



A review of computer vision technologies for plant phenotyping

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ARTICLE INFO

Keywords:

Computer vision
Plant phenotyping
Imaging system
Algorithms
Deep learning

ABSTRACT

Plant phenotype plays an important role in genetics, botany, and agronomy, while the currently popular methods for phenotypic trait measurement have some limitations in aspects of cost, performance, and space-time coverage. With the rapid development of imaging technology, computing power, and algorithms, computer vision has thoroughly revolutionized the plant phenotyping and is now a major tool for phenotypic analysis. Based on the above reasons, researchers are devoted to developing image-based plant phenotyping methods as a complementary or even alternative to the manual measurement. However, the use of computer vision technology to analyze plant phenotypic traits can be affected by many factors such as research environment, imaging system, research object, feature extraction, model selection, and so on. Currently, there is no review paper to compare and analyze these methods thoroughly. Therefore, this review introduces the typical plant phenotyping methods based on computer vision in detail, with their principle, applicable range, results, and comparison. This paper extensively reviews 200+ papers of plant phenotyping in the light of its technical evolution, spanning over twenty years (from 2000 to 2020). A number of topics have been covered in this paper, including imaging technologies, plant datasets, and state-of-the-art phenotyping methods. In this review, we categorize the plant phenotyping into two main groups: plant organ phenotyping and whole-plant phenotyping. Furthermore, for each group, we analyze each research of these groups and discuss the limitations of the current approaches and future research directions.

1. Introduction

Phenotype is the composite of the organism's observable characteristics or traits jointly affected by genotype and environment. Moreover, plant phenotype is formed during plant growth and development from the dynamic interaction between the genetic background and the physical world in which plants develop (Hemantaranjan, 2016). Plant phenotyping is an emerging science that links genomics with plant ecophysiology and agronomy. With the rapid development in phenotyping technologies, researchers have made significant progress in different fields. For example, the studies of the association between phenotypes and genotypes have improved the understanding of complex genetic traits, which provided opportunities for exploring functional genomics (Liu and Yan, 2019; Ogura and Busch, 2016). Various imaging technologies and phenotyping platforms (Bai et al., 2019; Ge et al., 2016; Virlet et al., 2017) for high-throughput screening have greatly enhanced our capability in obtaining phenotypic data for the multidimensional quantitative study of complex plant traits (Fahlgren

et al., 2015; Roitsch et al., 2019). Multi-domain phenotypic information databases have been established to store, manage, and retrieve a large amount of unstructured data effectively (Arend et al., 2016; Seren et al., 2017). Researchers have utilized computer vision and pattern recognition technologies, combined with data mining methods and machine learning algorithms, to study image-based non-invasive phenotype data analysis or evaluation (Perez-Sanz et al., 2017; Singh et al., 2020). However, there are many challenges that plant phenotyping needs to address in the future, especially the approaches to characterize and evaluate the structure and function of plants in the natural environment.

In the past, phenotypic measurement and analysis were laborious, expensive, and time-consuming. Reliable, automatic, multifunctional, and high-throughput phenotyping technologies are increasingly considered important tools for the rapid advancement of genetic gain in breeding programs (Zhao et al., 2019). With the popularization of image-based methods (Rahaman et al., 2019), non-invasive, fast, high-precision automatic quantification has become the core of current

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<https://doi.org/10.1016/j.compag.2020.105672>

Received 24 March 2020; Received in revised form 14 July 2020; Accepted 27 July 2020

Available online 05 August 2020

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research. Compared with manual measurements (e.g., ruler and weighing machine), image-based plant phenotyping aims to develop computer vision techniques and tools for obtaining quantitative data from massive plant images. Plants are complex and constantly changing systems which grow in highly variable natural environments, so plant phenotyping reveals more challenging computer vision problems: (1) In order to adapt to complex image background, quantifying plant phenotypic properties requires more accurate and robust image segmentation algorithms, which not only distinguish different components of plants, but also different instances of components. (2) Plant growth description and estimation require the quantitative establishment of rapid and precise dynamical models. (3) Root phenotyping is challenging, primarily attributed to the difficulty of imaging root system architecture nondestructively, which means designing special imaging systems and analysis methods; (4) 3D descriptions are particularly valuable, but the reconstruction of 3D from images becomes complicated due to frequent occlusions. (5) Plant stresses have only barely visible effects on plants in their early stages, and they must be accurately detected to maximize treatment effect. These issues spawned specialized workshops that presented challenging topics and provided benchmark datasets and appropriate performance evaluation methods, such as *IAMPS* (*The International Workshop on Image Analysis Methods for the Plant Sciences*), *CVPPP* (*Computer Vision Problems in Plant Phenotyping*), *Phenome*, etc. Many organizations (Fig. 1) are leading the efforts in the field, and they have made outstanding contributions to the plant phenotyping research based on computer vision.

