

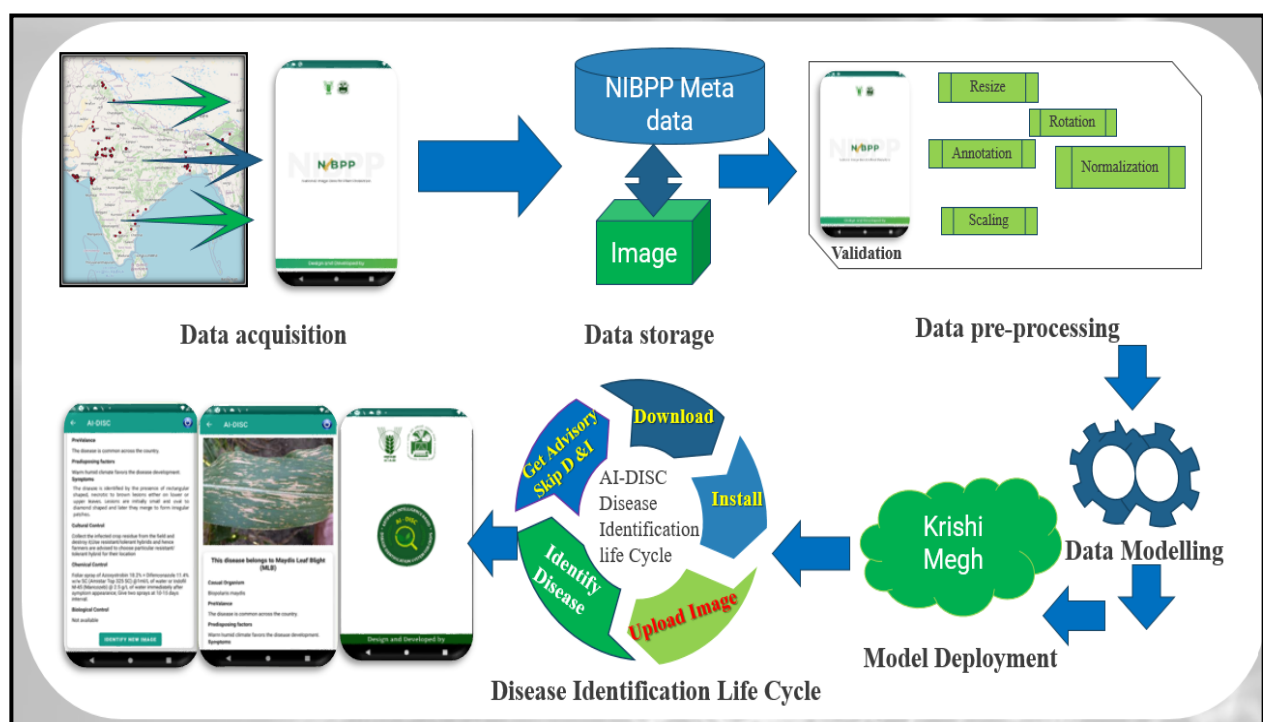


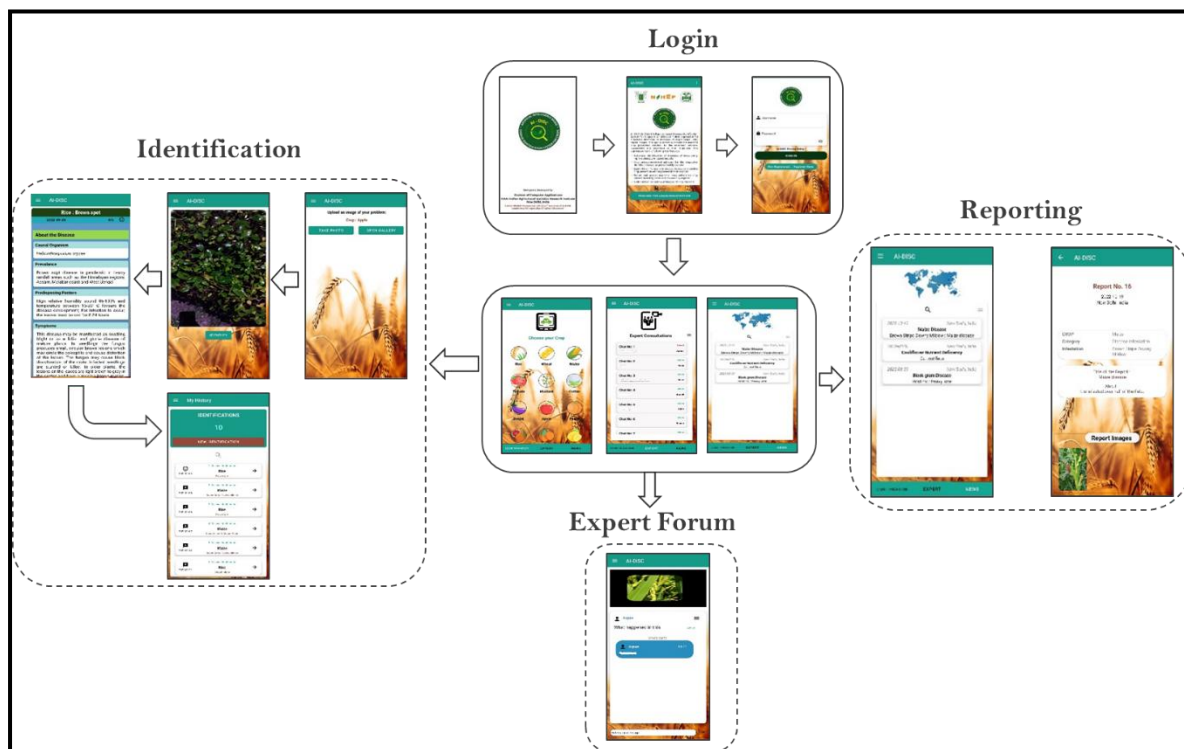
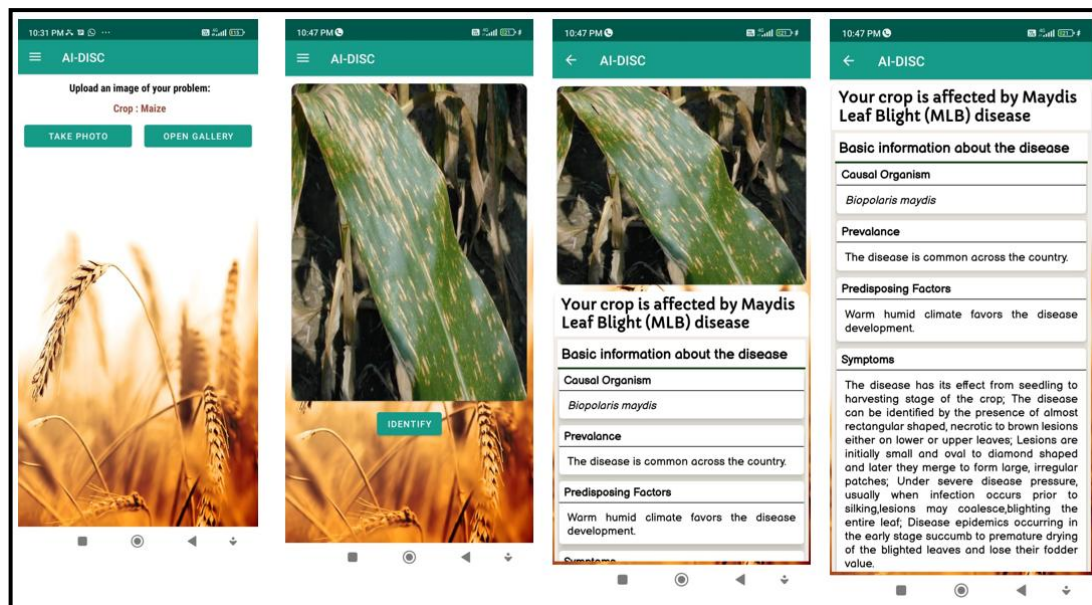
Achievements in Research and Development in Artificial Intelligence & Robotics: ICAR-IASRI, New Delhi

