Prediction of Important Insect of Soybean According to Weather Parameters using Genetic Algorithm based Optimized Ensemble Classifier

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Abstract –

Soybean cultivation is one of the most important crops in the world in terms of production, economic value and the relevance of its products and by-products as possible famine thugs in the face of the continuous growth of the global population. In India, more than 40 species of insect pests of this crop were registered, one of the most relevant being Blue beetle adult/ mrl Larvae/ mrlG.gemma Larvae/mrl, .acuta, Heliothis, Grey weevil adult/ mrl, Stem fly incidence % Plant inf./ mrl Girdle, beetle.This paper presents prediction of important insect of soybean utilizing the Genetic algorithm optimized ensemble classifier. MATLAB based simulations exhibits the accuracy performance for various types of insects.

Keywords –**AdaBoost, Bagging, Boosting, Genetic Algorithm, Soybean, etc.**

I. INTRODUCTION

Soybean (Glycine max (L.) Merr.) is used for human food for more than 4000 years, being from that moment considered as the legume most relevant of civilization [1]. This crop has grown sustainably since its inception in the country in terms of production and cultivated area, occupying a region with an enormous variety of climatic conditions and flora [2][3]. During the 2015 - 2016 campaign in our country,

After cotton, soybeans are the crop that suffers the most attacks from pestsanimals, in which we find a list of more than 40 phytophagous species of insects that they feed on different organs of the oilseed in different areas of India,causing direct physical damage that oscillates around 10% [4] [5].

The Heteroptera, within the Order Hemiptera, are a group of insectscommonly referred to as bedbugs [6]. This group is composedfor 42,347 species [7] It includes the family Pentatomidae, very important foragriculture because several species that are harmful to crops belong to it,either because of the economic importance due to its damage to the seeds in formation or because ofthe costs of its management [6][7]. These phytophagousspecies cause damage to crops both in their juvenile life and in their adult life[8].

Although 206 species and 85 genera of Pentatomidae have been recorded in Argentina,the phytophagous bug complex that affects soybean crops is made up of somefew species, Nezaraviridula (Green bug), Piezodorusguildinii(legume bug), Dichelopsfurcatus (Little horned bug) and Edessa meditabunda (Small Alquiche), insome soybean regions in the center of our country, the occasional presence ofEuschistusheros (Brown or Brazilian bug) [6][9][10] [11]. Bed bugs are the most important pests in the periodreproductive of soybean and are present in all soybean cultivation areas varying theirimportance according to the

region [3] [9] [12][13] [14]. Some species of thiscomplex can occur in high population densities and those conditionscause losses in yield and grain quality, as well as the syndrome offoliar retention and green stem of soybean [15] [16].

In many cases, the natural enemies are the first force of regulation of the population of pests, and the biological management can be used against all types of pests, including vertebrates, phytopathogens, weeds, as well as insects [17][18]. In annual crops such as soya, in early stages the natural enemies have the potential to reduce the population of pests, before reaching high population levels [19]. This is due to high densities of natural enemies in the first six weeks of cultivation [20]. Learning to recognize, manage and conserve natural enemies can help reduce their population and maintain them below economic levels, with the aim of reducing crop losses and necessary costs in control measures that also cause undesirable effects on the environment [21].

The populations of natural enemies in the soy agro-ecosystems may differ due to factors such as the climate, the sibling season, the phenology of the crops and the crop management practices [22] [23]. The objective of the present work was to compare the abundance and richness of predatory insects and parasitoids associated with the cultivation of soy (Glycine max L. Merrill) in normal and late harvests collected from ICAR, Indian Institute of Soybean Research Indore. The most frequent insects are Blue beetle adult/ mrl Larvae/ mrlG.gemma Larvae/mrl, .acuta, Heliothis, Grey weevil adult/ mrl, Stem fly incidence % Plant inf./ mrl Girdle, beetle.

II. PROPOSED METHODOLOGY

A. Dataset

Weekly larval populations of Blue beetle adult/ mrl Larvae/ mrlG.gemma Larvae/mrl, .acuta, Heliothis, Grey weevil adult/ mrl, Stem fly incidence % Plant inf./ mrl Girdle, beetle incidence collected from ICAR, Indian Institute of Soybean Research Indore under Crop Pest Surveillance during 2009-2018 was evaluated to see what effect meteorological variables had on the incidence of this insect on soybean. Larvae were seen throughout the soybean growing season, with the highest occurrence occurring between the third and first weeks of August.