With the level of computer hardware and the innovation of algorithms continuously improving, the research of plant phenotyping gets to be more in-depth, the image data tends to be multi-domain, and analysis methods verge to be diversified. Different types of sensors are used to collect multi-dimensional phenotypic data, such as red, green, and blue (RGB) camera, RGB-depth (RGB-D) camera, hyperspectral camera, thermal infrared camera, near-infrared camera, light detection and ranging (LiDAR) device, computed tomography (CT) scanner, etc. Multi-domain data are integrated to analyze plant structural characteristics and different analysis algorithms are combined to provide strategic solutions for system decision-making, such as traditional image processing, traditional machine learning, deep learning, etc. Applying computer vision and pattern recognition technologies to plant phenotyping can reduce the work intensity of scientific researchers,

accelerate scientific research progress, and automatically quantify phenotypic indicators, which is conducive to crop breeding optimization and improved agricultural management (Afonnikov et al., 2016; Dreccer et al., 2019). This field is undergoing a historic change, which will shift toward automation precision in the upcoming day.

As far as we know, the reviews about plant phenotyping based on computer vision are lacking. There are several papers we have searched just as below. In 2015, Minervini et al. comprehensively discussed the bottlenecks and future trends in the field of image-based plant phenotyping (Minervini et al., 2015). Unlike the above review, some papers explained and summarized the relevant methods in a particular phenotyping task from the perspective of technical theories and principles. They have been published in the last three years that provide reviews for plant stress phenotyping (Singh et al., 2018; Toda and Okura, 2019) and plant 3D phenotyping (Vandenberghe et al., 2018). Recently, a review paper (Jiang and Li, 2020) effectively summarized the existing knowledge, limitations, and good solutions to applying deep learning techniques in plant phenotyping. And it primarily focuses on studies published in the use of convolutional neural network (CNN) for image-based plant phenotyping in the most recent 5 years.

This paper manages to seek non-invasive plant phenotypic measurement and evaluation approaches to replace traditional artificial and destructive extraction ways, which attract more researchers in the field of computer vision to work in image-based plant phenotyping. In this paper, we introduce the hot research topics and theoretical analysis of plant phenotyping based on computer vision. The goal of this review is to scrutinize thoroughly the current efforts for imaging-based plant phenotyping. In particular, it covers rich phenotypic data and multiple processing strategies. The former includes spatial scales ranging from plant organ to whole-plant, imaging technologies ranging from visible light imaging to hyperspectral imaging, and image quality ranging from perfect to noise-contaminated. The latter includes the feature extractions ranging from manual design to representation learning, learning styles ranging from supervised learning to unsupervised learning, and algorithm types ranging from traditional machine learning to deep learning. First of all, we summarize two research perspectives according to the plant observation scales and image features, including organ and whole-plant. Secondly, we review typical solutions and compare the effects of these methods in terms of experimental results and application scope. Then, we find out the bottlenecks and challenges of



Fig. 1. The distribution of organizations that conduct research in plant phenotyping.

