A methodology of weed-crop classification based on autonomous models choosing and ensemble

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\textbf{ABSTRACT}

Neural networks play an important role in crop-weed classification high accuracy more than 95%. Manually choosing models and fine-tuning are laborious, yet it is indispensable in most traditional practices and researches. Moreover, classic training metric are not thoroughly compatible with farming tasks, that a model still have a noticeable chance of miss classifying crop to weed while it reach higher accuracy even more than 99%. In this paper we demonstrate a methodology of weed-crop classification based on autonomous models choosing and ensemble that could make models choosing and tuning automatically, and improve the prediction with high accuracy(>99% for both dataset) in specific class with low risk in incorrect predicting.

1. Introduction

Weeding is a big issue for farmers for long time, especially for those who work in a gigantic fram. Industrial agriculture uses chemical method to control weed, but leads to a great increase of herbicide resistance and a rising harm to the ecological environment. Therefore, more and more research focus on precision weed management. Meanwhile, effective farming works also demand precision crop cultivation, that can increase the yield of crop in fields. Under the two conditions above, each kind of plant should be treated in different strategies. It’s time consuming and laborious to conduct this work manually, thence a lot of work has been carried out aiming to facilitate autonomous farming, for which various of agriculture robotics are designed to replace manpower.

Implementing autonomous farming has been a focus of research for modern agriculture, especially for Agriculture 4.0 (Rose et al. (2021)), yet weed classification still remains a big problem in this realm (Wang et al. (2019)). Motivated by the need for weeding precisely, many studies base on weed-crop classification have been carried out over past few decades. Generally, these studies can be divided into three categories: 3D point cloud classification, spectrum classification and images classification. 3D point cloud classification relies on sophisticated radar and dense computing to determine the label of each 3D entity, which gets 3D data from field by LiDAR (Malavazi et al. (2018)), then classifies them by shape features. For spectrum information classification, it uses monochrome camera with different lasers to get matched spectral reflectance for classification (Strothmann et al. (2017)). As for images classification (Hall et al. (2018)), it simply uses camera to capture images from field. 3D feature and spectrum feature are proved to be pretty feature for weed classification, but requires expensive instrument and rich computing capability.

Utilizing images to fight weeds can be achieved by machine vision or artificial neural network (Patrício and Rieder (2018)). Machine vision has a good sets of tools for image processing and weed classification, but neural networks do much better than machine vision, which has accuracy of higher than 95% when machine vision can only reach 80% to 90% (Kamilaris and Prenafeta-Boldú (2018)). Neural networks are statistics models that use brain-like functions to find the correlation of input data, produce remarkable results in diverse fields of computer science, such as image classification and object segmentation. It use different models to fit the data to make the prediction of plant images: classic models or new models, simple models or deep models, etc (Kamilaris and Prenafeta-Boldú (2018)). However, there is no published studies focusing on autonomous models choosing and mis-prediction risk reduction in farming tasks.

The core contribution of this paper is the presentation of a methodology of weed-crop classification based on autonomous models choosing and ensemble. This method can search and choose a compatible neural network model for data set without additional model selection, use different metrics to train models and ensemble them to reduce the risk of inaccurate prediction. This article has tackled three main issues in crop-weed classification's technological innovation, of which the key contributions of methodology are as follows:

1. Different from traditional machine learning where models choosing needs to build and test different models manually, an automatic and fast procedure of models selection based on auto machine learning is proposed. In this paper, all sub models are picked by the algorithm which allows us to search compatible models within given data set.
2. Sampled data usage is posed to eliminate the preference of prediction existing in models when using complete data. Sampled data usage is posed for fixing the problem of unbalanced data set and making crop to have similar weight with weed.
3. New metrics for weeding task are employed. To re-
duce the risk of predicting crop as weed, two metrics in models training are employed to improve models performance in farming task.