B. Development of Prediction Model
1. AdaBoost Algorithm

Given $X \subseteq \mathbb{R}^p$, $Y \subseteq \mathbb{R}$ vector spaces. Let be the set $S = \{(x_1, y_1), \ldots, (x_N, y_N)\}$ formed by the Npairs (x_i, y_i), called the training set. Let $x_i \in X$ be the feature vector of the ith pair (also known as regressor variables), and $y\_i \in \mathbb{R}$ its response variable.

A statistical learning algorithm is one that searches for a function $f(x)$ that is capable of predicting, given a new datum with a feature vector x_0, its correct response variable y_0.

Depending on whether the variable to be predicted is continuous or categorical, we will be faced with a regression or classification problem, respectively.

Similar to the bagging methods, the boosting techniques will also train a number L of base models$h_1, \ldots, h_L$. However, instead of training the L models in parallel on bootstrap perturbations of the set S to later add them, the training is done sequentially, where each base model is repeatedly trained on modified versions of S, whose modifications depended on the results obtained by the previous model.

The AdaBoost algorithm was the first adaptive boosting algorithm, thus solving many of the limitations of the methods presented up to that time. Created with the aim of improving the predictive capacity of binary classifiers, AdaBoost is designed so that at each training step the distribution of data S adapts to the results of the current classifier, in order to put more weight on the points $x \in S$ that the model

classifies incorrectly. Finally, a weighted average of all these sequential models is used to produce the final assembled forecast.

The main hyperparameters to adjust in a boosting model are the following:

- **The number of base trees L.** Although in bagging and Random Forest the fact of increasing the number of base models to be trained does not usually produce an overfitting by itself, boosting can give rise to an overfitting of the data when L is very large (although it is unusual, and if it does occur it does so very slowly). This parameter is usually selected using cross-validation or making use of the out-of-bag error as the model is trained.

- **The weight α_l of each model in the final assembly.** Also called the shrink parameter, this will control the speed of learning the boosting method. In some cases a constant value is selected, typically $\alpha_l = \alpha = 0.01$ or 0.001 depending on

the problem, and also adjusted by cross-validation. In other cases, like the already mentioned AdaBoost, the contraction parameter α_l will be adaptive, being recalculated at each iteration l.

- **The parameters to be adjusted for the chosen family of base models h_l.** Although any type of base model can be boosted, the most common is to do it with decision trees, due to its low bias and its computational ease. Thus, the main parameter to adjust in this case would be the number of segmentations d that are allowed for each tree h_l created, which will control the complexity (i.e., the size) of the tree. A popular choice in practice is $d = 1$, thus making each tree consist of a single segmentation on a single variable (thus giving trees with $|T| = 2$ terminal nodes). These trees are also known as stump trees.

Algorithm -1:AdaBoostAlgorithm for Multiclass Classification Problems

Input: *Training set $S = \{(x_1, y_1), \ldots, (x_N, y_N)\}$, with $x_i \in \mathbb{R}^p$, $y_i \in \mathcal{G} = (\mathcal{G}_1, \ldots, \mathcal{G}_K)$.*
Number of base classifiers L.
Output: *A classifier $h_{ada} : \mathbb{R}^p \to \mathcal{G}$.*

1. *We start by defining the set B of all pairs of points x and classes y such that the correct class of x is not y. That is, the pairs (i, y) where the point S with index $i(x_i)$ does not have class $y \in \mathcal{G}$ Thus, we defineB $= \{(i, y)|i \in (1, \ldots, N), \ y \neq y_i\}$.*

2. *The weights are initialized, in this case having one for each data $x_i \in S$ and class $y \in \mathcal{G}: w^1(x, y) = \frac{1}{|B|},$ for all $(i, y) \in B$.*

3. *For $l = 1, \ldots, L$, it is calculated:*

   a. *A weak base classifier $h_l(x)$ is fitted to the training set S using the current weights $w^l(i, y)$. In this case, unlike the original AdaBoost, the definition of each base model is $h: \mathbb{R}^p \times \mathcal{G} \to [0, 1]$, so the base models will return more information (and not just the predicted class). Intuitively, each pair (i, y) can be interpreted as asking the algorithm to choose between class y_i (the correct one for x_i) or y (one of the incorrect ones). Thus, in this context the weight $w^l(i, y)$ would be the importance that it would have in our problem, for x_i, to distinguish between the incorrect class y and the correct class y_i.*

   b. *The pseudo-error is calculated with the following formula:*

$$\epsilon_l = \frac{1}{2} \sum_{(i,y) \in} w^l(i,y)\big(1 - h_l(X_i, y_i) + h_l(X_i, y)\big)$$