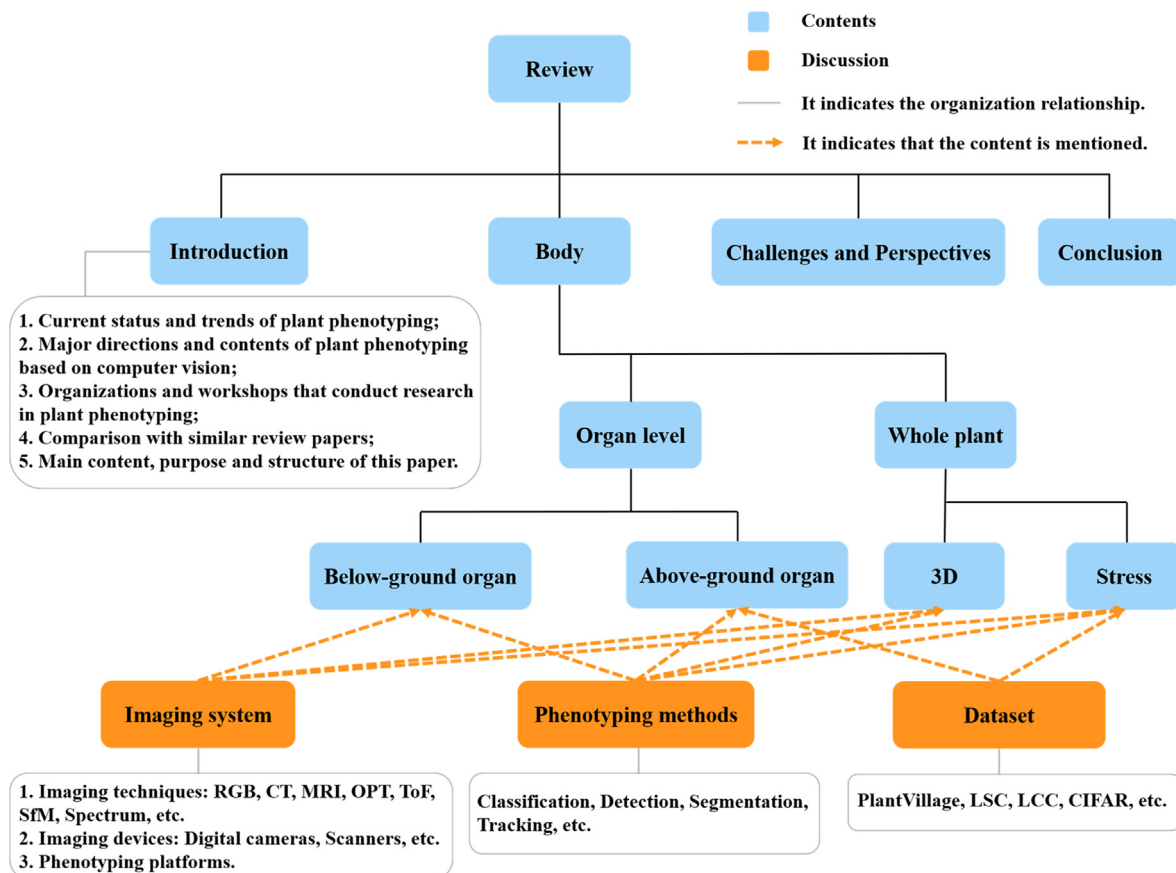


Fig. 2. The organization of the paper.

computer vision in the plant phenotyping field and put forward to the research focus. In summary, we discuss the most advanced methods, provide insights, and identify potential research directions.

The organization of the paper is shown in Fig. 2. In addition to the introduction, the rest of the review is organized as follows. Section 2 introduces the phenotyping researches of plant organs, including below-ground organs and above-ground organs. Section 3 discusses the studies of whole-plant phenotyping, including 3D phenotyping and plant stresses. In addition, we introduce the imaging systems (imaging techniques, devices, and platforms), phenotyping methods (classification, detection, segmentation, tracking, etc), and datasets. Section 4 points out some bottlenecks and potential directions for future research. Finally, Section 5 provides conclusions for the review paper.

2. Plant organ phenotyping

The importance of plant organs in the phenotypic analysis is self-evident. Generally, according to measurement contents and research purposes, plant organ phenotypes are broadly classified into three categories, namely, structural, physiological, and temporal (Das Choudhury et al., 2019). Structural phenotypes refer to the morphological properties of organs, including the shape, area, angle, etc. (Panjvani et al., 2019; Xu et al., 2019). Physiological phenotypes are related to traits affecting plant processes that regulate growth and metabolism, including water content, chlorophyll content, etc. (Esgario et al., 2020; Fariñas et al., 2019; Yao et al., 2018). Different organs of plants grow incongruously in space and time and this inhomogeneity of growth is also regulated by genotype. By analyzing image sequences, temporal phenotypes can be calculated, including elongation, angular trajectory, etc. (Agarwal, 2017; Duan et al., 2016; Sun et al., 2018).

Plant above-ground and below-ground organ phenotyping will be introduced from the perspective of the structural phenotype and

temporal phenotype in Section 2.1 and 2.2. In particular, Section 2.1 includes morphology and counting while Section 2.2 includes imaging and segmentation. In addition, the physiological phenotype of plants is the external manifestation of the interaction between multiple organs. Therefore, this content will be introduced in detail in Section 3.2.