1. Artificial Intelligence based Disease Identification System for Crops (AI-DISC) App

S.No.	Item	Description
1.	Area of the Technology/Output	AI & Robotics
2.	Name of the Technology/Output	Artificial Intelligence based Disease Identification System for Crops (AI-DISC) App
3.	Descriptions (Not more than 150 words)	AI-DISC is an intelligent mobile application which facilitates automated, image-based identification of crop diseases and pests through advanced artificial intelligence-based techniques. In this app, latest AI-based algorithms were integrated with the smartphones through a dedicated application interface. The application utilizes the National Image Base for Plant Protection (NIBPP) as its foundational knowledge repository and image database for developing the advanced deep learning models. AI-DISC App is aimed to provide real-time crop protection solutions and expert-level advisory to the farmers on their fingertips. This mobile app presently automatically detects 55 diseases of 22 crops and 66 insect-pests of 8 crops
4.	Potential Application in the Field Agriculture	The AI-DISC app provides real-time crop protection solutions using images and expert-level advisory to the farmers on their fingertips.
5.	Impact Evaluation Summary (if applicable)	This mobile application has more than 10K downloads in google playstores. Additionally, the models of AI-DISC have been shared in the form of APIs with POCRA and NPSS.
6.	Potential Stakeholders	Farmers, Researchers, Subject Matter Specialists, ICAR-Institutes, KVKs, etc.
7.	Expected Benefit	In a vast country like India where the number of experts is very scarce, it is not possible to reach every farmer at their doorstep and give the advice to cope with the consistently occurring pests and diseases in the crop field. Lack of proper and timely disease identification causes tremendous loss in crops, which leads to huge loss in economic sector of the country. In order to identify the diseases and pests of crops properly along with the scientific advisory in proper

		time an app like AI-DISC is a very beneficial tool to the farm community.
8.	Constraints (if any)	Development, monitoring and maintenance of the AI-based models requires huge computational resources and a dedicated human force.
9.	Intervention Required (if any)	Expanding the app's coverage for all the major crops (agricultural as well as horticultural crops) in India, coordinated interventions and support from the ICAR institutes are required. This objective can be operationalized through a multi-institutional network project, supported by some funding to deliver AI-enabled crop protection solutions towards farmers
10.	Future Plan of Action	In future, the app's scope could be expanded to cover a wider variety of crops (agricultural crops, horticultural crops etc) including their major diseases, insect-pests, and physiological disorders. To better reach farming communities, crop protection advisory services can be provided subjected to specific locations and be delivered in regional languages.
11.	Remarks	NA





2. KCC-CHAKSHU: Collated Historically Aggregated Knowledge-based System with Hypertext User-interface

S.No.	Item	Description
1.	Area of the Technology/Output	Space Technology/ AI & Robotics
2.	Name of the Technology/Output	KCC-CHAKSHU: Collated Historically Aggregated Knowledge-based System with Hypertext User-interface
3.	Descriptions (Not more than 150 words)	The KCC-CHAKSHU portal is a data-driven initiative developed by ICAR-IASRI, New Delhi, to enhance the efficiency of India's Kisan Call Center (KCC) system. It integrates Artificial Intelligence (AI) and Big Data technologies to analyze the nationwide farmer queries effectively. The portal aims to provide real-time insights into agricultural issues, enabling faster and more accurate responses. The KCC-CHAKSHU portal provides access to over 40 million preprocessed farmer queries, along with data-driven insights to enhance agricultural decision-making and advisory services. Under this activity we have developed multiple AI-driven frameworks to strengthen agricultural support systems by enabling real-time assistance, spatial-temporal analysis, and disease forecasting. The AgriResponse framework delivers text-based plant protection solutions to farmers and experts. The AgriMine pipeline extract national-scale spatial and temporal patterns from helpline data, with Temporal Convolution Networks (TCNs) outperforming other models in forecasting seasonal crop needs. The AgrIntel framework focuses on food-production challenges and disease outbreak prediction, exemplified by rice blast, using deep learning models (CNN, LSTM, GRU) for hotspot detection and demand forecasting. Collectively, these frameworks guide policymakers, agri-industrialists, and marketers in designing targeted interventions, training, and sustainable agricultural policies.
4.	Potential Application in the Field Agriculture	The KCC-CHAKSHU system can significantly strengthen agricultural extension and advisory services by enabling real-time, data-driven responses to farmer queries. It supports policymakers and researchers in identifying emerging issues, regional trends, and resource gaps to design targeted interventions. By

		leveraging AI and machine learning on a large repository of farmer interactions, it helps deliver personalized, evidence-based recommendations to improve farm productivity and sustainability. In addition, it can guide the development of new decision support tools, training modules, and policy frameworks for more efficient agricultural knowledge dissemination.
5.	Impact Evaluation Summary (if applicable)	N.A.
6.	Potential Stakeholders	Farmers, Agricultural extension workers, Policy makers and government agencies, Agricultural researchers and institutions, Agritech companies and service providers
7.	Expected Benefit	The KCC-CHAKSHU portal is expected to enhance the efficiency and accuracy of farmer advisory services by providing real-time, data-driven insights. It will reduce response time and improve the quality of solutions offered to farmers, leading to better decision-making at the field level. Policymakers and researchers will gain access to valuable trend analyses for developing targeted interventions and resource planning. Overall, it will foster a more responsive, transparent, and technology-driven agricultural support ecosystem in the country.
8.	Constraints (if any)	N.A.
9.	Intervention Required (if any)	N.A.
10.	Future Plan of Action	Future work aims to develop high-resolution, real-time disease surveillance systems by integrating crop-specific severity maps with weather, soil, IoT, and agronomic data, supported by cloud platforms for large-scale processing. The portal will be upgraded with an advanced and scalable database architecture alongside a redesigned, user-friendly interface to improve accessibility, visualization, and analytics for diverse stakeholders. Season-wise and region-specific analysis of farmer queries will be incorporated to deliver more targeted insights and advisory services. Automated query generation, large language models (LLMs), and AI-based outputs will further enhance data retrieval, forecasting accuracy, and personalized support for farmers.
11.	Remarks	N.A.



KCC - CHAKSHU

ICAR-Indian Agricultural Statistics Research Institute, New Delhi, India



HOME

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RELEVANT LITERATURE

ABOUT

Kisan Call Center Data Repository

CHAKSHU - Collated Historically Aggregated Knowledge-based System with Hypertext User-interface

Over 39 million farmers' call-log records available and ready to be used

About the Kisan Call Center program

The Ministry of Agriculture and Farmers Welfare, Govt. of India launched Kisan Call Centers nationwide on January 21, 2004, to deliver extension assistance to the farming community. The purpose of these call centers is to answer issues raised by farmers immediately in their local language. There are call centers for every state which are expected to manage traffic from any part of the country. Questions related to agriculture and allied sectors are being addressed through these call centers. A farmer from any part of the state can contact the Kisan Call Center by dialing the toll-free Telephone No. 1551 or 1800-180-1551 and explain their problems/queries related to agriculture. The operator at the Kisan Call center attempts to answer the problems/questions of the farmers immediately. If the operator at the Call Center cannot address the farmer's query directly, the call will be forwarded to identified agricultural specialists.

About the KCC data Repository

Each query-call from the farmers is logged with the information requested by the farmers and the information delivered to the farmer. The query-call logs are made available to the public by the Indian government on the open data platform (data.gov.in) and through API. In the presented data repository, query-call log records are made available with the 11 attributes, (given in table) received from January 2006 till present.

S.No.	Attribute Name	Description
1.	BlockName	Block name of farmer
2.	DistrictName	District name of farmer
3.	StateName	State name of farmer
4.	CreatedOn	Year, month, date and time of the query
5.	Season	Season of year
6.	Category	Query Category
7.	Crop	Target crop of query
8.	QueryType	Type of Query
9.	Sector	Target sector of query
10.	QueryText	Query in textual format
11.	KccAns	Query Response

About

The Kisan Call Center data repository is compiled and hosted by ICAR-Indian Agricultural Statistics Research Institute, New Delhi, India, under the project entitled, "Development of Artificial Intelligence integrated Big-Data based system for automatic query-response generation and analysis of Indian farmers' queries".