(1)

c. Is calculated $\beta_l = \frac{\epsilon_l}{1-\epsilon_l}$

d. The weights to be used in the next iteration are calculated for each point of the training set S:

$$w^{l+1}(i,y) = \frac{w^l(i,y)}{Z_l} \cdot \beta_l^{\left(\frac{1}{2}\right)\left(1 - h_l(x_i, y_i) + h_l(x_i, y)\right)}, \quad i = 1, 2, \dots, , N$$

(2)

where $Z_l \sum_{i=1}^{N} w_i^l(i,y) \cdot \beta_l^{\left(\frac{1}{2}\right)\left(1 - h_l(x_i, y_i) + h_l(x_i, y)\right)}$ is a normalizing factor.

4. Qualifying Phase: Given an x to classify, the class y (equivalently, $\mathcal{G}_k$) that maximizes the following expression would be associated:

$$h_{ada}(x) = \arg \max_{y \in \mathcal{G}} \sum_{l=1}^{L} \log\left(\frac{1}{\beta_l}\right) h_l(x,y)$$

(3)

2. Bagging

The Bagging method [24] in its "classical" version is part of the category of data manipulation methods in the taxonomy of the induction principles of set of classifiers that we presented in the previous section. It applies the principle of Bootstrap or Bootstrapping [24] to the aggregation of classifiers; hence its name Bagging for Bootstrap Aggregating.

Let us assume that a set $T = \{x_1, x_2, x_3 \dots, x_N\}$ of N observed data of our population, and that we are interested in a statistic written $S(T)$.

The bootstrap will consist in forming L samples $T_k^* = \left(x_1^*, x_2^*, x_3^*, \dots, x_{N'}^*\right)$ for $k = 1, \dots, L$, where each T_k^* is constituted by random pulling with N' data given in T. These L samples are usually called bootstrap samples.
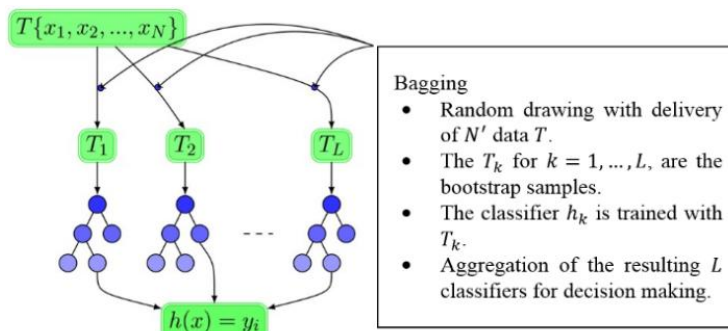

Figure 1: Illustration of the principle of Bagging for a set of decision trees [24]

We can then calculate $S(T_k^*)$ for each bootstrap sample, and thus obtain L estimates of our statistics. So instead of having a single estimate for a sample, we have an empirical distribution of our statistics. We can then calculate the empirical average from all these values (see equation 4), which will then give us a more precise estimate of the statistic, or else its standard error to measure its dispersion (see equation 5).

$$S_{boot} = \sum_{k=1}^{L} S(T_k^*)/L$$

(4)

$$\widehat{se}_{boot} = \sqrt{\frac{\sum_{k=1}^{L}(S(T_k^*) - S_{boot})^2}{(L-1)}}$$

(5)

It is simply a question of considering that the statistic that one seeks to study is a learning algorithm noted $h(x)$ and to then apply the principle of bootstrap as we have just explained it. Thus each elementary classifier $h_k(x)$ of the set will be trained on one of the L bootstrap samples so that they are all trained on a different learning set. Figure 1 illustrates the Bagging process applied to a set of decision trees.

3. Boosting

The name Boosting [24] refers to a learning principle method and is therefore a family of several algorithms. The basic principle is to gradually specialize the classifiers of the set iteratively, and then combine each of the classifiers obtained at each iteration. Typically, it is at theiteration k to concentrate the learning of the classifier h_k on the errors of classifiers $h_{k-1}, h_{k-2}, \ldots, h_1$, obtained at the previous iterations. In the Boosting principle, this objective is achieved by a weighting of the learning data. The weighting is then updated on the basis of these prediction errors, so as to increase the weight of the learning data that has been misclassified by this classifier, while simultaneously decreasing the weights of the well-ranked data. Thus, classifiers are gradually specialized to concentrate on learning previously poorly classified data.