2.1. Plant above-ground organ phenotyping

2.1.1. Morphology and growth

Morphological changes in plant organs play a vital role in the growth and development of vegetation. For example, leaf area and leaf shape (e.g., leaf length, leaf width, leaf inclination, etc) are closely related to various biological and physical processes of plants, such as photosynthesis, respiration, transpiration, and carbon and nutrient assimilation. Stem width is directly related to crop yields while stalk inclination contributes to determining plant lodging and measuring crop lodging rates. Flowers and fruits of different species also vary in characteristics such as shape, size, and color so that quantitative research on their diversity is crucial for genome-wide association studies. Observation of organs can reveal their growth status and ultimately help us identify genetic contributions, provide selection basis and reference standards for improving plant genetic characteristics, and increase crop yield (McCormick et al., 2016). Therefore, the estimation of plant organ morphological structure and physiological parameters is of great significance for vegetation growth monitoring. In the high-throughput phenotypic analysis, the automatic segmentation of plant organs is a prerequisite for measuring more complex phenotypic traits. Despite the outward appearance and shape characteristics, the occlusion of organ and change of organ shape and size, as well as imaging conditions, make image segmentation challenging (Lomte and Janwale, 2017; Scharr et al., 2016).

Since the 1980s, lots of effective methods have been proposed to

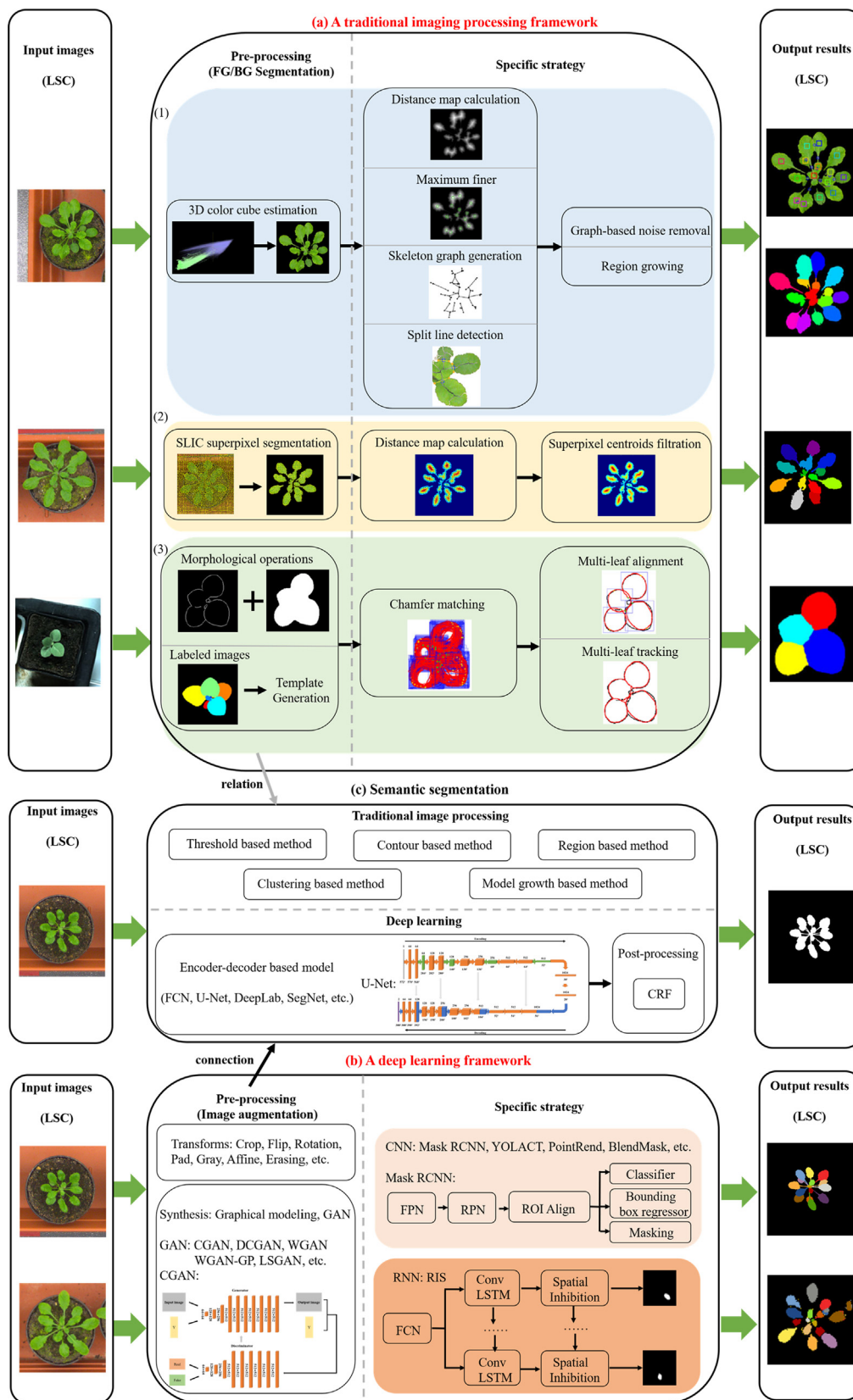


