

## RESEARCH ARTICLE

# Identification of promising genotypes in varietal trials of sugarcane using deep learning

Syed Sarfaraz Hasan<sup>\*1</sup> and Sanjeev Kumar<sup>2</sup>

<sup>1</sup>Agriculture Knowledge Management Unit, ICAR – Indian Institute of Sugarcane Research, Raebareli Road, PO Dilkusha, Lucknow 226002

<sup>2</sup>Division of Crop Improvement, ICAR – Indian Institute of Sugarcane Research, Raebareli Road, PO Dilkusha, Lucknow 226002

\* Corresponding author: Email: syed.hasan@icar.gov.in

(Received: 16 June 2022; accepted: 09 January 2023)

### Abstract

Identification of promising sugarcane genotypes in varietal trials undergoes analytical studies of data collected from location-based and multi-phase varietal trials. Data on more than twenty characters such as germination %, tillers, shoots, NMC, fibre, brix, sucrose, CCS, cane yield, etc are collected frequently, starting from germination stage till harvesting at different stages of crop. It is a quite complex and time-consuming task and information about some important parameters may remain unnoticed by experts despite best efforts. Deep learning algorithms can be developed for such complex task to extract high level features from trial data and make intelligent decisions based on it for identifying promising genotypes. Deep learning works on the principle of artificial neural networks in which multiple layers of processing are used to extract progressively higher-level features from data. In this paper, we have demonstrated use of deep learning for identification of promising genotypes. We have developed sequential model using tensor-flow libraries in Python programming platform. To construct, train and test deep learning model, datasets of 181 genotypes accepted in coordinated trials for the duration 2016-21 have been used. Model uses crop characters viz. cane yield, sucrose%, CCS%, and CCS yield along with score of monitoring and red rot screening. Data management practices allowed to pre-process data for learning and testing model from it. Deep learning in this study consists of input layer, two hidden layers and output layer. Output classes are 'Promising' and "Non-promising" in binary form corresponding to promising genotype or otherwise. Model performed well with accuracy of prediction worked out to be 91.67% with loss value as 0.2832, while F-measure for both promising and non-promising genotypes got a high equivalent score of 0.91 and 0.92 respectively.

**Keywords :** Deep Learning; Sugarcane; Varietal Trial; Machine Learning; Artificial Intelligence

### Introduction

Varietal improvement programmes are most essential component of sugarcane research system with aim of achieving not only production and productivity requirements but also to deter biotic and abiotic stresses. Identification of promising genotypes of sugarcane undergoes location-based and multiphase testing for both plant and ratoon crop under these programmes. In India, multi-location trials of sugarcane genotypes are conducted both at state and national level by coordinated efforts of agricultural universities, research institutes, and private sector under ambit

of All India Coordinated Research Project on Sugarcane. Varietal trials of proposed genotypes are conducted at over 22 locations under four agro-climatic zones of the country. A series of four trials are conducted of these genotypes under programme of Initial Varietal Trial, Advance Varietal Trial (Plant Crop 1), Advance Varietal Trial (Plant Crop 2), and Advance Varietal Trial (Ratoon Crop) (Pathak 2021). Data on more than twenty characters such as germination %, tillers, shoots, NMC, fibre, brix, sucrose, CCS, cane yield, etc are collected frequently, starting from germination stage till harvesting at different

stages of crop at all centres. Crop is monitored by centre's staff as well as monitoring team to judge the performance of genotypes. Promising genotypes are identified after a series of analysis and discussions on centre data and pooled data of zones. Accurate and reliable analysis of characters for identifying promising genotypes for further commercial release is important to improve performance of sugarcane sector. It is a quite complex and time-consuming task in traditional computing world and information about some important parameters may remain unnoticed by experts despite best efforts, and need intervention of artificial intelligence techniques.