Algorithm -2:Boosting Algorithm

Input:$\mathcal{L}$ a weak learner.

Input:L the number of classifiers in the final set.

Input:T a set of N learning data

1: $D_1(x_i) = \frac{1}{N}, i = 1, \ldots, N$**Initialization of weights (equal probability)**

2: for $t = 1, \ldots, L$ do

3: $h_t = \mathcal{L}(D_t)$**Learning h_t**

4: $\hat{\epsilon}_t = \sum_{i:h(x_i)\neq y_i} D_t(x_i)$**Calculation of the weighted error of h_t**

5: if $\hat{\epsilon}_t = \frac{1}{2}$ then

6: stop the loop

7: $\beta_t = \frac{\hat{\epsilon}_t}{(1-\hat{\epsilon}_t)}$**Calculation of the weighting coefficient of h_t**

8: for $i = 1, \ldots, N$ do

9: if $h_t(x_i) = y_i$ then

10: $D_{t+1}(x_i) = \frac{D_t(x_i)}{Z_t} \times \beta_t$

11: Else

12: $D_{t+1}(x_i) = \frac{D_t(x_i)}{Z_t}$

13: $h_c(x) = \arg\max_{y \in Y} \sum_{t=1}^{L} \log\frac{1}{\beta_t} \times \mathbb{I}_{h_t(x)=y}$

Main idea: Boosting is based on a deterministic principle for the creation of diversity in sets, whereas random forests by definition do so via the principles of randomization.

4. Genetically Optimized Ensemble Classifier

Genetic algorithms (GA) are search methods based on the principles of natural evolution and genetics. In this method, a population of possible solutions to the problem in question evolves under the application of probabilistic operators idealized from biological processes. Thus,

there is a tendency for elements of the population become better and better approximations of the solution as the algorithm develops [25].

The individuals of the population are represented in a coded way, being common the binary representation, expressed by a string of bits called chromosome. The positions in the chain are called gene and these normally assume the binary values 0 and 1, called alleles.

GAs are iterative algorithms, with each iteration called a generation. In most applications the initial population is generated randomly.

GAs assign to each member of the population a non-negative value of an objective function to be optimized called "fitness" or suitability. This value indicates the quality of the individual in the population, being a measure of its adaptability to the environmentindividuals stronger, with better fitness, will have a better chance of surviving and passing on to the next generation. GA simple is composed of 3 basic operators: selection, crossover or "crossover" and mutation. At selection each individual "i" of the population is selected or not according to a selection probability $p_i = P_{fi}$ where fi is your "fitness". The selected individuals are grouped into pairs and subjected to the crossover operator. It occurs according to a fixed probability P_x, simulating sexual reproduction, where chromosome fragments (sub-bit strings) are exchanged.

The mutation occurs according to a probability Pm and consists of selecting a position in the chain chromosome and change its binary value. The mutation introduces new genetic material into the population and allows the exploration of new regions in the parameter space. After applying these operators a new population of possible solutions is obtained. The process continues until some stopping criterion. GAs only need information about the value of an objective function, not requiring derivatives or any other kind of knowledge. GAs can be applied to problems of global optimization, in multidimensional spaces and with objective functions strongly not linearby introducing weights w_{cj}, base classifier scores are p_{cj} are represented by equation (6).

$$p_{cj}(x_t) = w_{cj} \sum_{i=1}^{n} \alpha_i y_i k(x_i, x_t) + b$$

(6)