Fig. 3. Diagram of the pathway of imaging-based plant organ segmentation (with leaf segmentation as the example). A key first step is to gather a large and diverse set of data (with LSC dataset (Scharr et al., 2014) as the example). **(a)** A traditional imaging processing framework. A pipeline typically consists of two stages. Stage A: the foreground and background are segmented by pre-processing. Stage B: using some specific strategies distinguishes different instances of plant organs. The blue (1), yellow (2), and green (3) backgrounds represent three different approaches, respectively. These methods were reproduced using figures from (Agapito et al., 2015; Scharr et al., 2016). **(b)** A deep learning framework. A pipeline typically consists of two stages. Stage A: using transforms or GAN augments images. Stage B: using CNN or RNN distinguishes different instances of plant organs. The red and orange backgrounds represent two types of methods: CNN (Mask RCNN) and RNN (RIS). RIS was reproduced using figures from (Romera-Paredes and Torr, 2016). **(c)** The middle part of the (a) and (b) refers to semantic segmentation methods, including traditional image processing and deep learning. This part is the supplement of the pre-processing methods in (a). In addition, the expanded images in (b) can improve the accuracy and robustness of semantic segmentation methods. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

deal with the problem of plant organ segmentation, especially leaf segmentation. Most of them considered plant organ segmentation as a semantic segmentation task (Fig. 3(c)) and used traditional image processing methods (Table 1), such as the threshold-based method, edge-based method, region-based method, and clustering-based

method. In general, researchers do not apply these strategies alone, but combine them to improve the accuracy and robustness of image segmentation algorithms. For instance, the threshold-based method is often assisted by region-based methods to trim the segmentation results and correct for the excessive segmentation (Jun Pang et al., 2011;

Table 1
Summary of 2D plant organ image segmentation methods.