4. Models ensemble strategy based on new metrics has been used to improve the accuracy and reduce the risk of miss prediction. For the accuracy of the model under the same conditions, the value of ensemble model is similar to the best one in single models. But for handling possible consequences of incorrect predictions, ensemble model is significantly better than single models.

| Glossary | Definition |
|----------|------------|
| Num\_a | In model’s prediction, the number of objects which were predicted as ‘a’ and labeled as ‘b’ |
| AutoML | Autonomous machine learning |
| DS.1 | Our data set |
| DS.2 | Plant Village 2 data set |
| VCNN | Vanilla convolution neural network |
| CNN | Convolution neural network |
| DCNN | Dilated convolution neural network |
| CD | Complete data usage |
| SD | Sampled data usage |
| Acc | Training metric : Accuracy |
| MWA | Percentage of ‘miss weed’ in all objects |
| MWC | Percentage of ‘miss weed’ in crop |
| Tol | Mediator of training metric : Tolerance |
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Then we label these images manually to establish our dataset, as auto-labeling is not our focus, yet, precise framing with position record can accomplish this task effectively.

2.2. Plant classification

The main focus of our work is the second step of main workflow, plant classification, which enable us to get a combined model from a given data set with good performance. The pipeline of this step is shown in Fig. 1, S2.. Best models searching uses AutoML (Thornton C (2015)) to search different type of models in data set, and we apply Algorithm 1 to get models from multiple data sets; data sampling build serveral sub sets from original data set, which make their ratio of weed to crop closer to 1:1. models training modify the last few layers of the models to fit our new metrics, and retrained them with different configurations; models ensemble parallel models to make sub predictions, then make final prediction by their constitution. In the following sections, these works will be presented in detail.

2.2.1. Best models searching

Given data set, in place of testing models manually, we use AutoML to reach the goal automatically. AutoKeras (Jin et al. (2019)), an open source machine learning package, widely used for AutoML, is chose as the frame work in our article. In this section, models selected from automatic searching are restricted to tiny model, which has less than 300,000 parameters. And one deep model as the base-line: ResNet (He et al. (2016)).

It is proved that deep models is more accurate than tiny models, but we still use small ones to ensemble. The reasons are below: complexity of target problem, when preprocessed properly, we can remove the irrelevant portion in images that they can be easily classified; the second is about the capacity of computing device, deep models require much more resources for computation, we can only use powerful GPU to make it works, yet it's only available in laboratory but not on the fields outside. Hence, we choose tiny models to reach the goal, and select a deep model as baseline of so models, which has almost 100 times more parameters of a tiny model.

*Pr.* : Preparation before steps

*Sn.* : Step n, e.g., s1. for step 1

Given a type of models, models searching by AutoML might be heterogeneous for different data set, that would cause inconsistency in the next step. We overwrite the algorithm of models ranking in AutoKeras, make searching procedure possible in multiple data sets, that it allows us to get similar model structure for same type. The detail of this algorithm are as follows:

**Preparation:** Initialize best model table; Iterate model type in search type-space for all steps;

**step 1:** For each data set, use AutoKeras to search models within max trials, then save them in file;

There are two parameters required for "search" function:
Algorithm 1  Best models in multiple data set

Pr.  $\text{Best\_models} = \emptyset$

for $t$ in $T$, $T = \{T_1, T_2, ..., T_n\}$

S1. for $ds$ in $DS$, $DS = \{DS.1, DS.2, ..., DS.n\}$

$\text{trails}^{t, ds} = \text{search}(t, ds)$

S2. $\text{Common} = \text{trails}^{T_1, DS.1} \cap \text{trails}^{T_2, DS.2} \cap ... \cap \text{trails}^{T_m, DS.n}$

S3. if $\text{Common} \neq \emptyset$ then

$best_t = \text{max}(\text{Common})$

S4. else { $\text{Common} = \emptyset$ }

score\_table = $\emptyset$

S4.1. for $ds$ in $DS$, $DS = \{DS.1, DS.2, ..., DS.n\}$

score\_table += evaluate($\text{trails}^{t, ds}$, $DS$)

$best_t = \text{max}(\text{score\_table})$

end if

$\text{Best\_models}_t = best_t$

"t", type of neural network; 'ds', data set for training and testing. Return of this function is a list, each element contains a neural network model and its score.

step 2: Find the common models of all trails;

Common models here do not need to be exactly the same, but main parts do, require layers to be identical except for input layers and output layers. Operator of set intersection ($\cap$) is fixed to get same main parts between two elements, and if they have, return the common part and the sum of score; else, return nothing.

step 3: If all trials have common models, find the bests model by ranking their scores;

step 4: If there is no common models, use a score table to record scores for models;

step 4.1: For each trial, evaluate it by all data sets, and save the model with its score; Then find best models by ranking saved score;

Detail of these models are presented in Fig. 2.