Where c represents c^{th} ensemble classifier, $j$symbolize j^{th}base classifier of the cth ensemble classifier, and x_t is the test sample.
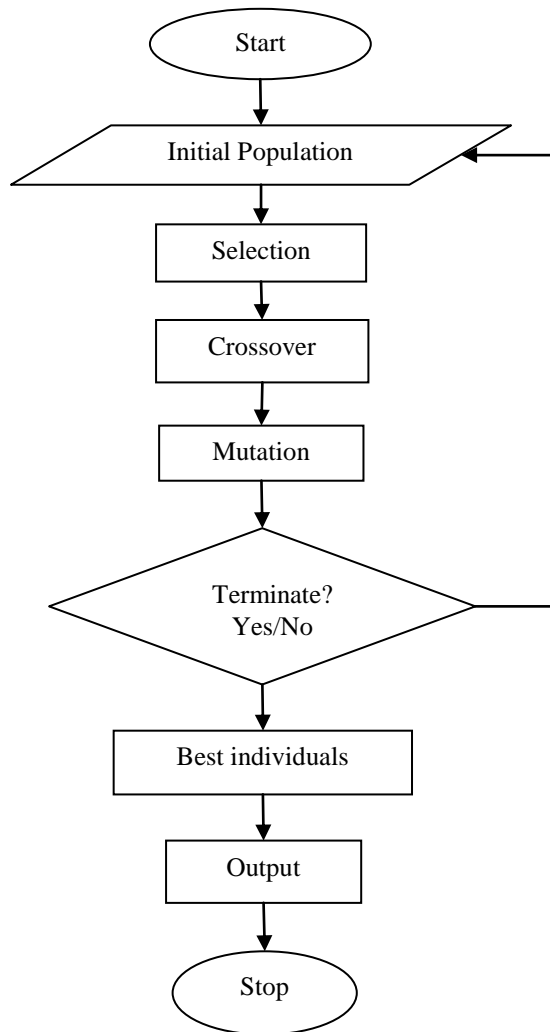
Figure 2: Genetic Algorithm Flow Chart

III. SIMULATION AND RESULTS

Following figures show the MATLAB based simulation results for the prediction of soybean insects.
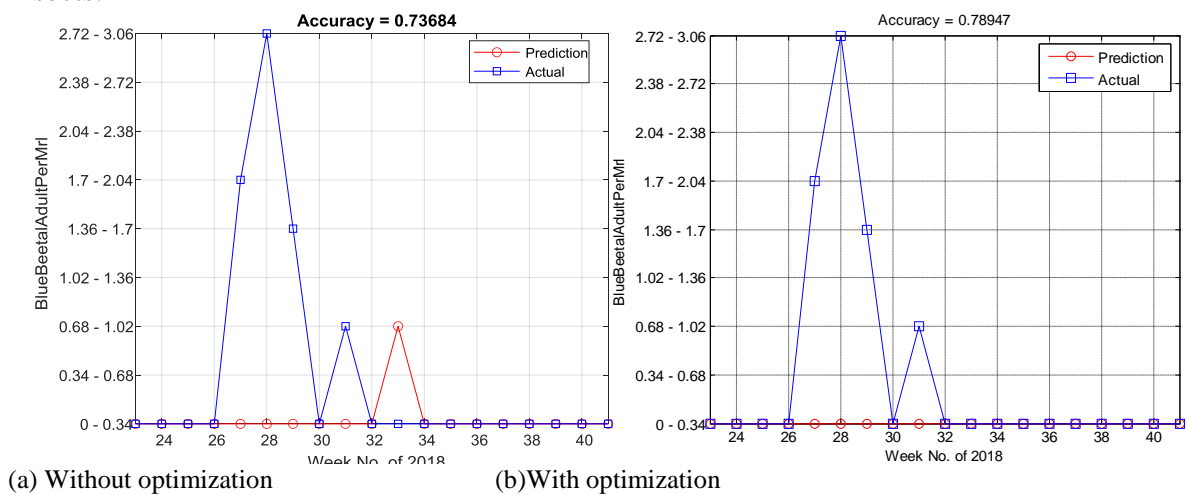

(a) Without optimization   (b)With optimization

Figure 3: Actual and predicted accuracy graphs for BlueBeetalAdultPerMrl insect

(a) Without optimization   (b)With optimization
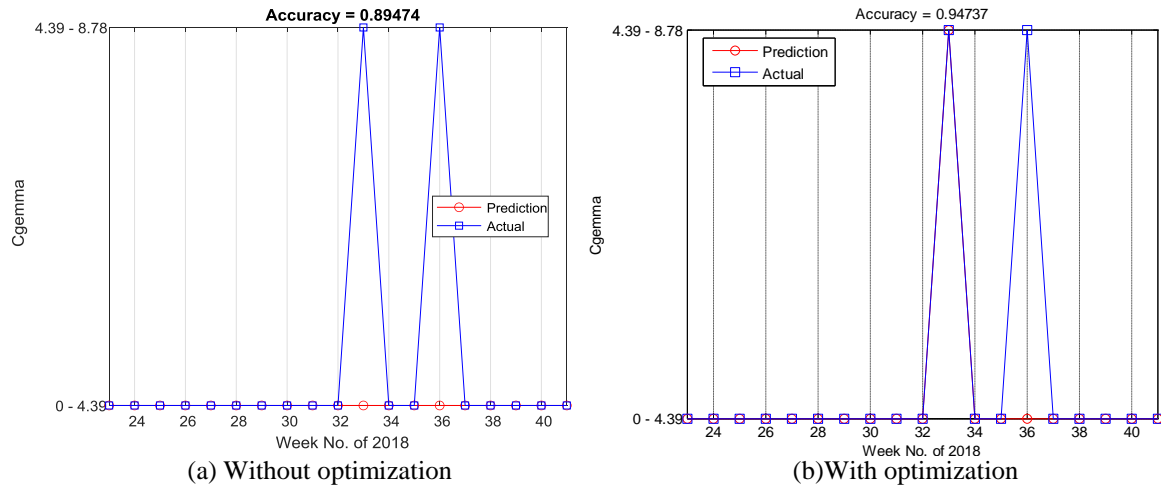
Figure 4: Actual and predicted accuracy graphs for Cgemma insect

