Counting of Pine Wood Nematode Disease Trees Based on Threshold Segmentation

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Abstract. Pine wood nematode disease is a very contagious and devastating forest pest. Finding infected trees in time, counting them, and clearing or selective cutting according to different diseased tree densities is the main way to control the spread of the disease. In this paper, threshold segmentation technology is used to reduce the adverse effects of interference factors such as buildings, rocks, and soil in the data set on density estimation, and finally a higher-quality density map is obtained to realize the counting of pine wood nematode diseased trees. Compared with the classic density estimation algorithm, the mean absolute error of this algorithm has dropped by 9.2, the root mean square error has dropped by 7.4, the variance of absolute error has dropped by 65.0, and the counting accuracy has increased by 19.6%.

1. Introduction

Pine wood nematode disease is a devastating forest pest caused by pine wood nematode. The latest announcement [1] shows that pine wood nematode disease has been found in 18 provinces in China, causing a large number of pine trees to wither and die, causing serious economic and ecological losses. Pine wood nematode diseased trees of different densities are treated differently[2], so counting the regional diseased trees is the key to the detection and control of pine wood nematode diseased trees.

In the traditional counting method, the detection-based method [3] generally counts by detecting each independent target in the image. Although this type of method has good results, the algorithm time complexity is relatively high. The detection methods Fast-RCNN [4] and YOLO [5] based on deep learning have high detection accuracy, but they are computationally intensive and require a large amount of data to support [6]. The detection-based counting method is simple and easy to implement, but it is not suitable for complex environments with high density and high occlusion. The counting method based on regression is to find the mapping relationship between image features and the number of targets [7~9]. Although it avoids the difficulty of target detection, it also loses the target spatial information. The concept of density function [10] makes up for the insufficiency of the regression-based counting method. This method counts the target through the mapping relationship between the image feature and the image count target density map, effectively retaining the spatial information of the counting target, and further optimizes the counting accuracy.

There are many interference factors such as buildings, rocks, and soil in the pine wood nematode disease area, which requires the counting algorithm to overcome the interference in complex scenes to improve the counting accuracy of diseased trees. In this paper, the density function counting method is
improved, and the threshold segmentation technology is used to eliminate the background to highlight the foreground pixel target, reduce the interference factors of the counting, and improve the counting accuracy of the pine wood nematode disease tree.

2. Materials and Methods

2.1. Density counting
The traditional density counting method [10] is suitable for medical cell images with uniform and single background pixels, but it cannot achieve the ideal counting accuracy in the image of the complex environment of the pine wood nematode diseased tree area. This is because there are a large number of interference factors such as terraces, soil, and buildings in the area of pine wood nematode diseased trees. The area indicated by the arrow in Figure 1 will have a negative impact on the density count results.

As shown in Figure 2, in order to reduce the influence of interference factors and improve the accuracy of target counting, threshold segmentation can be used to preprocess the original collected images. In this paper, threshold segmentation in HSV color space can reduce the influence of interference factors in complex images. Improve the counting accuracy of pine wood nematode diseased trees. The structure of the complete algorithm is shown in Figure 2. The input image is first subjected to threshold segmentation in the HSV color space to obtain the filtered image, and then the density count is used to process the filtered image, and the count result and the corresponding density image are output.

2.2. Threshold segmentation
In this paper, the threshold segmentation of HSV color space is used to directly remove background pixels. After segmentation is completed, the pixel value \( f(x, y) \) at the pixel coordinate point \((x, y)\) is:
Where $f(x, y)$ represents the value of the H channel or the V channel, and $Y$ represents the threshold. When there are more than two gray thresholds, formula (1) becomes:

$$
\overline{f(x, y)} = \begin{cases} 
1, & f(x, y) \geq Y \\
0, & f(x, y) < Y 
\end{cases}
$$

(2)

In the image, in addition to the target diseased tree that needs to be counted in the foreground pixels, there are also a large number of interference factors such as healthy trees, soil, terraces, and buildings in the background pixels. These interference factors and the scatter plots of the H and V channel values of the target diseased tree are as follows As shown in Figure 3.

The red, green, yellow, blue, and purple dots in the picture represent diseased trees, healthy trees, soil, terraces, and buildings, respectively. The color of healthy trees is significantly different from that of the target diseased tree. The H channel of the HSV color space can be used to set the threshold to remove. Although the H channel value of soil, terraces, and buildings are similar to the H channel value of the target diseased tree, the V channel Most of the values are higher than the target disease tree, you can use the V channel of the HSV color space to set the threshold to remove these interference factors, randomly select 50 disease tree centers in the data set, extract and analyze the H channel and V channel values respectively, and draw them into a histogram As shown in Figure 4 and Figure 5.
From Figure 4 and Figure 5, it is found that the H channel values of the disease tree are basically distributed between 9 and 35, and the V channel values are basically distributed between 29 and 46. You can set 9 to 35 as the H channel threshold. Set 29 to 46 as the V channel threshold, perform the H channel filtering operation and the V channel filtering operation on Figure 1, and the results are shown in Figure 6.