2.2.2. Data sampling

In the procedure of data collection, there is usually a consensus that, don’t kill the weed totally, which leads to more weed than crop in field, also due to the rapid growth rate of weed. Unsymmetric distribution in data set will affect the prediction of models, model tend to trick us by classifying an object to categories that account for the majority of the data set. Therefore, we use sampling to get balanced sub sets from original data set, the procedure of sampling are as follows:

step 1: Select all crop in data set as crop part, noted as CROP; get weed part, noted as WEED.

step 2: Calculate sample rate $k$, $k = \frac{|\text{CROP}|}{|\text{WEED}|}$

step 3: For all types of models, do step 4 and step 5;

step 4: For sampling in WEED, enumerate all kinds of weed in WEED, sampling without replacement by sample rate $K$.

step 5: For each sampled weed, combine with CROP to get a new sub set.

Concerning the usage of data set, besides sampling, we also use intact set. DS.1 as well as DS.2 are both applied with these two strategies, that we can testify the feasibility of our methodology properly.

2.2.3. Models training

The training process of neural network is an optimization problem, that use different functions to measure the distance between label and prediction. On the other hand, this process is typically paralleled, that means input, label($y$ in Eq. (2)) and output($\hat{y}$ in Eq. (2)) are both vectors. For classification tasks, accuracy is the most common also the easiest function, that is shown in Eq. (5): For each element in label
and output $\hat{y}$: result is one if they are same, else zero.

$$
y = \begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \\ \end{bmatrix}, \quad \hat{y} = \begin{bmatrix} \hat{y}_1 \\ \hat{y}_2 \\ \vdots \\ \hat{y}_n \\ \end{bmatrix},
$$

(2)

$$
equal^*(a, b) = \begin{cases} 
1 & a - b = 0 \\
0 & a - b \neq 0 
\end{cases}
$$

(3)

$$
equal(\begin{bmatrix} a_1 \\ a_2 \\ \vdots \\ a_n \end{bmatrix}, \begin{bmatrix} b_1 \\ b_2 \\ \vdots \\ b_n \end{bmatrix}) = \begin{bmatrix} equal^*(a_1, b_1) \\ equal^*(a_2, b_2) \\ \vdots \\ equal^*(a_n, b_n) \end{bmatrix}
$$

(4)

$$
Acc = equal(\hat{y}, y)
$$

(5)

Although accuracy is widely used, it still has deficiency in farming tasks. It leads model to predict as accurate as possible by one unified rule: one for correct and zero for wrong, are inconsistent with farming rules. The cost of misclassification depends on the situation: it’s reasonable to ignore sprouts since they are too small to be classified; it’s bearable to leave a few weeds alive; but it’s harmful to kill part of crops.

In order to lower the risk of killing the crops, new metrics are used in our training procedure: Eq.(11) and DM. Before making a definitions for new metrics, we need to explain some notions below (Eq.(6)): weed in data set is noted as W, which has p kinds of weed; crop in data set, noted as C, which has q kinds of crop in data set; none group, which do not exists in original set, we add them for new metric. A column vector $Vec^t(e)$ with n elements $e$, noted as Eq.(7).

In Eq.(8), $contain(G, v)$ function could provide a result between type list G and vector v, the position of vector that contains any elements of list.

$$
W = \begin{bmatrix} w_1 \\ w_2 \\ \vdots \\ w_p \end{bmatrix}, \quad C = \begin{bmatrix} c_1 \\ c_2 \\ \vdots \\ c_q \end{bmatrix}, \quad N = \begin{bmatrix} n_1 \\ n_2 \\ \vdots \\ n_r \end{bmatrix},
$$

(6)

$$
Vec^t(e) = \begin{bmatrix} e \\ e \\ \vdots \\ e \end{bmatrix}, \quad dim(Vec^t(e)) = t
$$