(a) Without optimization   (b)With optimization
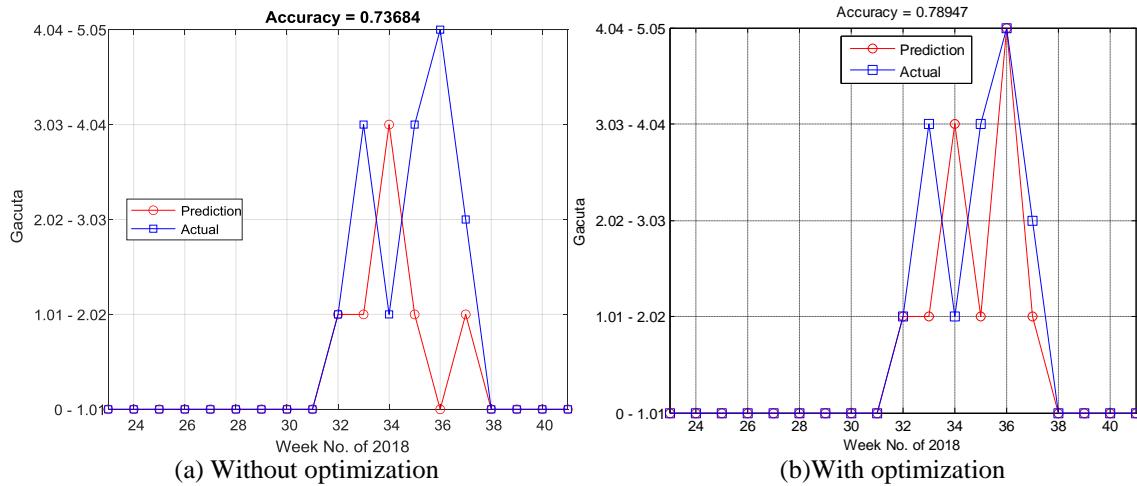
Figure 5: Actual and predicted accuracy graphs for Gacuta insect

(a) Without optimization   (b)With optimization
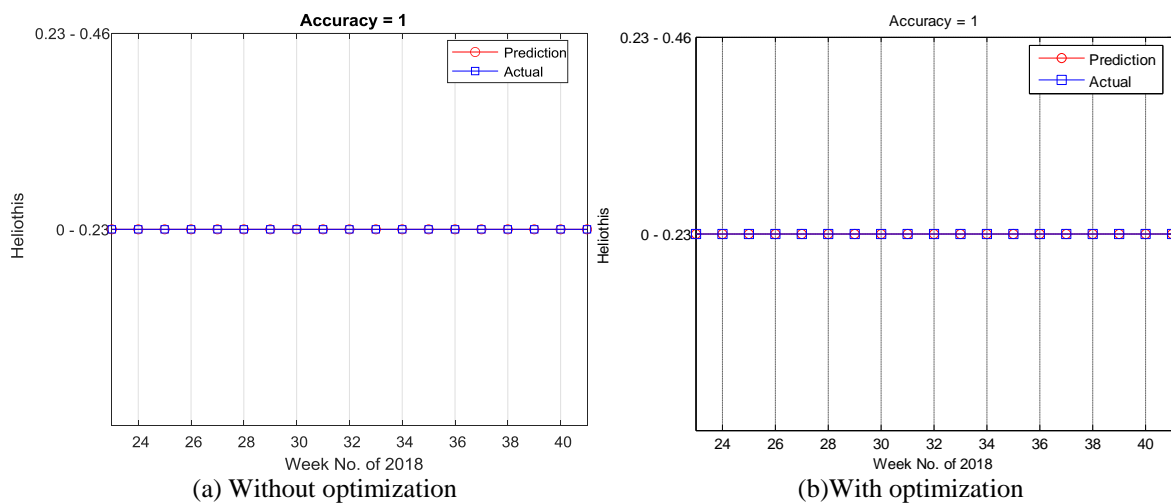
Figure 6: Actual and predicted accuracy graphs for Heliothis insect