![Figure 6. H channel and V channel filter diagram.](image)

As shown in Figure 6, interference factors such as healthy trees, soil, terraces, and buildings have been filtered, and what is left is the preliminary estimated area of pine wood nematode diseased trees.

3. Results & Discussion

3.1. Data set acquisition
The experimental data is an image of a pine wood nematode epidemic area in a county in Hubei Province collected by a DJI drone. The camera model is FC6310. The data set includes 92 images, and the flying height of the drone is 350 meters. In order to optimize the calculation speed, the data set images are resampled, and the resolution of the obtained images is unified to 972x728. According to the ratio of 7:3, the data set is divided into 65 training images and 27 test images, and each image has a corresponding ground-truth manual annotation file.

3.2. Evaluation index
In order to compare the performance difference between the classic density counting algorithm and the algorithm in this paper, the mean absolute error (MAE), root mean square error (RMSE) and variance of absolute error (VAE) are used as evaluation indicators. The definitions of MAE, RMSE and VAE are as follows:

\[
\text{MAE} = \frac{1}{N} \sum_{i=1}^{N} |z_i - \hat{z}_i| 
\]

\[
\text{RMSE} = \sqrt{\frac{1}{N} \sum_{i=1}^{N} (z_i - \hat{z}_i)^2} 
\]

\[
\text{VAE} = \frac{1}{N} \sum_{i=1}^{N} (|z_i - \hat{z}_i| - \text{MAE})^2 
\]

Where \(N\) is the number of test images, \(z_i\) is the actual number of diseased trees in the \(i\)-th image, and \(\hat{z}_i\) is the number of diseased trees estimated by the algorithm in the \(i\)-th image. Generally, the smaller the MAE value and RMSE value, the higher the prediction accuracy of the model, and the smaller the VAE value, the higher the robustness of the model.
In order to make the evaluation index more intuitive, the counting accuracy rate is used as the fourth evaluation index, and its calculation formula is as follows:

$$P = 1 - \frac{\text{MAE} \times N}{\sum_{i=1}^{N} \left( z_i \right)}$$  \hspace{1cm} (6)$$

3.3. Contrast experiment

In order to verify the effectiveness of the algorithm in this paper, Lempitsky's Density Learning Algorithm (DL) [10], Density Learning with Threshold Segmentation of HV channel (DLTSHV) are selected for comparative experiments. Among them, DLTSHV belongs to the density counting method that uses the threshold segmentation of HSV color space. The evaluation indexes of different algorithms are shown in Table 1.

| Method        | MAE  | RMSE | VAE  | P (%) |
|---------------|------|------|------|-------|
| DL            | 21.3 | 22.2 | 137.2| 54.7  |
| DLTSHV        | 12.1 | 14.8 | 72.2 | 74.3  |

It can be seen from Table 1 that the three evaluation parameters of DLTSHV algorithm MAE, RMSE and VAE are better than Lempitsky's DL algorithm [10]. Compared with the DL algorithm, the MAE of the DLTSHV algorithm has dropped by 9.2, and the RMSE of the DLTSHV algorithm decreased by 7.4, the VAE of the DLTSHV algorithm decreased by 65.0, and the counting accuracy of the DLTSHV algorithm increased by 19.6%. It can be seen that threshold segmentation using HSV color space can effectively improve the counting accuracy of the density function model.

Figure 7 shows the density map of the counting effect of different algorithms in multi-building, multi-soil, and dense forest areas. The red arrow in the figure indicates missed or misdetected target diseased trees.

Figure 7. Density map of the counting effect of different algorithms in different areas.

It can be seen from Figure 7 that Lempitsky's DL algorithm has a large number of false detections and missed detections for diseased trees in pine wood nematode disease areas. Compared with the DL algorithm, the DLTSHV algorithm in this paper counts the count areas of interference items such as multi-buildings, soil, and rocks. The effect is good, and the position of the disease tree marked in the density map is accurate, and there are only a small number of false detections and missed detections of
the disease tree, which proves that DLTSHV has the ability to deal with counting problems in complex backgrounds.

4. Conclusions
In this paper, the density function is used to solve the problem of pine wood nematode disease tree counting. At the same time, the threshold segmentation of HSV color space is used to optimize the data set to eliminate the influence of interference factors such as buildings, rocks, and soil on the counting results in complex environments. Experimental results show that this method can effectively solve the problem of pine wood nematode disease tree counting.

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