Machine learning is an application of artificial intelligence (AI) that provides systems the ability to automatically learn and improve from experience without being explicitly programmed. It can be defined as a process of building computer systems that automatically improve with experience (Ayodele 2010). While deep learning is a class of machine learning algorithms that extract higher-level features from the raw input for making intelligent decisions (Deng and Yu 2014). Inspired by the structure and function of the human brain, deep learning works on the principle of artificial neural networks in which multiple layers of processing are used to extract progressively higher-level features from data (Grossi and Buscema 2007). Deep learning algorithms can be developed for such complex task to extract high level features from trial data and make intelligent decisions based on it for identifying promising genotypes.

Although it is a new technique of artificial intelligence, but as of now it drives many artificial intelligence (AI) applications and services that improve automation, performing analytical and physical tasks without human intervention. Santos et al. (2020) performed a survey of different deep learning techniques applied to various agricultural problems, such as disease detection/identification,

fruit/plants classification and fruit counting. The conclusions indicate that deep learning provides high accuracy results, with occasional exceptions. Lac et al. (2020) proposed a deep neural network-based algorithm able to detect, locate, and track the stem position of crops in images which is suitable for precision actions in vegetable fields such as mechanical hoeing within crop rows. UAV-based camera systems and a deep learning image analysis pipeline are implemented for a fully automated plant counting in sugar beet, maize, and strawberry fields in the study conducted by Barreto et al. (2021). Selectively picking a target fruit surrounded by obstacles remains a challenge for fruit harvesting robots. Xiong et al. (2021) developed vision system that combined two neural networks and colour thresholding for real-time detection, tracking and localization of strawberries.

However, very little applications of deep learning has been found in sugarcane domain limited to insect-pest identification and sugarcane mass estimation. Hamdan et al. (2020) used deep learning to develop and test a vision system that can accurately estimate the mass of sugarcane while running in real-time on a sugarcane harvester during operation. The deep neural network (DNN) succeeds in capturing the mass of sugarcane accurately and surpasses older volumetric-based methods, despite highly varying lighting and material colours in the images. Thenmozhi and Reddy (2019) in his study proposed an efficient deep CNN model to classify insect species on three publicly available insect datasets. The results demonstrated that the proposed CNN model is effective in classifying various types of insects in field crops than pre-trained models and can be implemented in the agriculture sector for crop protection.

Inspired by deep learning abilities and concerns of varietal trials, we have used this technique

to identify promising genotypes in sugarcane varietal trials. Paper describes the methodology used in our approach for building deep learning model and then presented results of its evaluation and prediction of genotypes.

## Materials and Methods

Deep learning approach is data driven and results depend on quality of data to learn a model from. Data is bifurcated in training and testing datasets, out of which training set is used for training and building the model, while testing dataset is used for testing model. We have taken zonal varietal trials data of sugarcane generated in AICRP trials. AICRP on Sugarcane is serving the nation by coordinating research work on sugarcane since 1970 through a network of sugarcane research stations of ICAR, state agricultural universities, state govt. departments and non-government organizations. As per the mandate, main emphasis is laid on the development of improved sugarcane varieties, crop production and protection technologies suited to commercial cultivation under different agro-climatic conditions in the country. AICRP receives request for multi-location trials of genotypes proposed by various states of four agro-climatic zones of the country. Technical programme is scheduled for these genotypes to pass through Zonal Varietal Trials (ZVT) consisting of Initial Varietal Trial, Advance Varietal Trial (Plant Crop 1), Advance Varietal Trial (Plant Crop 2), Advance Varietal Trial (Ratoon Crop). Further, crop protection trials under disciplines of Plant Pathology and Entomology are also conducted for evaluation of genotypes for resistance to various diseases and insect-pest. Data is collected at regular interval as per technical programme and then compiled, analysed and reported in AICRP meetings for selection of promising genotypes.

In our study, we have taken pooled data of ZVTs, monitoring reports of trials and red rot evaluation data for duration 2016-21. Data was collected from

secondary sources such Principal Investigator's Reports of AICRP. Our methodology goes through two major phases viz. data management and deep learning model building.