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INDIAN COUNCIL OF AGRICULTURAL RESEARCH

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of

ICAR-Indian Agricultural Statistics Research Institute, New Delhi

has developed the technology

**KCC-CHAKSHU: Collated Historically Aggregated
Knowledge-based System with Hypertext User-interface
(<https://kcc-chakshu.icar.gov.in/>)**

16th July, 2023
New Delhi

(Bimlesh Mann)

Assistant Director General (EP&HS)

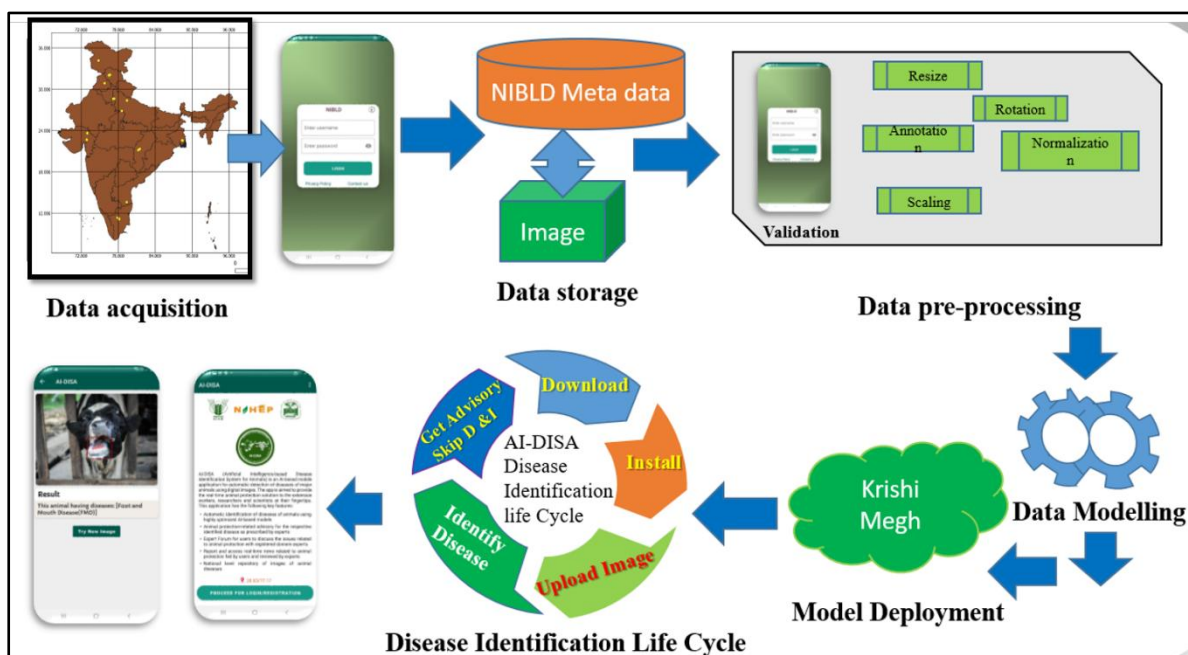
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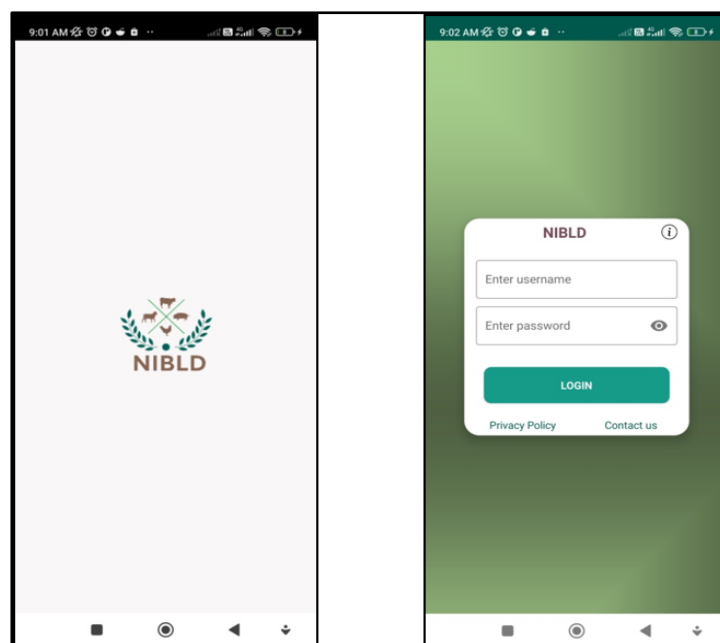
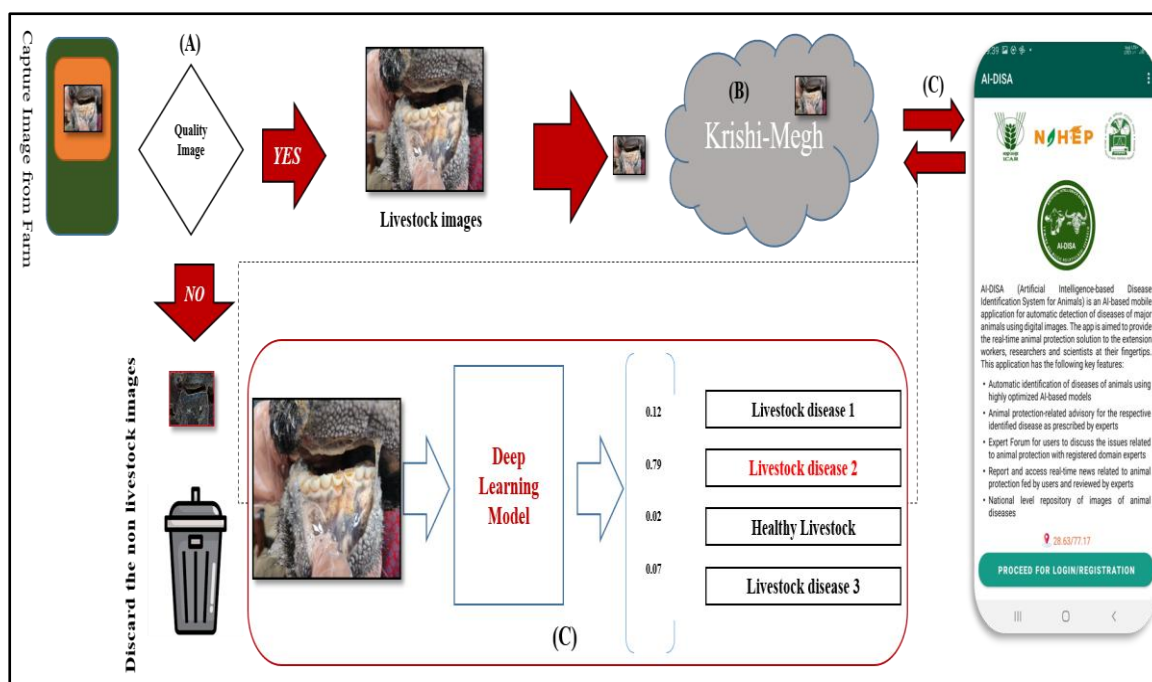
Deputy Director General (Agril. Edn.)