(7)

$$
contain(G, v) = \sum_{g} v \cdot Vec^{dim(v)}(g)
$$

(8)

The first metric NMW is abbreviation of "no miss weed", which is composed of three parts: Accuracy, we has explained in Eq.(5); Tolerance of homogeneous (Eq.(9)), yield one if prediction and label are in same group, else 0; Tolerance of unknown (Eq.(10)), yield one if prediction are in none, else 0. $Tol_{homo}$ allow models to predict one object to other label but in a same group, and $Tol_{unknown}$ allows models to predict one object to unknown. These two parts disclose some latent information to models, or some tolerance when models predict in slight errors. Then we apply a "logic or" between accuracy and tolerance, so that NMW will yield one when accuracy is one no matter what tolerance is, vice versa. In short, NMW is not like accuracy that only returns 1 when the classification is correct, but also returns 1 when it has no grouping errors.

$$
Tol_{homo} = contain(W, \hat{y}) \cdot contain(W, y) \quad \text{||} \quad contain(C, \hat{y}) \cdot contain(C, y)
$$

(9)

$$
Tol_{unknown} = contain(N, \hat{y})
$$

(10)

$$
NMW = Acc \quad \text{||} \quad (Tol_{homo} + Tol_{unknown})
$$

(11)

$$
DM = [Acc, \quad NMW]
$$

(12)

DM means "dual metric": refers to accuracy and NMW (Eq.(12)), and is a vector of metrics instead of a single metric like accuracy and NMW. In the training of the model, if model’s optimizer accepts a vector of metrics, the model will optimize them separately instead of optimizing their sum. Since the optimization method of the model will not affect other parts of the experiment, and for the unification of the notion in the article, we also call the vector of metrics as metric.

We add a few nodes on models to make models fit the new metrics, that ‘none’ is invalid in original data set. After randomizing weights, we trained these models by two kinds of new metrics: NMW and DM.

2.2.4. Models ensemble and prediction

The algorithm of models ensemble is shown in Fig. 1, S2.4, where model A, B and C have been trained in same configuration; $P_1$, $P_2$ and $P_3$ are predictions of three models, and their order are arbitrary; in Pred_{mix} block, cate is category of prediction, like potato, tomato or apple; $type$ is the group of this prediction, crop, weed or none; and $Act(m)$ shows how models suggest to deal with these objects. Key points of model ensemble are as follows:

(1) If three models reach a consensus, that give a same prediction in specific category, go ahead.

(2) If three models give totally different prediction, mark this object as none.

(3) For crop like object, which means two of models have a same prediction and the prediction is crop, then check the total number of crop in result: if there still have a gap between current number and record, then we assume the more part make a right desicion; or, it is none.
(4) For weed like one, we just mark it as none.

When dealing with consensus and disagreement, our method is the same as other method of ensemble, but we have different opinions on processing crop-like and weed-like predictions. For farming task in real world, to treat a weed as crop occasionally would do a little harm to field. But for weed-like conditions, it will cause a considerable damage to field that kill a crop if the predictions are wrong, so we simply classify all weed-like object to none.

3. Result and discussion

3.1. Models from searching

Except for the baseline model, ResNet, other three models are generated by Algorithm 1, as presented in Fig. 2, and their training curves are presented in Fig. 3, a. Although these model are generated by AutoKeras, we name them by their characteristic of structure: Vanilla neural network, has similar structure with an earlier neural network, AlexNet (Krizhevsky et al. (2012)); Convolution neural network, has similar structure with a famous convolution neural networks, VGG (Simonyan and Zisserman (2014)); Dilated convolution neural network, has similar structure with VGG-16 but having a new kind of convolution block (Yu and Koltun (2016)). These models are small (less than 300,000 parameters, that means their saved file are less than 4MB) and shallow (less than 15 layers), but have accuracy more than 98%. For all models belonging to same type, they have only a little divergence in structure that their last two layers are determined by data sets, since the count of labels are
unequal between different data sets.