In first phase following data management activities were performed to prepare the dataset for next phase:

1. Collected following data of four agro-climatic zones for both early and midlate genotypes for duration 2016-21 from the Principal Investigator's Reports of Crop Improvement, Varietal Improvement Programme, All India Coordinated Research Project on Sugarcane, ICAR-Sugarcane Breeding Institute, Coimbatore (for the years, 2017, 2018, 2019, 2020 and 2021) and Plant Pathology (Technical Report, Plant Pathology, All India Coordinated Research Project on Sugarcane, ICAR-Sugarcane Breeding Institute, Coimbatore for the years, 2017, 2018, 2019, 2020 and 2021) and recorded in Excel Sheet.
  - a. Pooled varietal trial data of four major characters of sugarcane viz. cane yield, CCS yield, CCS% and sucrose % at harvest.
  - b. Monitoring data of trials.
  - c. Red rot screening data of genotypes.
  - d. Information about promising and non-promising genotypes was recorded with the help of domain experts.
2. Data was transformed into common units, wherever required.
3. Quality data was converted into quantitative form in fixed scale as per following criteria:
  - a. Monitoring score was converted into scale of 1-4, where 4 indicates best genotype and 1 indicates poor.
  - b. Red rot score was converted into binary form. Resistant and moderately resistant

genotypes was given 1, while moderately susceptible and susceptible genotypes was given 0.

- c. Promising genotypes were given a score of 1 while 0 for non-promising one.
4. Above data was pooled together to get single record per sugarcane genotype using averaging techniques.
5. Since selection of promising varieties is done based on improvement of genotypes in comparison to best standard of the zone. We have calculated and used difference of all four characters data from their best standard for the zone.
6. Removed unwanted columns and rows from Excel sheet and converted into CSV format.

After preparation of dataset, building of deep learning model, evaluation and testing was performed in second phase. Python programming language along with tensor flow libraries have been used to perform these tasks. Various activities performed under this phase are as follows:

1. Imported TensorFlow and other important libraries in Python.
2. Imported datasets created above to be used in our program.
3. Scaled the data to bring it in same scaling range.
4. Balancing of datasets was performed using Oversampling technique.
5. Bifurcated datasets into training and testing in ratio of 4:1.
6. Built a Sequential model of deep learning.
7. Above model was compiled and fitted with training and testing datasets using inbuilt functions of tensor flow.
8. Model was evaluated for accuracy, precision, recall and F-measure for desired performance.

These matrices were calculated with following formulae

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

$$Precision = \frac{TP}{TP + FP}$$

$$Recall = \frac{TP}{TP + FN}$$

$$F1 = \frac{2 * Precision * Recall}{Precision + Recall}$$

Confusion matrix helped in identifying True Positive (TP), True Negative (TN), False Positive (FP) and False Negative (FN) cases out of the model to evaluate above metrics.

9. Prediction of test genotypes was made using above model.

## Results and Discussion

Trial data of 181 genotypes was collected, which were proposed for multi-location trials from states of peninsular, north-west, north-central & north-eastern, and east-cost zones during 2016-21. Table 1 shows the zone-wise list of genotypes entries used along with standards in this study. Number of genotypes for early and midlate are 69 and 72 respectively for north-west, north-central & north-eastern, and east-cost zones while 40 genotypes are of peninsular zone. Crop characters covered are cane yield, CCS%, CCS yield and sucrose % along with monitoring score and red rot score. Thus, there are six attributes used to predict the promising genotypes as shown in data structure given in Table 2. Table 3 shows the sample processed data used by the system. First six columns in this table corresponds to monitoring score, red rot resistance score and four crop characters (cane yield, CCS %, CCS yield, sucrose %) difference from standards, while last column signifies the score 1 and 0 for promising and non-promising classes respectively.