3. AI-DISA: Artificial Intelligence-based Disease Identification System for Animals

S.No.	Item	Description
1	Area of the Technology/Output	AI & Robotics
2	Name of the Technology/Output	AI-DISA: Artificial Intelligence-based Disease Identification System for Animals
3	Descriptions (Not more than 150 words)	AI-DISA is an AI-powered mobile designed for the intelligent detection, and advisory of animal diseases. Developed under ICAR initiatives, the system combines deep learning-based image analysis and knowledge-driven modules to identify visible symptoms of Bovine and canine diseases. Presently, AI-DISA can detect three bovine diseases—Foot and Mouth Disease (FMD), Mastitis, and Lumpy Skin Disease (LSD)—and five canine diseases, covering a total of nine diseases across two animal groups. The platform generates real-time advisories for farmers, veterinarians, and livestock owners, while also enabling participatory disease surveillance through crowdsourced, geo-tagged data. Its integration of AI models with field-ready advisory frameworks enhances animal health management, reduces diagnostic delays, and supports policy decisions for disease control.
4	Potential Application in the Field (Animal Health & Agriculture)	AI-DISA can strengthen veterinary extension and surveillance systems by enabling rapid, on-farm detection of livestock and canine diseases. It supports farmers, para-vets, and veterinarians with instant, evidence-based advisory solutions, thereby reducing mortality and productivity losses. The platform also empowers policymakers and researchers with spatio-temporal analytics for early warning systems, targeted vaccination campaigns, and region-specific disease management strategies.
5	Impact Evaluation Summary (if applicable)	Pilot testing with bovine and canine datasets has demonstrated accurate disease identification with high adoption potential. Early results indicate reduced diagnostic gaps, improved response times, and enhanced veterinary service efficiency.
6	Potential Stakeholders	Livestock farmers and pet owners, Veterinarians and para-vets, State Animal Husbandry Departments, Policy makers and government agencies, Veterinary researchers and ICAR/SAUs, Animal health companies and start-ups.
7	Expected Benefit	Faster and more accurate animal disease diagnosis, improved animal welfare and productivity, reduced economic losses, strengthened veterinary extension, and data-driven policymaking.

8	Constraints (if any)	Requires continuous dataset expansion with diverse field images; smartphone access and digital literacy in rural areas; model accuracy may be influenced by image quality and environmental conditions.
9	Intervention Required (if any)	Infrastructure for large-scale image collection and annotation, integration with national livestock health platforms, multilingual support, and training modules for field veterinarians and farmers.
10	Future Plan of Action	Expand coverage to additional livestock and companion animal diseases, incorporate explainable AI for transparent diagnostics, integrate with IoT biosensors for multimodal surveillance, and establish national-level dashboards for real-time disease intelligence.
11	Remarks	AI-DISA aligns with India's vision of One Health by enabling smart, AI-driven animal disease management and advisory systems.





4. Artificial Intelligence & Robotics (AI-enabled softwares for High Throughput Plant Phenotyping)

S.No.	Item	Description
12.	Area of the Technology/Output	Artificial Intelligence & Robotics (AI-enabled softwares for High Throughput Plant Phenotyping)

13.	Name of the Technology/Output	PhenoVision-AI: An Artificial Intelligence Enabled High Throughput Plant Phenotyping Platform for Abiotic Stress Tolerance
14.	Descriptions (Not more than 150 words)	This technology is an AI-enabled High Throughput Plant Phenotyping (HTP) platform that integrates computer vision, deep learning, and automated pipelines to address the phenotyping bottleneck and accelerate crop improvement. It provides end-to-end solutions for non-destructive trait characterization, stress assessment, and yield prediction in wheat, mustard, and other crops. Work done so far includes the development of specialized modules: MuSiC (Deb et al., 2023) for siliqua counting in mustard, WheatSpikeSense for real-time wheat ear detection, SpikeSegNet and Web-SpikeSegNet (Misra et al., 2020; 2021) for spike identification, m-Senescencia (Kumar et al., 2020) for senescence staging, and SlypNet (Maji et al., 2022) for spikelet detection, PanicleDet: Automated Paddy Stage Detection (Chaurasia et al., 2024). Future work focuses on unifying these pipelines into an Integrated Analysis Platform (IAP) , incorporating sensor datasets and scalable web applications. This unified platform will accelerate genetic gain, support breeder-friendly tools, and contribute to developing climate-resilient, high-yielding crops.
15.	Potential Application in the Field Agriculture	• Automated trait extraction for wheat, mustard, rice and other crops • Senescence monitoring for abiotic tolerance studies. • Yield prediction and growth stage identification for precision agriculture. • Integration into breeder workflows to accelerate selection of superior genotypes. • Real-time, non-destructive crop monitoring for controlled conditions.
16.	Impact Evaluation Summary (if applicable)	N.A.
17.	Potential Stakeholders	• ICAR institutes • Plant breeders and crop physiologists. • Agricultural universities and research stations. • Policymakers and agri-tech startups.

		Seed companies adopting digital agriculture.
18.	Expected Benefit	- High-throughput phenotyping replacing laborious manual methods. - Breeder-friendly decision-support tools. - Open-source pipelines and web applications for wider adoption.
19.	Constraints (if any)	NA
20.	Intervention Required (if any)	- National-level collaboration for standardized datasets and field validation of pipelines. - Investment in affordable imaging and computational infrastructure. - Training programs for breeders, physiologists and researchers on AI-based phenotyping tools. - Policy support for adoption of digital phenomics in breeding programs.
21.	Future Plan of Action	- Development of an Integrated Analysis Platform (IAP) combining all modules. - Scaling web-based applications for multi-crop. - Deployment of mobile and edge-AI solutions for decision support.
22.	Remarks	NA

5. Conversational virtual agents or Chatbots for improving livestock, pet and poultry health and production.

S.No.	Item	Description
1.	Area of the Technology/Output	AI & Robotics
2.	Name of the Technology/Output	Conversational virtual agents or Chatbots for improving livestock, pet and poultry health and production.
3.	Descriptions (Not more than 150 words)	SHRIA (Smart Heuristic Response-based Intelligent Assistant) is an advanced educational platform designed to provide instant, scalable, and personalized assistance to stakeholders in the livestock farming sector. Utilizing cutting-edge Natural Language Processing (NLP) and AI methodologies, SHRIA delivers real-time, context-specific information to

		users. Its multilingual feature supports 10 Indian languages and features voice input and output for enhanced accessibility and user experience. Three specialized SHRIA chatbots have been developed to cater to Dairy, Sheep & Goat, and Swine farming. These bots offer comprehensive guidance on topics such as breeding strategies, optimal feeding, preventive healthcare, general management, calf rearing, and organic practices. SHRIA serves as a holistic solution for livestock-related queries, helping users adopt scientifically recommended practices. By ensuring timely access to relevant information, SHRIA contributes to improved animal health, reduced mortality rates, and increased profitability in livestock-based enterprises.
4.	Potential Application in the Field (Animal Health & Agriculture)	In the context of agriculture and animal healthcare, SHRIA plays a transformative role by providing timely, accessible, and scientifically sound guidance to livestock farmers. Designed specifically for the agricultural sector, SHRIA serves as an intelligent, multilingual chatbot platform that addresses the practical challenges faced by farmers involved in dairy, sheep & goat, and swine farming. Its voice-enabled interaction in 10 Indian languages ensures that farmers, regardless of literacy or technical skills, can access vital information easily. SHRIA thus bridges the knowledge gap in rural farming communities, contributing to more sustainable and profitable livestock practices.
5.	Impact Evaluation Summary (if applicable)	The SHRIA chatbots have been demonstrated to livestock farmers and evaluated using real-world queries during field testing conducted by students of ICAR-IVRI, Izatnagar. A dedicated web dashboard, developed to support the mobile applications, captures and displays user feedback on the chatbot responses. The average response time recorded across the bots is 2.37 seconds. To date, the Dairy SHRIA bot has responded to approximately 2,550 queries, while the Sheep & Goat SHRIA and Swine SHRIA bots have resolved around 7,000 and 1,000 queries, respectively.
6.	Potential Stakeholders	Livestock farmers and pet owners, Veterinarians and para-vets, State Animal Husbandry Departments, Policy makers and government agencies, Veterinary researchers and ICAR/SAUs, Animal health companies.
7.	Expected Benefit	• Offers accurate, science-based guidance on livestock management practices • Reduces misinformation from unverified sources • Improved Animal Health and Productivity • Lower mortality