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(a) Without optimization   (b)With optimization
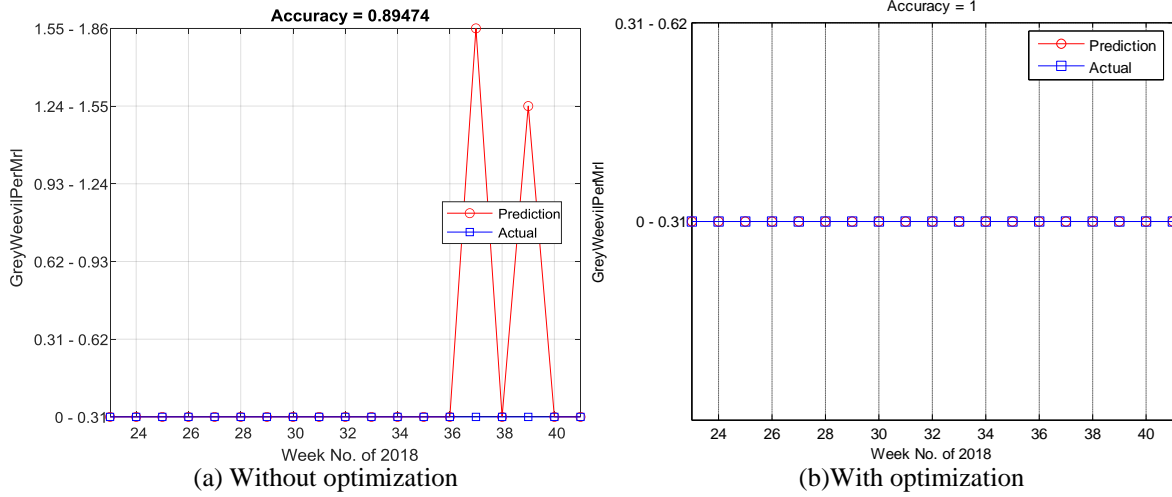
Figure 7: Actual and predicted accuracy graphs for GreyWeevilPerMrl insect

(a) Without optimization   (b)With optimization
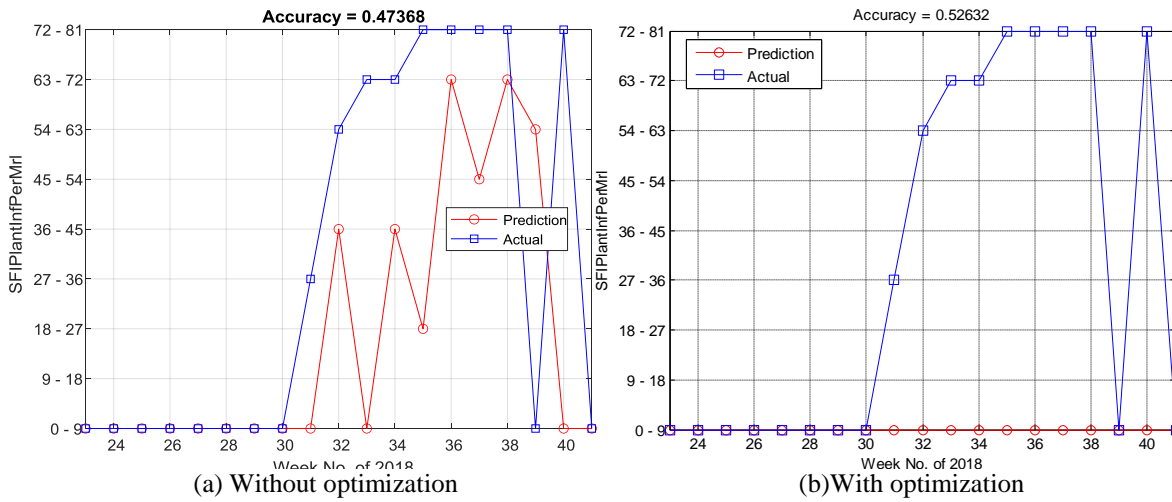
Figure 8: Actual and predicted accuracy graphs for SFIPlantInfPerMrl insect

