mediated pathogenesis of Parkinson`s disease and its implication via Akt signaling , Neurochemistry International, Elsevier,152,105344, IF - 4.297.
- 16 Sahu S., Dholaniya, Pankaj Singh*, T Sobha Rani*. (2022) , Identifying the candidate genes using co-expression, GO, and machine learning techniques for Alzheimer`s disease , Network Modeling and Analysis in Health Informatics and Bioinformatics, Springer,11,10,.
- 15 Manukonda Radhika, Yenuganti Vengala Rao, Nagar Nupur, Dholaniya Pankaj Singh, Malpotra Shivani, Attem Jyothi, Reddy Mamatha M., Jakati Saumya, Mishra Dilip K, Pallu Reddanna, Krishna Mohan Poluri, Vemuganti Geeta K., and Kaliki Swathi (2022) , Comprehensive Analysis of Serum Small Extracellular Vesicles-Derived Coding and Non-Coding RNAs from Retinoblastoma Patients for Identifying Regulatory Interactions , Cancers, ,14 (17),,4179 IF - 6.575.
- 14 Kumari, Baby., Dholaniya, Pankaj Singh* (2022) , Parkinson`s disease gene prioritising using an efficient and biologically appropriate network-based consensus strategy , Journal of Computational Science, Elsevier,65,,101879 IF - 3.817.
- 13 S, Neha., Ahmad, Mohammad., Kumari, Baby., Ali Zainul MD., Dholaniya, Pankaj Singh* (2022) , Early Diagnosis of Parkinson`s Disease: Utility of Animal Models , Parkinson`s Disease - Animal Models, Current Therapies and Clinical Trials, IntechOpen,,,.
- 12 Muttineni, Radhakrishna., Kammili, Nagamani., Bingi, Thrilok Chander., Rao M, Raja., Putty, Kalyani., Dholaniya, Pankaj Singh., Puli, Ravi Kumar., Pakalapati, Sunitha., Doodipala, Mallikarjuna Reddy., Upadhyay, Amit A., (2021) , Clinical and whole genome characterization of SARS-CoV-2 in India , Plos one, Public Library of Science San Francisco, CA USA,16,2,e0246173 IF - 3.752.
- 11 Dholaniya, Pankaj Singh*, Rizvi, Samreen. (2021) , Effect of various sequence descriptors in predicting human protein-protein interactions using ANN-based prediction models , Current Bioinformatics, Bentham Science,16,8,1024 - 1033 IF - 4.850.

- 10 S, Neha., Dholaniya, Pankaj Singh*, (2021) , The Prevailing Role of Topoisomerase 2 Beta and its Associated Genes in Neurons , Molecular Neurobiology, Springer,58,,6443–6459 IF - 5.628.
- 9 Kumari, Baby., Mandal, Mukulika., Dholaniya, Pankaj Singh*, (2020) , Analysis of multiple transcriptome data to determine age-associated genes for the progression of Parkinson`s disease , Meta Gene, Elsevier,25,,100712.
- 8 Gupta, Prateek., Dholaniya, Pankaj Singh., Devulapalli, Sameera., Tawari, Nilesh Ramesh., Sreelakshmi, Yellamaraju., Sharma, Rameshwar., (2020) , Reanalysis of Genome Sequences of tomato accessions and its wild relatives: Development of tomato genomic variation (TGV) database integrating SNPs and INDELs polymorphisms , Bioinformatics, Oxford University Press,36,20,4984-4990 IF - 6.931.
- 7 Kakade, Aishwarya., Kumari, Baby., Dholaniya, Pankaj Singh* (2018) , Feature selection using logistic regression in case–control DNA methylation data of Parkinson`s disease: A comparative study , Journal of theoretical biology, Academic Press,457,,14-18 IF - 2.405.
- 6 Bollimpelli, V Satish., Dholaniya, Pankaj S., Kondapi, Anand K., (2017) , Topoisomerase II β and its role in different biological contexts , Archives of biochemistry and biophysics, Academic Press,633,,78-84 IF - 4.114.
- 5 Gupta, K Preeti., Dholaniya, Pankaj Singh., Chekuri, Anil., Kondapi, Anand K., (2015) , Analysis of gene expression during aging of CGNs in culture: implication of SLIT2 and NPY in senescence , Age (GeroScience), Springer International Publishing,37,3,1-14.
- 4 Dholaniya, Pankaj Singh., Ghosh, Soumitra., Surampudi, Bapi Raju., Kondapi, Anand K., (2015) , A knowledge driven supervised learning approach to identify gene network of differentially up-regulated genes during neuronal senescence in Rattus norvegicus , Biosystems, Elsevier,135,,9-14.
- 3 Meetei, Potshangbam Angamba., Singh, Pankaj., Nongdam, Potshangbam., Prabhu, N Prakash., Rathore, RS., Vindal, Vaibhav., (2012) , NeMedPlant: a database of therapeutic applications and chemical constituents of medicinal plants from north-east region of India , Bioinformation, Biomedical Informatics Publishing Group,8,4,209.
- 2 Arun, PV Parvati Sai., Bakku, Ranjith Kumar., Subhashini, Mranu., Singh, Pankaj., Prabhu, N Prakash., Suzuki, Iwane., Prakash, Jogadhenu SS., (2012) , CyanoPhyChe: a database for physico-chemical properties, structure and biochemical pathway information of cyanobacterial proteins , PloS one, Public Library of Science,7,11,e49425.
- 1 Singh, Pankaj., Suryavanshi, R., Sailu, S., Vindal, V., Kondapi, AK., Rathore, RS., (2010) , HIV Information REsources (HIRE): An Integrated Knowledgebase for Immunodeficiency Viruses , Proceedings of 2010 First International Conference on Cellular, Molecular Biology, Biophysics and Bioengineering (Volume 3), ,,,.