Accuracy can also be an evaluating metric that measures how models predict correctly in the whole set. Besides, we propose a evaluating metric to measure the performance of models for weeding task: MWP (Eq. (13)), miss weed probability, percentage of miss classified crop in entire set, which focus on problem of manslaughter in crop. The status of models are shown in Table 1 and Table 2.

\[
MWP = \frac{\sum_{crop}^C \sum_{weed}^W \text{NMW}_{crop}^{weed}}{|C|} \tag{13}
\]

| Table 1 | Models status for DS.1 |
|---------|------------------------|
| Model   | Accuracy | MWP |
| Vanilla | 98.06%   | 6.64% |
| Dilated | 98.34%   | 5.76% |
| Conv    | 97.51%   | 6.28% |
| ResNet  | 99.58%   | 1.56% |

| Table 2 | Models status for DS.2 |
|---------|------------------------|
| Model   | Accuracy | MWP |
| Vanilla | 99.24%   | 2.24% |
| Dilated | 99.53%   | 1.36% |
| Conv    | 99.06%   | 3.12% |
| ResNet  | 99.51%   | 1.28% |

These models get high accuracy in both data sets, however the values of MWP are not low. Even for the models that reach 99.5%+ accuracy, they still kill 1.2%+ crop in test set, and for other models it could have almost 6% crop killed by wrong classification. The reasons for this situation may be caused by the following: unsymmetric data set provides information if the model predicts weed, it is more likely to be correct. when accuracy is used to determine the specific class, all group information will be lost. And when accuracy is used to determine the group, the class information will be lost. Thus we try to use sampled data set to fix the problem of unsymmetric distribution, and new metrics to fix training problem of accuracy.

3.2. Models training

As presented in Figure 3, we applied our experiments on both data sets, DS.1 and DS.2, that are located in the upper and lower parts of the first three colours. For each data set it will be divided into three parts first, training set, validation set and test set, the percentage of them are 64%, 16% and 20%; then used for 6 different sub experiments, which can be found in the top block of the last column. For each sub experiment, we record its training history and illustrate as curves in first two colours: experiments trained with metric Acc only have plots with Val Accuracy titled, which means the accuracy curves in validation set; experiments trained with metric NMW only have plots with Val No Miss Weed titled; experiments trained with DM, have both of Val Accuracy and Val No Miss Weed titled. Then we group the MWA by data set and its usage, and get four bar charts as presented. So we get 12 sub experiments in models training, which are named in format of "<data set> <data set usage> <training metric>". Note that experiments f), use a vector with two metrics for optimization, so it has training curves for both metrics.

For training curves, we can see all of the curves become stable after about 60 epochs, so we stop training at 64 epochs, or our models will be overfitted that has poor performance on evaluation. The curves of ResNet have more fluctuation than others, that may be caused by its deep and special structure. And the curves that use NMW as metric are more stable than Acc, that might be caused by the tolerance, similar with DM. All of the sub experiments get high score on their metric, most of them more than 96% after 64 epochs training. By the curves we get, though the score of some models are not so high, they are good enough for next task.

For MWA plots, there are some obvious difference between each other: in most cases, Acc get the most higher values than other two metric, especially in DS.2; NMW is lower than Acc in most cases for DS.2, but sometimes higher in DS.1; DM get the lowest scores in most cases; We can see that both of new metric decrease the MWA and keep the accuracy at a same level with classic metric Acc, but it’s hard to say which is best within these experiments. So we use gathered model to testify which configuration is better, in other words, which one can have lower risk in killing crops.

3.3. Models ensemble and predicting

| Table 3 | Accuracy of ensemble models |
|---------|-----------------------------|
| Exp     | DS.1 Best | DS.1 Ensemble | DS.2 Best | DS.2 Ensemble |
| a)      | 99.58%   | 99.27%   | 99.53%   | 99.02%   |
| b)      | 99.03%   | 99.76%   | 99.41%   | 99.64%   |
| c)      | 99.58%   | 99.76%   | 99.48%   | 99.84%   |
| d)      | 99.24%   | 99.52%   | 99.11%   | 99.92%   |
| e)      | 99.27%   | 99.76%   | 99.56%   | 99.88%   |
| f)      | 99.24%   | 99.76%   | 99.87%   | 99.96%   |

As there are 12 difference sub experiments in models training, we use the algorithm shown in Fig. 1, S2.3 to build twelve ensemble models, and evaluate them in same data as its sub models, and their accuracy is similar with the best models as shows in Table 3, where Exp is abbreviation of experiments. We can see that the accuracy of ensemble models are similar to the best models of its sub models. Then we use two kinds of plot to show how ensemble model can decrease the risk of wrong predictions, which are presented in Fig. 4.