**Table 1.** List of genotypes entries and standards used

<b>Zone and Entry Group</b>	<b>Test Entries</b>	<b>Standard</b>
East Coast Zone (Early)	Co 13023, CoA 12321, CoA 12322, CoA 12323, CoA 13322, CoA 13323, CoA 14321, CoA 16321, CoC 13336, CoC 13337, CoC 14336, CoC 15336, CoC 15338, CoC 16336, CoC 16337, CoOr 12346, CoV 12356, CoV 13356, CoV 15356, CoV 16356	Co 6907, CoA 92081, CoC 01061, CoOr 03151
East Coast Zone (Midlate)	Co 13028, Co 13029, Co 13031, CoA 11326, CoA 12324, CoA 14323, CoC 13339, CoC 14337, CoC 15339, CoC 16338, CoC 16339, CoOr 13346, CoOr 15346, CoV 16357, PI 14377	Co 06030, Co 86249, CoV 92102
North Central Zone + North Eastern Zone (Early)	CoLk 12207, CoLk 14206, CoLk 15466, CoLk 15467, CoP 11436, CoP 11437, CoP 11438, CoP 12436, CoP 13437, CoP 14437, CoP 15436, CoSe 11451, CoSe 12451, CoSe 13451, CoSe 13452, CoSe 14451, CoSe 14454, CoSe 15452, CoSe 15455	BO 130, CoLk 94184, CoSe 01421, CoSe 95422
North Central Zone + North Eastern Zone (Midlate)	BO 155, CoLk 09204, CoLk 12209, CoLk 14208, CoLk 14209, CoLk 15468, CoLk 15469, CoP 12438, CoP 14438, CoP 14439, CoP 15438, CoP 15439, CoP 15440, CoSe 11453, CoSe 11454, CoSe 11455, CoSe 12453, CoSe 14455, CoSe 15453, CoSe 15454	BO 91, CoP 06436, CoP 9301, CoSe 92423
North West Zone (Early)	Co 13034, Co 14034, Co 15023, Co 15024, Co 15027, CoH 11262, CoLk 11201, CoLk 11202, CoLk 11203, CoLk 14201, CoLk 15201, CoLk 15205, CoPb 13181, CoPb 14181, CoPb 14211, CoPb 15212, CoS 13231	Co 0238, Co 05009, CoJ 64
North West Zone (Midlate)	Co 11027, Co 12029, Co 13035, Co 14035, CoH 11263, CoH 12263, CoH 13263, CoH 14261, CoLk 11204, CoLk 11206, CoLk 12205, CoLk 13204, CoLk 14203, CoLk 14204, CoPant 12226, CoPant 13224, CoPb 11214, CoPb 12211, CoPb 13182, CoPb 14184, CoPb 14185, CoS 11232, CoS 12232, CoS 14233	Co 05011, CoPant 97222, CoS 767, CoS 8436

Zone and Entry Group	Test Entries	Standard
Peninsular Zone (Early + Midlate)	Co 09009, Co 10004, Co 10005, Co 10006, Co 10015, Co 10017, Co 10024, Co 10026, Co 10027, Co 10031, Co 10033, Co 11001, Co 11004, Co 11005, Co 11007, Co 11012, Co 11019, Co 12007, Co 12008, Co 12009, Co 12012, Co 12019, Co 12024, Co 13002, Co 13003, Co 13004, Co 13006, Co 13008, Co 13009, Co 13013, Co 13014, Co 13018, Co 13020, Co 14002, Co 14004, Co 14012, Co 14016, Co 14027, Co 14030, Co 14032, CoM 10083, CoM 94008, Co 99004, CoC 671, 11081, CoM 11082, CoM 11084, CoM 11085, CoM 11086, CoM 12085, CoSnk 05103 CoN 13072, CoN 13073, CoN 14073, CoSnk 13101, CoSnk 13103, CoSnk 13106, CoSnk 14102, CoSnk 14103, CoT 10366, CoT 10367, CoT 10368, CoT 10369, CoT 14367, CoTI 14111, CoVC 10061, CoVC 14062, MS 13081, MS 14081, MS 14082, PI 10131, PI 10132, PI 13132, VSI 12121	