Method Type	Advantages	Disadvantages	Year	Specific Methods	Plant Organs (Species)	Reference
Threshold based	(1) Simple calculation (2) High efficiency	(1) It just depends on the pixel gray value and does not consider spatial details. (2) Sensitive to noise and has low robustness	2012	Otsu's method	Flower (Oxford flower dataset)	(Najjar and Zagrouba, 2012)
			2013	Adaptive thresholding & Otsu's method & Canny edge detection	Leaf (Jujube)	(Wang et al., 2013)
			2016	Otsu's method	Flower (Oxford flower dataset)	(Patil and Shaikh, 2016)
			2017	Otsu's method	Leaf (Mango)	(Prasetyo et al., 2017)
			2017	Otsu's method	Stem (Maize)	(Choudhury et al., 2017)
			2019	Otsu's method	Fruit (Kiwifruit)	(Fu et al., 2019)
Edge based	(1) Accurate edge positioning (2) Fast computing	(1) The continuity and closure of edges cannot be guaranteed. (2) Not suitable for too many edges	2009	Edge detection fuzzy numerical morphology calculation	Leaf (Tobacco)	(Pan et al., 2009)
			2009	Canny edge detection	Flower (Oxford flower dataset)	(Nilsback and Zisserman, 2009)
			2012	Sobel edge detection	Fruit (Orange)	(Patel et al., 2012)
			2014	Canny edge detection	Fruit (Orange)	(Thendral et al., 2014)
			2018	Sobel edge detection & Chan–Vese model	Leaf (Cucumber)	(Wang et al., 2018)
			2009	Watershed	Fruit	(Zeng et al., 2009)
Region based	(1) Good segmentation effect for complex images (2) It works well for images having good contrast between regions.	(1) Complicated algorithm (2) Heavy computing	2011	Watershed	Fruit (Apple)	(Deepa and Geethalakshmi, 2011)
			2016	Watershed & Simple linear iterative clustering	Leaf (Arabidopsis & Tobacco)	(Scharr et al., 2016)
Clustering based	(1) It can eliminate noisy spots. (2) It can obtain more homogeneous regions.	(1) Sensitive to noise and gray inhomogeneity (2) Difficult to determine the initial parameters	2011	Ant colony optimization clustering	Flower (Oxford flower dataset)	(Aydn and Uğur, 2011)
			2012	Fuzzy clustering & Fuzzy thresholding	Leaf	(Valliammal and S.N.Geethalakshmi, 2012)
			2013	K-means	Fruit	(Dubey et al., 2013)
			2014	Spatial fuzzy C-means	Leaf (Corn)	(Premalatha et al., 2014)
			2014	K-means	Leaf (Wheat)	(Niu et al., 2014)
			2016	DBSCAN	Flower (Jasmine)	(Abinaya and Roomi, 2016)
Deep learning	(1) Strong learning ability (2) High accuracy (3) Strong portability	(1) Large-scale training data (2) Complex networks (3) Poor interpretability (4) Computationally expensive	2016	RNN	Leaf (Arabidopsis)	(Romera-Paredes and Torr, 2016)
			2017	SegNet	Leaf (Arabidopsis & Tobacco)	(Aich and Stavness, 2017)
			2018	Pyramid CNN & Washed	Leaf (Tree)	(Morris, 2018)
			2019	Mask RCNN	Leaf (Arabidopsis & Tobacco)	(Ward et al., 2019)
			2019	FCN	Leaf (Arabidopsis & Tobacco)	(Itzhaky et al., 2019)
			2019	Graph-based method	Leaf (Arabidopsis & Tobacco)	(Praveen Kumar and Domnic, 2019)
			2019	U-Net & Watershed	Leaf (Arabidopsis & Tobacco)	(Sapoukhina et al., 2019)
			2019	FCN	Fruit (Grape)	(Grimm et al., 2019)
			2019	DCNN & Simple linear iterative clustering	Fruit (Wheat)	(Sadeghi-Tehran et al., 2019)

Scharr et al., 2016). Additionally, the above methods are also combined with some specific tools (e.g., genetic algorithm, wavelet transform, active contour, etc.). Therefore, a study applied wavelet transform to leaf segmentation based on fuzzy threshold and clustering, eliminating noisy spots and providing good segmentation results in the serrated part of the leaf edge. Another study proposed a method based on the Sobel operator and Chan-Vese model to extract the target leaf from cucumber leaf images with complex backgrounds and overlapping regions (Wang et al., 2018). Combining these multiple methods in some way would improve the generalizability and accuracy of plant organ segmentation. In summary, these methods only segment the organs from the background but would not segment the various special instances in these organs. Therefore, they are mainly used in the pre-processing stage of instance segmentation or in aerial image analysis.

After segmentation, we can calculate values regarding plant basic parameters such as length, width, length-to-width ratio, eccentricity, etc. However, shapes and branching architectures are hard to quantify. Persistent homology, a mathematical method that captures topological features across scales, is well suited to quantify the shapes and branching architectures of plants (Li et al., 2017). A study applied persistent homology algorithm to characterize complex shape parameters in American cranberry (*Vaccinium macrocarpon* L.) (Diaz-Garcia et al., 2018). In this study, the method divided the fruit image into subsets of features utilizing increasing annuli emanating from the center of the shape. It discretized each Euler feature curve into 30 values, and then spliced them on 4 annuli. This study demonstrated the potential of persistent homology for shape description, which can be very useful for quantitative trait locus (QTL) mapping and fruit quality assessment. Inflorescence is the arrangement of flowers on the axis, which are major adaptations of the angiosperm lineage whose architectural variation affects fertilization, fruit development, dispersal, and crop yield (Chanderbali et al., 2016). A very recent study explored the use of persistent homology to describe the inflorescence structure of wild grapes and evaluate phylogenetic signals under inflorescence structural characteristics (Li et al., 2019). The output of persistent homology is a barcode that summarizes topological information including branching hierarchy, branch arrangement, and branch lengths, which can be used to compare topological similarity between two inflorescences. This would not only inspire future studies related to shape and branching architectures measurement but also reveal genetic structure.