In order to measure wrong predictions more accurately, we divide them into four categories, that measure the sever-
Fig. 4: Models ensemble and predicting

1. Moderate error, it happens when model classify an object to "none", only occurs in new metrics.
2. Minor error, it happens when model’s prediction is inconsistent with its label, but both of them are in the same type, say the prediction is $\text{weed}_1$ and its label is $\text{weed}_2$.
3. Considerable error, it occurs when models has different prediction with its labels and its type, but those predicted to be weed but labeled crop;
4. Dangerous error is that models predict one crop to one weed.

These errors are ranked by their outcome in practice, that moderate error means we have chance to rectify it manually, minor error means it will do no harm to field even it has made
a mistake already, considerable error means it left a weed alived, dangerous error means it kill a crop by mistake.

In order to show the detail of how ensemble model works, we present severral radar charts in the third coloumn of Fig. 4. The radial coordinate to the interval [95%, 100%) consist of two parts: accuracy and moderate error. The angular coordinate is label, which consists of labels contained in DS.1 and labels of DS.2, specific name of labels are shown in the third legend of last row. Solo models are plotted in curves only, while curves of ensemble models have filled color inside, so that we can see the overlap of ensemble models clearly. For sub models, we can see that the crop parts get the lower value than weed in most cases, and the value of the part marked potato of DS.2 is also relatively low. The lower points have a same feature: less volume of data than others. And we notice that DM behave better than Acc and NMW, as the experiments of DM have more smooth curves than others with same data set, shown in experiment c). and f) in Figure 4. Baseline model, ResNet, have higher accuracy than other solo models. But for ensemble models, we find that they cover most of the areas. According to Table 3, ensemble models are not significantly improved in accuracy compared to their sub-models. However, the bar charts prove that ensemble models are significantly better in terms of error distribution, because most of their errors are minor rather than serious.

Instead of specifying model by model, we count the minimum and the maximum of error rate in sub models, and group them in two sets: best of solo, and worst of solo. Best of solo means the minimums of all solo models in sub experiments, including ResNet. Worst of solo uses the maximums. Then we present the ensemble model as the third part. It’s obvious that the ensemble models can reduce the percentage of errors which are more serious, and they can convert some serious errors into safer, but they also have different effects on various sub experiments. We summarise the key points of our findings in these bar charts as below:

1. For different data sets. Experiments with DS.1, are placed in the first coloumn of chart, showing that ensemble models remove all dangerous errors, since this data set is small and simple. For experiments with DS.2, the second one, ensemble models can remove most of dangerous errors, but still have a little reamin in experiments a), b), c). and d).

2. For different data usage. Experiments with complete data usage, are placed in first three rows of chart, a), b), and c), showing that there are still some dangerous errors in ensemble models. As for experiments with sampled data usage, d), e), and f), ensemble models have performed better than complete usage.

3. For different training metrics. Experiments with classic training metric, accuracy, are placed in row a) and d), showing that more serious errors than other experiments come with new metrics. And for experiment e). and f), they have no dangerous error in both data sets.

4. Conclusion

This work propose a methology of weed-crop classification based on autonomous models choosing and ensemble. AutoML helps us to automatically choose the neural network models for a data set with high accuracy(>97%), though its max parameters was limited. Two kinds of new traing metrics, NMW and DM, can reduce risk of miss prediction without lowering accuracy to a great extent. Data sampling can remove the preference in models. Then we ensemble the models to improve the preformance in farming task, which can convert most serious errors to some safer ones. Overall, we can conclude: (a) models trained with NMW are compatible for weeding task, models trained with DM can be used in precise farming task; (b) <Data set> - SD - <new metric> has good enough accuracy with lowest risk among other experiments.

Based on the automation of model selection, this method can be easily used on other data sets. For the high accuracy and low risk of final model, we hypothesize that the use of this method could have a good performance in precise farming task.

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