

Dr. Rakesh Kaundal

Department of Biochemistry and Molecular Biology

Dr. Rakesh Kaundal joined the Oklahoma State University faculty in early 2011 as a research scientist of bioinformatics and metagenomics in the National Institute for Microbial Forensics & Food and Agricultural Biosecurity (NIMFFAB). He earned his bachelor's degree in agriculture and master's in plant breeding & genetics from CSK Himachal Pradesh Agricultural University, Palampur, India. A profound love for agricultural science and a relentless urge to serve the farming community encouraged him to complete his doctoral studies at University, Agra India. Although his Ph.D. research involved extensive molecular biology and genetic analysis work, he always wished to integrate the advances in the areas of computer science and information technology to solve complex biological problems. Bioinformatics being the key to handle this prompted him to earn a post-graduate diploma in bioinformatics as an additional qualification from Sikkim Manipal University, Gangtok, India.

Before joining OSU, Kaundal served as a postdoctoral research fellow at The Samuel Roberts Noble Foundation, Ardmore, Okla. for about four years where he was actively involved in the basic plant biology research aimed at software development in computational biology, bioinformatics and genomics for biological discovery.

The research in Kaundal Bioinformatics Laboratory focuses on a range of topics in applying statistical pattern recognition, artificial intelligence and machine learning technologies in the area of agricultural biosecurity, metagenomics, regulatory mechanisms of gene expression, genome-wide host-pathogen interaction networks and genome annotation for functional studies. He has developed a range of bioinformatics tools that are useful within the real biological situations. Currently, his lab is involved in developing novel computational tools and algorithms for pathogen detection and discrimination, such as discriminating genotypes in a fundamentally different way from distance-based and BLAST algorithms and instead, using the Neural Networks, Support Vector Machine or Decision Tree classifiers to build patterns from genome regions (e.g. DNA barcodes) that are under selective pressure; and ultimately incorporating them into searchable databases / visualization tools.



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