**Table 2.** Data structure of dataset developed in first phase

Field Name	Field Type	Field Description
Monitoring Score	Float	Average numeric score of monitoring team score for trial
Red Rot Resistance Score	Binary	Binary value of 1 to indicate genotype is red rot resistant / moderately resistant otherwise 0
Cane Yield Difference	Float	Difference of cane yield t/ha from best standard of the zone
CCS % Difference	Float	Difference of CCS% from best standard of the zone
CCS Yield Difference	Float	Difference of CCS yield t/ha from best standard of the zone
Sucrose Difference	Float	Difference of sucrose % from best standard of the zone
Identified Class	Binary	Promising genotype indicator. 1 for promising, 0 for non-promising

**Table 3.** Sample of dataset developed in first phase

Monitoring Score	Red Rot Resistance Score	Cane Yield Difference	CCS % Difference	CCS Yield Difference	Sucrose Difference	Identified Class
1.964286	1	-13.96	0.4	-1.21	0.46	0
2.422078	1	-13.22	-0.84	-2.43	-1.2	0
2.275974	1	0.6	-0.23	-0.23	-0.34	1
2.208333	0	-1.36	-0.62	-0.85	-0.81	0
2.214286	1	2.7	-0.35	-0.04	-0.44	0
2.574675	1	-9.84	-0.513	-0.703	-0.712	0
2.003846	1	-9.36	-0.45	-1.76	-0.63	0
2.62013	1	16.13	-0.65	1.39	-1.15	1
2.555195	1	-7.79	-0.7	-1.81	-0.93	0
2.613636	1	-9.13	-0.77	-2.12	-1.02	0
2.674603	1	-13.22	0.19	-1.53	0.27	0
2.766484	1	-2.5	0.25	0.16	0.34	0
2.90232	1	-3.38	0.06	-0.35	0	1
2.708181	1	1.58	-0.1	-0.1	-0.39	0
2.252442	1	-11.08	0.03	-1.11	0.29	0

Oversampling technique came out to be beneficial, as there is huge imbalance in number of promising and non-promising genotypes in varietal trial data. It is a technique used to adjust the class distribution of a dataset. After oversampling technique total size of dataset came out to be 296, out of which 60 records have been used by the system as testing datasets and rest as training dataset to train the model. Final sample scaled dataset used by system for training and testing purpose has been given in Table 4.

**Table 4.** Scaled dataset developed in second phase

Monitoring Score	Red Rot Resistance Score	Cane Yield Difference	CCS % Difference	CCS Yield Difference	Sucrose Difference	Identified Class
0.687012	1	0.730957	0.631836	0.634766	0.404297	0
0.358887	0	0.579102	0.190186	0.500488	0.223389	0
0.418457	1	0.637695	0.528809	0.729004	0.606445	0
0.524414	0	0.441895	0.008545	0.294922	0.042480	1
0.864258	1	0.688965	0.689453	0.602539	0.283691	0
0.519043	0	0.156494	0.495605	0.250977	0.510742	0
0.421387	1	0.966797	0.223145	0.854980	0.148926	1

Monitoring Score	Red Rot Resistance Score	Cane Yield Difference	CCS % Difference	CCS Yield Difference	Sucrose Difference	Identified Class
0.358887	1	0.130371	0.289062	0.211182	0.301270	0
0.306641	1	0.799316	0.491455	0.820312	0.567383	1
0.321777	1	0.901367	0.557617	1.000977	0.680664	1
0.614746	1	0.468506	0.285156	0.492676	0.343750	0
0.208984	1	0.533691	0.247925	0.549805	0.273193	0
0.290527	1	0.723145	0.058105	0.598633	0.102783	0
0.230957	1	0.490723	0.499756	0.620117	0.506836	0
0.465820	1	0.241943	0.247925	0.247314	0.276611	1