		• Higher milk and meat yield and Quality production • Increased income from Livestock Enterprises • Can serve millions of users simultaneously, ensuring consistent information dissemination across geographies
8.	Constraints (if any)	• Limited Understanding of ambiguous queries • Scientific information is available for queries that are only available in the knowledge corpus
9.	Intervention Required (if any)	• Training programs for sensitization of the bots • Resource needs to strengthen the data used for development of the chatbot
10.	Future Plan of Action	Future development of the SHRIA chatbot require focus on enhancing its knowledge coverage and making it more dynamic e.g. extraction of knowledge from dynamic sources like PDF documents or other relevant URLs available on the Internet. Expansion of the knowledge base to incorporate a broader, dynamically updated corpus sourced from authenticated agricultural and veterinary repositories will enable more comprehensive query resolution. Enhancing the fallback strategies through interactive clarification prompts or guided follow-ups will help mitigate user dissatisfaction when direct matches are unavailable.
11.	Remarks	-

6. Survey weighted machine learning models in complex surveys for crop yield estimation

S. No.	Item	Description
1.	Area of the Technology/Output	AI & Robotics
2.	Name of the Technology/Output	Survey weighted machine learning models in complex surveys for crop yield estimation
3.	Descriptions (Not more than 150 words)	• Estimation of crop yield is complex process due to its multifactorial behaviour. Traditionally, yield is estimated through sample surveys under the General Crop Estimation Surveys (GCES) scheme using Crop Cutting Experiments (CCEs). The introduction of the Pradhan Mantri Fasal Bima Yojana (PMFBY) has increased the number of CCEs required. With this context, Survey-Weighted Support Vector Regression (SWSVR) and Survey-Weighted Random Forest (SWRF) models were developed for yield prediction in both sampled and non-sampled areas. Based on

		these models, an estimator of population total/mean was developed and is expected to be more efficient in yield estimation and will potentially reduce the number of CCEs required. The incompleteness of data in survey due to non-sampling errors is one of the common problems in the survey data. The imputation of missing observations by plausible values enhance the model accuracy. With this context, a new machine learning methodology was developed for dealing with the missing observations in the survey data.
4.	Potential Application in the Field Agriculture	- The developed machine learning models for complex survey for crop yield estimation will be useful for PMFBY Scheme stake holders and PMFBY policy makers for early settlement of claims made by farmers. - The new developed methodology can be an alternative of GCES method.
5.	Impact Evaluation Summary (if applicable)	Nil
6.	Potential Stakeholders	- PMFBY Scheme stakeholders and PMFBY Scheme policy makers. - Social Scientists and Statisticians working in National Agricultural Research and Education System (NARES). - NSSO and other organizations involved in generating official statistics. - Students and Research Scholars working in the area of Sample Surveys.
7.	Expected Benefit	- Improved accuracy in crop yield estimation - Timely settlement of crop insurance claims - Efficient handling of missing data
8.	Constraints (if any)	- Availability of high-quality survey data - Computational requirements of advanced ML models - Need for skilled manpower for implementation
9.	Intervention Required (if any)	- Policy support for adopting ML methodologies in official statistics - Pilot studies for large-scale validation
10.	Future Plan of Action	- Integrate survey-based models with satellite/remote sensing data - Collaborate with government agencies for large-scale adoption in national agricultural surveys

11.	Remarks	The proposed models align with national priorities of strengthening agricultural statistics and supporting PMFBY. They have strong potential to improve accuracy and efficiency in crop yield estimation.
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7. Model-assisted estimators using survey weighted artificial neural network (SWANN) in complex surveys

S. No.	Item	Description
1.	Area of the Technology/Output	Space Technology/ AI & Robotics
2.	Name of the Technology/Output	Model-assisted estimators using survey weighted artificial neural network (SWANN) in complex surveys
3.	Descriptions (Not more than 150 words)	- Survey Weighted Regression (SWR) is a widely used technique that incorporates survey weights into linear regression models for modelling and prediction. However, SWR relies on strong assumptions such as linearity between dependent and independent variables, multivariate normality etc. In practice, these assumptions are often difficult to satisfy, particularly when the functional relationship between variables cannot be explicitly specified or when the underlying population distribution is unknown. Under such circumstances, non-parametric models like Artificial Neural Network (ANN) are preferred because they make no prior assumptions about data distribution and can capture complex nonlinear relationships. Therefore, Survey Weighted Artificial Neural Network (SWANN) model was developed which combine survey weighting with Artificial Neural Networks, which will be able to learn complex nonlinear relationships in a data-driven manner without making any assumption on the population distribution under complex surveys. - Model-assisted SWANN estimator of population mean/total based on SWANN model was developed along with its variance and variance estimator for finite population sampling.
4.	Potential Application in the Field Agriculture	The model-assisted SWANN estimator can be applied to agricultural surveys to obtain more accurate and representative estimates

		of crop yields. SWANN can capture complex, nonlinear relationships in agricultural data such as interactions between climate, soil quality, and farming practices providing policymakers and researchers with robust insights for planning and intervention.
5.	Impact Evaluation Summary (if applicable)	• Nil
6.	Potential Stakeholders	• Government Agencies: Ministry of Agriculture and Farmers Welfare, National Sample Survey Office (NSSO) • Research Institutions & Universities • Policy Makers and Planners: State and national-level policymakers using survey data for decision-making and resource allocation. • Data Scientists and Statisticians: Developing models and analyzing survey data for improved estimation.
7.	Expected Benefit	• The model-assisted SWANN estimator offers more accurate, precise, and reliable estimates for agricultural surveys, reducing bias from unequal selection probabilities. It enhances efficiency by capturing complex, nonlinear relationships in the data, supporting better-informed policy decisions.
8.	Constraints (if any)	• Limited availability of large high-quality survey datasets for training. Model can be developed using survey data but for the development of model assisted estimator, the unit level data of auxiliary variables is required for whole population. • High computational requirements • Need for expertise in AI/ML and statistical survey methods.
9.	Intervention Required (if any)	• Nil
10.	Future Plan of Action	• Development of user-friendly software packages and training modules for wider adoption of the developed estimators • Validate with large-scale agricultural datasets • Develop user-friendly R packages for wider adoption
11.	Remarks	• Model-assisted SWANN estimator shows strong potential as an innovative methodology for survey-based agricultural research.

S.No.	Item	Description
1.	Area of the Technology/Output	Space Technology/ AI & Robotics
2.	Name of the Technology/Output	BufAMPpred: a deep learning-based AMP prediction server
3.	Descriptions (Not more than 150 words)	An improved buffalo-specific AMP prediction server was developed using a deep neural network based on a CNN+LSTM architecture, which demonstrated superior performance compared to existing prediction tools and servers. The server achieved a prediction accuracy of 98.72% and an AUC of 99.14% in classifying AMP and non-AMP sequences. Designed with a user-friendly interface, the web server allows users to input sequences in FASTA format either by directly pasting them or by uploading a sequence file on the Analysis Page. The prediction results are presented in a tabular format and can be conveniently downloaded using the provided link. A notable feature of this server is its ability to process multiple sequences simultaneously (up to 500 in a single submission), offering a significant advantage over most existing AMP prediction tools, which typically accept only one sequence at a time.
4.	Potential Application in the Field Agriculture	The output of this study will help improve disease resistance in buffalo but as well as contribute to the economy of the major dairy and meat-based industries across the globe. The computationally discovered AMPs have huge scope in management of rising AMR (antimicrobial resistance) across globe as an alternative to antibiotics livestock farming.
5.	Impact Evaluation Summary (if applicable)	NA
6.	Potential Stakeholders	Potential stakeholders include academic researchers in animal genomics, veterinary scientists, livestock breeders, pharmaceutical and biotech companies, animal health policymakers, government and livestock development agencies, and NGOs working in animal disease control. These groups can utilize the AMP prediction server for research, diagnostics, breeding, and disease management applications.
7.	Expected Benefit	The expected benefits include accurate and efficient prediction of antimicrobial peptides (AMPs) in buffalo species, enabling improved disease resistance research and therapeutic development. The tool's batch processing enhance accessibility and usability,