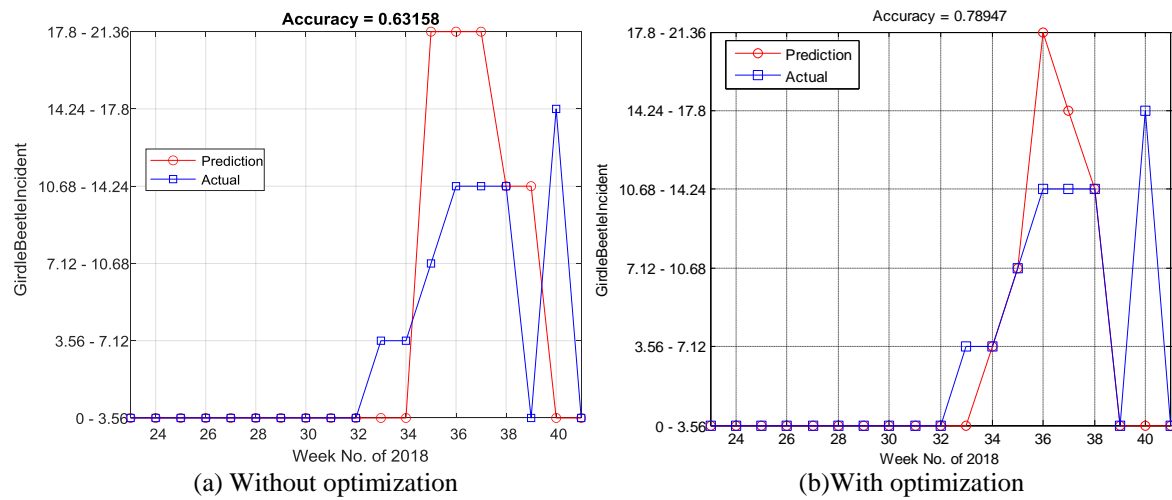(a) Without optimization   (b)With optimization

Figure 9: Actual and predicted accuracy graphs for GirdleBeetleIncident insect

Stem fly, Melanagromyzasojae (Zehntner)

During the Kharif–2017 season, investigations on the seasonal occurrence of soybean were done. The soybean crop was plagued by the stem fly throughout the crop season, however the infestation was minimal at first and peaked in the last week of September 2017. The stem fly infection began in the first week of August 2017 at 28 DAG, with 18% plant infestation and 1.35 percent stem tunnelling. The stem fly infestation persisted until the crop was harvested. Infestation spiked in the last week of September, reaching up to 78%, with the largest stem tunnelling (48.40%). In the fourth week of September 2017, the fly attacked practically every plant.

Girdle beetle, Obereopsisbrevis (Swed.)

The girdle beetle infestation began in the second week of August, when the crop was 35 days old and the infestation level was 3.08%. The girdle beetle's adult created a minor infestation at first. However, the number of infested plants gradually grew, reaching 9.20 and 15% in the second and second weeks of August and September, 2017, respectively. In the third week of September, there was a further reduction in infestation, with plant damage of 11.50%. In the month of September, the trend of diminishing plant infestations maintained.

During the first two weeks of October, there was some plant invasion, but it was minor. As a result, the pest was active for around two and a half months, or until the crop was harvested.

Table 1: Comparative analysis

Prediction	Without optimization	With optimization
BlueBeetalAdultPerMrl	0.7368	0.7895
Cgemma	0.8947	0.9474
Gacuta	0.7368	0.7895
Heliothis	1.0000	1.0000
GreyWeevilPerMrl	0.8947	1.0000
SFIPlantInfPerMrl	0.4737	0.5263
GirdleBeetleIncident	0.6316	0.7368
AVERAGE	**0.7669**	**0.8270**

IV. CONCLUSION

Bugs are one of the most important insect pests of soybeans. With a low population, they can cause a wide variety of damages with their corresponding negative impacts, both economic and quality, regardless of the destination of the production, grain or seed. The most important species of the complex begin to appear in the soybean lots in coincidence with the reproductive stage of the crop. The results of validationtechniques showed a minimum significantdifference between observedandpredicted values. The research shows a maximum overall accuracy of 82.70% with GA optimized ensemble classifiers.

There is a great variety of natural enemies of bedbugs in soybean crops and it is convenient to care for them and strengthen them. To take advantage of this environmental service, one should respect the treatment thresholds, use selective insecticides as well as expand the investigations of the biology and ethology of these beneficial organisms to achieve the complementation between different types of pest management tactics.

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