Sequential model used for deep learning consist of input, output and hidden layers as depicted in Fig. 1. Input layer consists of six neurons with respect to input parameters viz. Monitoring score, red rot resistance score, and difference of cane yield, CCS yield, CCS % and sucrose % from standards. Output layer corresponds to two classes of promising and non-promising genotypes represented by binary output of 1 and 0. Two hidden layers have been used in our model, which assist in extracting features in every iteration of learning.

Confusion matrix of predictions made by the deep learning model has been shown in Fig. 2. It provides insight into not only the performance of a predictive model, but also which classes are being predicted correctly or incorrectly,

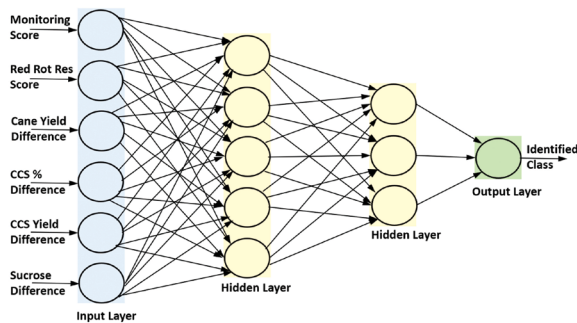


Figure 1. Deep learning model used

and what type of errors are being made. Two types of classes mentioned in the matrix are “Promising” and “Non-promising” corresponding to promising genotypes or otherwise. X axis displays the prediction results while true results are indicated on Y axis. As shown in this matrix, 26 trial genotypes have been predicted as true (promising) predictions for promising class, while 4 promising genotypes have been shown false (non-promising) by the model. Similarly, 29 non-promising genotypes have been predicted as true (non-promising) prediction while 1 genotype has been falsely predicted of promising class.

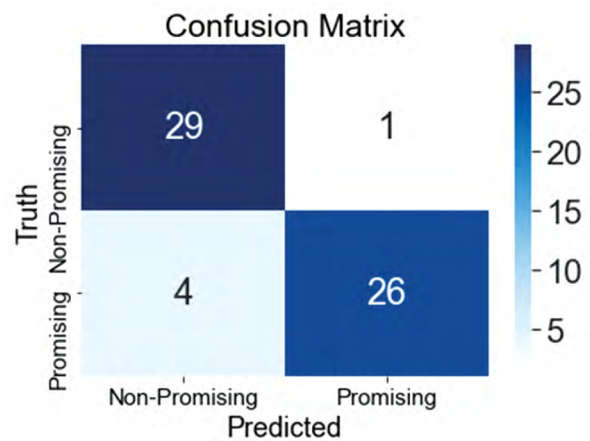


Figure 2. Confusion matrix of prediction made by model



**Table 5.** Classification report of prediction

Prediction	Precision	Recall	F-measure
Promising	0.96	0.87	0.91
Non-promising	0.88	0.97	0.92
Accuracy : 0.9167		Loss : 0.2832	

Table 5 above shows the classification report of model evaluation. Metrics shown in table describes the performance of the model in terms of accuracy, precision, recall, and F-measure. Classification accuracy is the total number of correct predictions divided by the total number of predictions made for a dataset. Accuracy of prediction worked out to be 91.67% with loss value as 0.2832. Precision is a metric that quantifies the number of correct positive (promising) predictions made. Precision of prediction for promising genotypes found to be 96%, as against 88% for non-promising genotypes. Recall metric quantifies the number of correct positive predictions made out of all positive (promising) predictions that could have been made. Unlike precision that only comments on the correct positive predictions out of all positive predictions, recall provides an indication of missed positive predictions. Recall values for promising and non-promising genotypes indicated by model are 87% and 97% respectively. F-measure provides a way to combine both precision and recall into a single measure that captures both properties. F-measure for both promising and non-promising genotypes got a high equivalent score of 0.91 and 0.92 respectively. Data on more than twenty crop characters is recorded in varietal trials of sugarcane for selection, however, our model performed well with only 4 crop characters along with the score of red rot screening and trial monitoring.