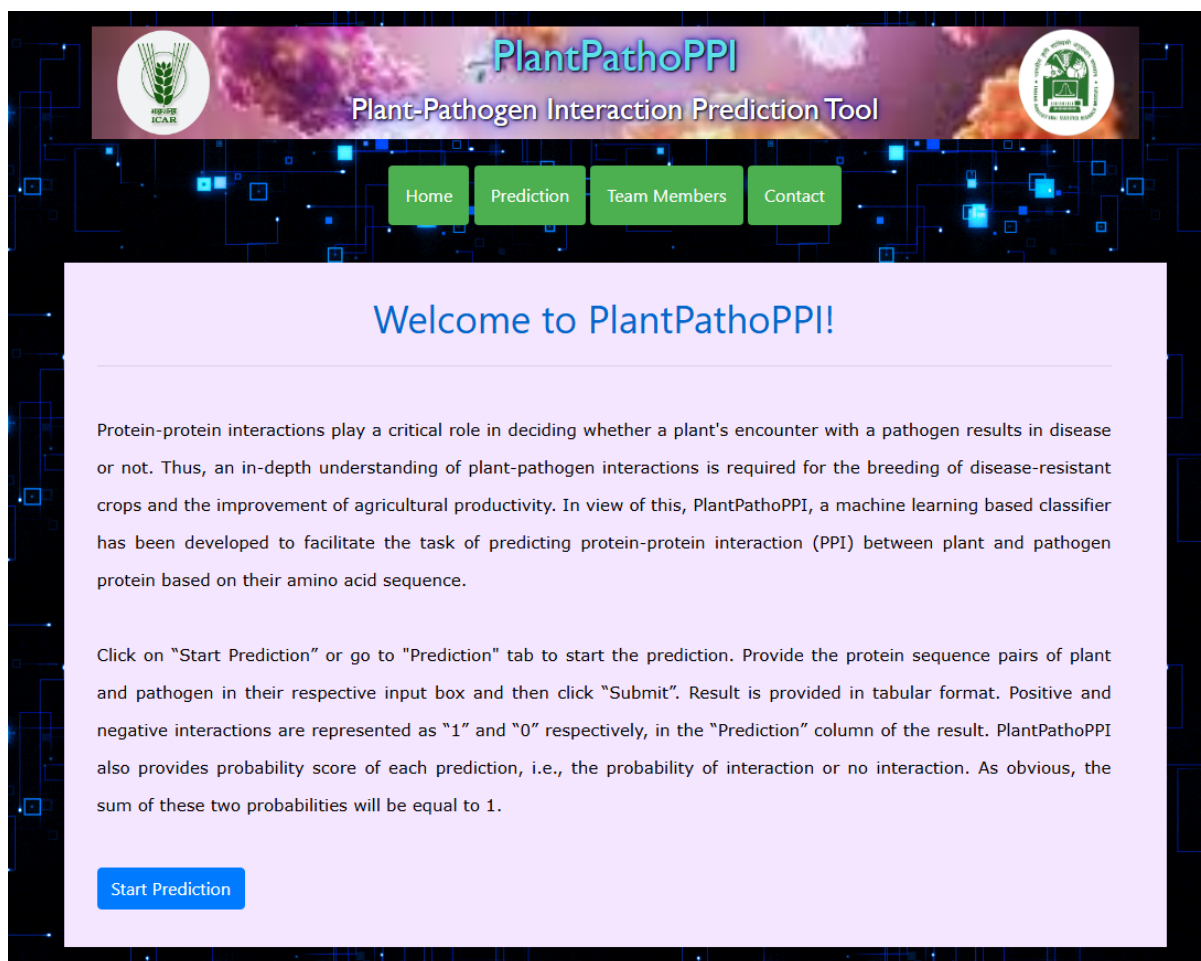
		supporting researchers, veterinarians, and breeders in accelerating buffalo health management and bioinformatics applications.
8.	Constraints (if any)	NA
9.	Intervention Required (if any)	NA
10.	Future Plan of Action	Future plans include expanding the prediction server to cover additional livestock species, integrating more advanced deep learning models for enhanced accuracy, and incorporating multi-omics data for comprehensive antimicrobial peptide analysis. Further development of the mobile app with added features and offline capabilities to support field usage is also planned.
11.	Remarks	Received Copyright in 2024: SW-19584/2024 BufAMPpred: Deep Learning AMP Prediction Server for Buffalo Authors: Aamir Khan, Kalpana Singh, Ajay Verma, Sarika, Varij Nayan, UB Angadi, TK Datta, Anil Rai, Dinesh Kumar, M. A. Iquebal

8. PM_ProInteract: A web application predict protein-ligand interaction in plants and microbes

S.No.	Item	Description
1.	Area of the Technology/Output	AI & Robotics
2.	Name of the Technology/Output	PM_ProInteract: A web application predict protein-ligand interaction in plants and microbes
3.	Descriptions (Not more than 150 words)	PM_ProInteract is a comprehensive web tool developed for predicting protein–ligand interactions in plants and microbes. Protein–ligand interactions are central to biological processes, influencing plant growth, development, immunity, and microbial pathogenicity. Understanding these mechanisms is vital for crop improvement and antimicrobial development, yet experimental approaches are time-consuming and computational scoring functions often oversimplify binding dynamics. To address this, PM_ProInteract leverages machine learning for flexible, data-driven modeling of diverse interaction types.

		The tool integrates two ML components: PhytoMicroBioPred, a classification model that predicts interactions between small molecules and plant or microbial proteins with accuracies of 86% and over 90%, respectively; and PlantPathoPPI, an ensemble model for plant–pathogen protein–protein interactions, achieving ~97% accuracy. Together, these modules provide a unified platform for exploring protein–ligand interactions, enabling the discovery of candidate targets and bioactive compounds. PM_ProInteract serves as a valuable resource for plant biology, crop protection, and microbial research.
4.	Potential Application in the Field Agriculture	PM_ProInteract can accelerate the discovery of novel bioactive compounds for plant protection by predicting interactions of phytochemicals with microbial targets and plant defense proteins. It supports the identification of virulence factors and host immune regulators, aiding in the development of disease-resistant crops. By integrating protein–ligand and protein–protein interaction predictions, it provides a computational platform for screening large compound libraries, reducing reliance on labor-intensive wet-lab assays, and enabling sustainable solutions for crop improvement and protection.
5.	Impact Evaluation Summary (if applicable)	NA
6.	Potential Stakeholders	Researchers, agro-biotech firms, agrochemical industries.
7.	Expected Benefit	PM_ProInteract will enhance agricultural research by providing a reliable platform for predicting plant–microbe molecular interactions and identifying potential bioactive compounds. This will accelerate the discovery of eco-friendly crop protection strategies, reduce time and cost of experimental screening, and support breeding programs for disease resistance. Ultimately, it empowers researchers, industries, and policymakers with data-driven solutions for sustainable agriculture.
8.	Constraints (if any)	NA

9.	Intervention Required (if any)	NA
10.	Future Plan of Action	The tool will be expanded with larger datasets, integration of molecular dynamics and docking modules. Collaboration with agro-biotech and crop protection industries will be pursued for validation, optimization, and commercialization to maximize its practical utility.
11.	Remarks	NA



PlantPathoPPI
Plant-Pathogen Interaction Prediction Tool

Home Prediction Team Members Contact

Welcome to PlantPathoPPI!

Protein-protein interactions play a critical role in deciding whether a plant's encounter with a pathogen results in disease or not. Thus, an in-depth understanding of plant-pathogen interactions is required for the breeding of disease-resistant crops and the improvement of agricultural productivity. In view of this, PlantPathoPPI, a machine learning based classifier has been developed to facilitate the task of predicting protein-protein interaction (PPI) between plant and pathogen protein based on their amino acid sequence.

Click on "Start Prediction" or go to "Prediction" tab to start the prediction. Provide the protein sequence pairs of plant and pathogen in their respective input box and then click "Submit". Result is provided in tabular format. Positive and negative interactions are represented as "1" and "0" respectively, in the "Prediction" column of the result. PlantPathoPPI also provides probability score of each prediction, i.e., the probability of interaction or no interaction. As obvious, the sum of these two probabilities will be equal to 1.