Projects

Title	Year	Duration	Amount(In Lakhs)	PI/I
DBT-Centre for Microbial Informatics (DBT-CMI)	2021	5	176	Prof. H.A.Nagarajaram (PI), Prof. Appa Rao Podile (Co-PI), Prof. Dayananda Siddavattam (Co-PI), Prof. Ch Venkataramana (Co-PI), Dr. Pankaj Singh (Co-PI), Dr. Vivek (Co-PI), Dr. Manjari Kiran (Co-PI)
Investigating the miRNA based biomarkers for early diagnosis of Parkinson's Disease for				

chemically induced PD model in Rat.2021 3 4000000000 Dr. Pankaj Singh Dholaniya
A novel computational approach to generate genome based barcode intended to catalog Indian
microbial species. 2020 5 68.6 Dr. Manjari Kiran, Dr. Pankaj S Dholaniya
Modulating the expression of topo2b to enhance the viability of CGNs through genome editing
2018 3 5920000000 Dr. Pankaj Singh Dholaniya

Research

Knowledge Discovery in Disease Biology:

As more sophisticated technologies in life science/healthcare are constantly being developed, an enormous amount of data has been generated and deposited on various platforms. Looking from the perspective of a particular disease, these data appear to be the pieces of a broken puzzle. This poses a challenge for data scientists to put these parts together and draw conclusive information out of it and to put forward the potential therapeutic targets for the disease. For example, in order to understand the disease mechanism, the data from heterogeneous resources could be collected and analyzed in relation to the molecular pathways centralized to the disease. The behaviour of such pathways can be studied under normal vs diseased conditions for identifying the probable drug targets for the disease. The data resources that can be considered for such studies are genome-wide expression/mutation studies of patients and healthy controls, patients' specific genetic mutations, expression of non-coding DNA elements, clinical characteristics, and integrated pathway information.

Understanding Sequence-Function Relationship in Proteins/DNA:

The behaviour of a protein inside or outside the cell is defined by its interaction with the elements present in the surrounding environment, which include small metabolites to the macromolecules such as RNA, DNA, or proteins. The interactions of a protein with these elements are determined by how it folds in 3-dimensional space, and this three-dimensional folding of a protein largely depends on the linear sequence of amino acids. In summary, it can be stated that the function of a protein is determined by its interaction, the interaction of a protein is determined by its structure and the structure of a protein is determined by its sequence. As determining the 3D structure of a protein is a challenging task (computationally as well experimentally), we deploy various ML-based to understand the molecular interactions of protein from its sequence properties. This has large application in terms of predicting potential interactions of a protein with that of small molecules (drug-like/metabolites) and macromolecules such as RNA, DNA, or proteins.

Neurological Disorders:

We are interested in investigating the mechanism and the molecular markers for neuronal senescence and age-associated neurodegenerative diseases. Currently, we are working towards the computational modelling of Parkinson's disease from an integrated analysis of the GWAS, gene expression, proteome, and pathway data to explain the disease and non-disease states in terms of the gene/protein interaction networks. We are also working on the characterization of the role of Topoisomerase 2 beta (Top2b) and its associated genes in neuronal senescence by modulating the expression of the Top2b enzyme through genome editing techniques.

Datasets and Databases

Genome Sequences:

7 Whole-genome sequences of Severe Acute Respiratory Syndrome Coronavirus 2 isolate (SARS-CoV-2) from Hyderabad, India#

MT415320.1; MT415321.1; MT415322.1; MT415323.1; MT477885.1; MT457402.1; MT457403.1

Tools and Databases:

RTGR-iTGV: Induced Tomato genomic variation database#: <http://psd.uohyd.ac.in/itgv/>

RTGR-TGV: Tomato genomic variation database#: <http://psd.uohyd.ac.in/tgv/>

Microarray Datasets:

E-MTAB-3977 - Transcription profiling by array of Human SUP-T1 cells infected with HIV and/or treated with curcum:

<https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-3977/>

E-MTAB-4552 - Expression profiling of cerebellar granule neurons from Rattus norvegicus cultured for four week:

<https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-4552/>

#Work in collaboration