### Conclusion

A key advantage of deep learning networks is that they often continue to improve as the size of data increases, which is advantageous as sugarcane

varietal trials are continuous activity. Automatic extraction of hidden features in deep learning is beneficial for such type of applications, as important features may be missed in traditional system of identifying promising genotypes in varietal trials. Results of deep learning model evaluation gave a good starting value of accuracy for the size of zonal varietal trial dataset and number of attributes. However, accuracy of model can be enhanced further with use of long-term zonal varietal trials data and addition of other crop characters while training and testing the model. As deep learning is a new machine learning method of artificial intelligence and recent research work has come out with many techniques for improving accuracy and minimising losses in prediction that needs to be tested in agriculture scenario. Model may be used further for developing mobile or web-based apps for decision support in varietal identification and to ultimately improve the performance of sugarcane sector.

### References

- Ayodele T. 2010. Machine Learning Overview. <https://doi.org/10.5772/9374>.
- Barreto A, Lottes P, Yamati FRI, Baumgarten S, Paulus S. 2021. Automatic UAV-Based Counting of Seedlings in Sugar-Beet Field and Extension to Maize and Strawberry. *Computers and Electronics in Agriculture*, 191. <https://doi.org/10.1016/j.compag.2021.106493>.
- Deng L, Yu D. 2014. Deep Learning: Methods and Applications. *Foundations and Trends in*

- Signal Processing, 7(3–4):197-387. <http://dx.doi.org/10.1561/20000000039>.
- Grossi E, Buscema M. 2007. Introduction to artificial neural networks. *European Journal of Gastroenterology & Hepatology*, 19(12): 1046-1054. <http://dx.doi.org/10.1097/MEG.0b013e3282f198a0>.
- Hamdan MKA, Rover DT, Darr MJ, Just J. 2020. Generalizable Semi-Supervised Learning Method to Estimate Mass from Sparsely Annotated Images. *Computers and Electronics in Agriculture*, 175. <https://doi.org/10.1016/j.compag.2020.105533>.
- Lac L, Costa JPD, Donias M, Keresztes B, Bardet A. 2022. Crop Stem Detection and Tracking for Precision Hoeing Using Deep Learning. *Computers and Electronics in Agriculture*, 192. <https://doi.org/10.1016/j.compag.2021.106606>.
- Pathak A D. 2021. Annual Report 2020-21. All India Coordinated Research Project on Sugarcane. ICAR-Indian Institute of Sugarcane Research, Lucknow.
- Santos L, Santos FN, Oliveira PM, Shinde P. 2020. Deep Learning Applications in Agriculture: A Short Review. In: Silva M., Luís Lima J., Reis L., Sanfeliu A., Tardioli D. (eds) *Robot 2019: Fourth Iberian Robotics Conference. ROBOT 2019. Advances in Intelligent Systems and Computing*, 1092. Springer, Cham. [https://doi.org/10.1007/978-3-030-35990-4\\_12](https://doi.org/10.1007/978-3-030-35990-4_12).
- Thenmozhi K, Reddy US. 2019. Crop Pest Classification Based on Deep Convolutional Neural Network and Transfer Learning. *Computers and Electronics in Agriculture*, 164. <https://doi.org/10.1016/j.compag.2019.104906>.
- Xiong Y, Ge Y, From PJ. 2021. An Improved Obstacle Separation Method Using Deep Learning for Object Detection and Tracking in a Hybrid Visual Control Loop for Fruit Picking in Clusters. *Computers and Electronics in Agriculture*, 191. <https://doi.org/10.1016/j.compag.2021.106508>.