[Start Prediction](#)



PM-BioPred: A Web-Server for Prediction of Compound Bioactivity against Plant and Microbes Proteins



Welcome to PM-BioPred

PM-BioPred predicts the bioactivity of small molecules against different biological targets using machine learning and chemical descriptors computed from SMILES.

- PM-BioPred is a web-based prediction server for assessing the bioactivity of compounds against plant and microbial proteins.
- The tool is built on curated datasets of experimentally validated active and inactive compounds, offering prediction accuracy of 86% (plants) and >90% (microbes).
- It addresses the gap in computational bioactivity prediction resources for non-human systems, particularly in agricultural and microbial research.
- The web interface allows users to query SMILES-formatted compounds and retrieve bioactivity classifications with interpretability.
- PM-BioPred is freely accessible to the academic community and supports early-stage screening of agrochemicals and antimicrobial agents.

Input: CSV file with molecule_id and SMILES
Output: Bioactivity prediction with probabilities
Target Options: Bacteria, Fungi, Virus, Plant

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ICAR-AED-IASRI-Product-2024-024



INDIAN COUNCIL OF AGRICULTURAL RESEARCH

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has developed the technology

**PlantMicrobeProinteract: A web application
to predict the protein-ligand interactions in plants
and microbes (Product)**

16th July, 2024
New Delhi

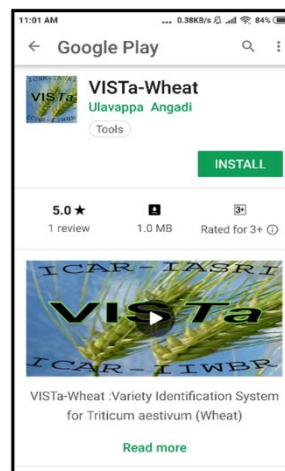
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9. VISTa: Variety Identification System for *Triticum aestivum*

S.No.	Item	Description
1.	Area of the Technology/Output	Space Technology/ AI & Robotics
2.	Name of the Technology/Output	VISTa: Variety Identification System for <i>Triticum aestivum</i>
3.	Descriptions (Not more than 150 words)	VISTa is a DNA-based forensic platform developed to accurately identify wheat varieties, supplementing traditional morphological distinctness, uniformity, and stability (DUS) testing mandated under the PPV&FR Act (2001). Conventional trait-based methods are time-consuming, environmentally influenced, and often insufficient for legal or commercial purposes. VISTa overcomes these limitations by using DNA signatures from 386 wheat varieties, providing rapid, reliable, and environment-independent varietal identification. The system ensures legal validity in resolving disputes over breeders' rights, germplasm sovereignty, and access-and-benefit-sharing (ABS) issues. It also supports global compliance with WTO and IPR guidelines for Plant Breeders' Rights. Hosted as a user-friendly web server, VISTa has already been accessed by more than 5,000 users worldwide. Beyond wheat, the methodology has broad potential for adaptation to other crops, offering an efficient, technology-driven solution for varietal protection, ownership dispute resolution, and strengthening agricultural innovation systems.
4.	Potential Application in the Field Agriculture	VISTa ensures accurate and legally valid wheat varietal identification, supporting breeders' rights, seed authenticity, and dispute resolution under the PPV&FR Act. It strengthens compliance with national and international IPR frameworks, minimizes adulteration, and safeguards farmers' and breeders' interests. The system also promotes investment in varietal development and can be extended to other crops for global application.

5.	Impact Evaluation Summary (if applicable)	NA
6.	Potential Stakeholders	Breeders, PPV&FR Authority, seed companies, policymakers, farmers.
7.	Expected Benefit	VISTa enhances varietal protection by providing fast, reliable, and legally valid DNA-based identification. It ensures seed authenticity, prevents economic losses, and protects breeders' and farmers' rights. By enabling transparent dispute resolution and supporting IPR compliance, it fosters innovation, boosts confidence in crop breeding, and strengthens agricultural sustainability.
8.	Constraints (if any)	NA
9.	Intervention Required (if any)	NA
10.	Future Plan of Action	VISTa will be expanded to other major crops for broader applicability. Integration with SNP chips and advanced genomic databases will improve precision and scalability. Plans include developing a global varietal identification platform, collaborating with national and international stakeholders, and enhancing accessibility through upgraded interfaces and training programs for end-users.
11.	Remarks	NA



10. Machine Learning–based Model of Mineral Nutrition Related Genes in Higher Plants

S.No.	Item	Description
1.	Area of the Technology/Output	Space Technology/ AI & Robotics
2.	Name of the Technology/Output	Machine Learning-based Model of Mineral Nutrition Related Genes in Higher Plants
3.	Descriptions (Not more than 150 words)	A comprehensive machine learning (ML) framework has been developed for the prediction and functional annotation of mineral transporter and homeostasis genes in higher plants. A curated dataset of 32,533 transporter protein sequences covering ten mineral classes (N, P, K, Ca, Mg, Mn, Fe, Zn, Cu, Na) was compiled from UniProt. Eight ML algorithms were trained and evaluated, with Random Forest (81.08%) and LightGBM (81.07%) demonstrating the highest accuracy. The models enable accurate classification of mineral transporter proteins across diverse classes, offering a robust computational pipeline for mineral nutrition research. This framework provides an important step towards the development of a prediction server to facilitate genome-wide mining of mineral-related genes in plants, thereby supporting studies on nutrient uptake, transport, and homeostasis.
4.	Potential Application in the Field Agriculture	Facilitates rapid identification of mineral transporter and homeostasis genes in crops, supporting molecular breeding for nutrient-efficient and climate-resilient varieties. Enhances annotation of genomic datasets and accelerates discovery of candidate genes for improving mineral use efficiency.
5.	Impact Evaluation Summary (if applicable)	NA
6.	Potential Stakeholders	Plant biologists, crop breeders, bioinformaticians, genomic researchers, seed companies, and policy planners in nutrient management.
7.	Expected Benefit	Provides a cost-effective and scalable computational platform for functional annotation of nutrient-related genes, reducing reliance on resource-intensive experiments. Supports breeding of nutrient-efficient crop varieties and improves agricultural sustainability.
8.	Constraints (if any)	NA

9.	Intervention Required (if any)	NA
10.	Future Plan of Action	Develop a web-based prediction server for mineral nutrition-related genes. Expand the framework to additional plant species and integrate deep learning models for higher accuracy. Collaborations with breeding programmes will be pursued for practical deployment.
11.	Remarks	NA

11. Prediction server for IRES

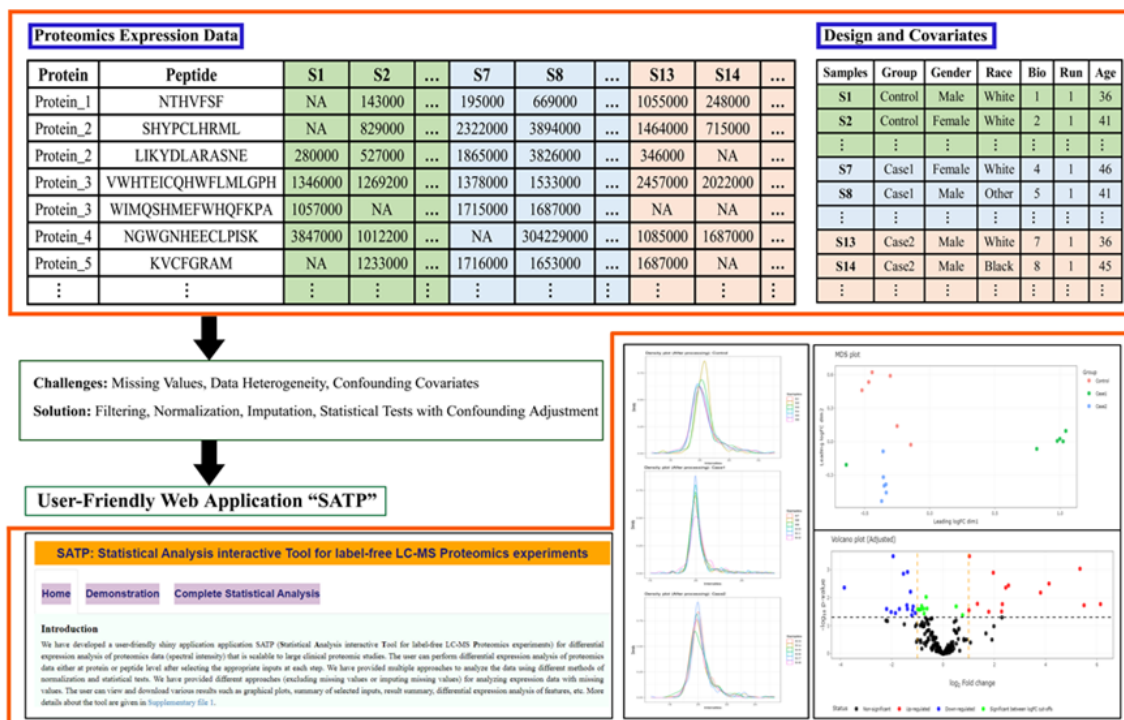
S.No.	Item	Description
1.	Area of the Technology/Output	Bioinformatics/machine learning/AI
2.	Name of the Technology/Output	Prediction server for IRES
3.	Descriptions (Not more than 150 words)	Translation initiation in eukaryotes occurs principally in a 5'cap-dependent manner. However, cell has many ways to regulate the production of proteins using 5'cap-dependent or independent protein translation mechanism. In the former case, scanning machine recognizes and binds to the methylated 5'-end cap structure of an mRNA and scans linearly downstream until it reaches an AUG codon for the initiation of protein translation. Whereas, in the later case, translation can initiate internally in a cap-independent manner because of the presence of internal ribosome entry site (IRES) sequences. It allows the initiation of translation in a cap-independent manner: ribosomes bind internally at the initiating AUG without scanning the 5' nontranslated region of the transcript The IRES directs the ribosomal translation due to formation of specific secondary and tertiary structures that interact directly with the translational machinery. The state-of-art machine learning technique like deep learning, SVM and RF will be implemented for the classification of IRES and non-IRES transcript. Also, compare the deep learning approach against RF and SVM. The comparison will be made through the various evaluation majors such as sensitivity, specificity, accuracy, ROC curve, AUC, precision, recall, F-score etc. Further, an attempt will be taken to identify the ORF length and amino acid sequence along with homologous genes.
4.	Potential Application in the Field Agriculture	The user will understand how small peptides from the UTR and non-coding regions participate in various economically important traits.
5.	Impact Evaluation Summary (if applicable)	Work is in progress

6.	Potential Stakeholders	Biotechnologist and plant breeders
7.	Expected Benefit	A robust tool will be freely available in the public domain
8.	Constraints (if any)	NA
9.	Intervention Required (if any)	NA
10.	Future Plan of Action	Develop a tool to identify the plant toxic peptide.protein translating from noncoding/UTR
11.	Remarks	

12.SATP (Statistical Analysis Interactive Tool for label-free LC-MS Proteomics experiments)

S.No.	Item	Description
1.	Area of the Technology/Output	Space Technology/ AI & Robotics
2.	Name of the Technology/Output	SATP (Statistical Analysis Interactive Tool for label-free LC-MS Proteomics experiments)
3.	Descriptions (Not more than 150 words)	Proteomics studies using LC-MS often face challenges such as missing values (due to random errors, poor-quality samples, or detection limits) and heterogeneity (arising from technical or biological variability). These issues can confound important findings. Additionally, clinical and pre-clinical metadata (e.g., sex, exposure) and field experiments data offer valuable covariates that are often underutilized. To address this, the SATP web application (URL: https://ulbbf.shinyapps.io/satp/) was developed as a user-friendly and scalable platform for differential expression analysis in label-free LC-MS proteomics. The SATP tool has significant scientific and technical impact by addressing key challenges in LC-MS proteomics data analysis, including missing values, heterogeneity, and the need for multi-factor statistical models. Its integration of normalization, imputation, and advanced analysis methods makes it a comprehensive platform for differential expression studies.
4.	Potential Application in the Field Agriculture	In agriculture, it enables the discovery of proteins linked to stress tolerance, growth, and yield, supporting crop productivity. In animal sciences, it helps to identify protein markers for disease

		resistance, reproduction, and growth traits, contributing to livestock improvement.
5.	Impact Evaluation Summary (if applicable)	N.A.
6.	Potential Stakeholders	It is relevant to researchers, clinical and pre-clinical scientists, biotechnology and pharma companies, and agricultural scientists working on plant and animal proteomics. It will also benefit academic researchers, students, and trainees involved in proteomics research and applications.
7.	Expected Benefit	This will lead to discovery of novel proteins and genes responsible for various economically important traits in plants and animals. This will aid in increasing the productivity.
8.	Constraints (if any)	N.A.
9.	Intervention Required (if any)	N.A.
10.	Future Plan of Action	The developed approach and web tool will be enhanced to better handle missing values and data heterogeneity, integrate additional clinical, pre-clinical, and field metadata, and support advanced multi-factor statistical models, including interaction effects. These improvements will make the tool more user-friendly and comprehensive, enabling accurate and insightful analysis of label-free LC-MS proteomics experiments. In the future, the platform will be extended to include other types of proteomics experiments, such as Data-Dependent Acquisition, Data-Independent Acquisition, and labeled proteomics experiments.
11.	Remarks	N.A.



13. Artificial Intelligence based Framework for Prediction of Protein 3D Structure

S.No.	Item	Description
1.	Area of the Technology/Output	Space Technology/ AI & Robotics
2.	Name of the Technology/Output	Artificial Intelligence based Framework for Prediction of Protein 3D Structure
3.	Descriptions (Not more than 150 words)	A model for protein structure prediction was developed using Long Short-Term Memory (LSTM) deep learning techniques, trained on datasets from the Protein Data Bank. This method extracts features from existing 3D structures by segmenting both protein sequences and structures, and then mapping sequence segments to corresponding structural segments. The mapped data are used to train the model using the LSTM approach. The model first generates the basic topology of the protein structure using only backbone atoms. Following this, side-chain packing is performed using the FASPR (Fast and Accurate Side-chain Packing and Refinement) tool. Finally, side-chain and overall energy minimization are carried out using ModRefiner to produce the final predicted structure.
4.	Potential Application in the Field Agriculture	The developed framework for protein 3D structure prediction has wide applications

		in agriculture. In crops, it helps uncover mechanisms of stress tolerance, plant–pathogen interactions, and nutrient uptake, while also guiding the design of protein-based biostimulants, resistant varieties, and safer agrochemicals. In animals, it supports the development of vaccines, disease-resistant breeds, improved feed efficiency, and the reduction of allergens or anti-nutritional factors in livestock products. Overall, this will lead to enhanced productivity, better health, and greater sustainability in agriculture.
5.	Impact Evaluation Summary (if applicable)	N.A.
6.	Potential Stakeholders	It has several potential stakeholders, including researchers and academics in agricultural sciences, plant breeders and animal geneticists, as well as biotechnology and agri-tech companies.
7.	Expected Benefit	It is expected to accelerate discoveries in plant and animal sciences by revealing protein functions and interactions, enabling the development of stress-tolerant crops, disease-resistant livestock, eco-friendly agrochemicals, and protein-based biostimulants. This will ultimately improve agricultural productivity, enhance food security, and promote sustainability.
8.	Constraints (if any)	N.A.
9.	Intervention Required (if any)	N.A.
10.	Future Plan of Action	The AI-based protein 3D structure prediction framework will be further refined and expanded to cover a broader range of proteins. Efforts will focus on improving prediction accuracy, integrating additional datasets, and enhancing the web tool for more user-friendly access.
11.	Remarks	N.A.