Plant growth is regulated by numerous metabolic reactions, physiological processes, and environmental factors. The dynamic fluctuations of plant organ growth reflect the adjustment of environmental conditions by endogenous processes, which can be important for us to understand the processes of biomass and yield formation (Walter and Schurr, 2005). The optical flow method can effectively track the slight changes and analyze the growth patterns or strain rates within organs. Growth estimates based on optical flow have been widely applied to study leaf (Nagano et al., 2019; Nugroho et al., 2016; Poire et al., 2010), hypocotyl (Bergougnoux et al., 2012), stem (Wakamori et al., 2019), and root (Nagel et al., 2009). However, growth estimation based on optical flow is sensitive to brightness fluctuations and must satisfy the brightness change constraint equation (BCCE), while requires continuous or small amplitude of structural pattern motion. This not only means that a constant brightness must be maintained but also inevitably increases the size of the image sequence and the volume of data. Template matching is a classic method of target tracking, which is simple, accurate, fast, good noise-insensitive, and does not have to fulfill BCCE requirements. A study established an approach based on template matching that allows monitoring of diel leaf growth fluctuation in various illumination conditions, revealing typical features of diel leaf growth patterns, without further consideration of base-tip gradients or other spatial growth differences within the leaf lamina (Mielewicz et al., 2013). However, the above methods are unable to adapt to the drastic changes of illumination and target shape, especially for

perennial and field crops. For example, perennial crops (e.g., ryegrass, apple, grape, blueberries, bell pepper, etc.) are cut or picked repeatedly throughout the season and need to resume growth from existing tillers and form new ones, which requires to evaluate growth-related parameters during a full growing season or even over several seasons (Lootens et al., 2016). For field crops, researchers could not guarantee the imaging quality, because outdoor light conditions varied throughout the day and season. To solve these problems, people employed deep learning (such as convolutional long short term memory (LSTM)) to track plant growth and morphological changes (Lee et al., 2020; Namin et al., 2018; Reddy and Prasad, 2018; Sakurai et al., 2019). This method can automatically adapt to changes of the external environment, so as to improve the accuracy and robustness of tracking. Convolutional neural networks (CNNs) are used to extract the features of plant images, while LSTMs can remember the state of plants and obtain the temporal relation. In this way, plant growth patterns could be encoded by an encoder-decoder architecture to model the representation of plant growth effectively. Yet, deep learning requires lots of sequences of labeled images and lacks visualization tools to enhance the interpretability. All in all, no mature and effective method for plant growth has been published so far when time intervals become larger, or plant and background complexity is higher.

2.1.2. Counting

With the segmentation and tracking analysis, the computer could automatically and correctly calculate the organ area (De Maria et al., 2018; Koma et al., 2018), measure the length and width (Guy and Aharon Bar-Hillel, 2019; Panjvani et al., 2019; Paproki et al., 2012), visualize the leaf vein characteristics (Schneider et al., 2018), estimate inclination and azimuth angle (Itakura and Hosoi, 2018; Xu et al., 2019), monitor growth and movement dynamically (Duan et al., 2016; Herrero-Huerta et al., 2018), and so on. In addition to the above tasks of quantifying organ characteristics, automatic counting has become the focus of people's attention in recent years. From the phenotypic perspective, the number of plant organs, especially leaves and fruits, is directly related to the developmental stage, growth regulation, flowering time, and yield potential. However, automatic counting is a challenging task because the shape and size of the organs will change over time, the position of the organs will rotate and move and the organs may overlap, leading to severe occlusion (Pape and Klukas, 2015). Due to the rapid growth and complexity of plants, automatic counting has drawn more and more attention. *Leaf Counting Challenge (LCC)* has attracted a large number of researchers and proposed many advanced and effective methods (Aich and Stavness, 2017; Dobrescu et al., 2017; Giuffrida et al., 2019). In recent years, in order to attract a large number of scholars to the field of leaf counting and encourage researchers to propose various solutions (Scharr et al., 2016), the *Leaf Segmentation Challenge (LSC)* and *LCC* provided a dataset of Arabidopsis and Tobacco under different varieties, while developed a lot of good methods. Recently, the methods of plant organ counting are mainly summarized into two categories, namely, the methods based on image detection or segmentation and the methods based on direct regression.

2.1.2.1. Counting based on detection or segmentation. Object detection is an intuitive method for counting plant organs in plant images. The accuracy of counting is completely dependent on the detection results. Multi-instance segmentation is considered a more difficult task than object detection, which requires to obtain a per-pixel segmentation mask. Compared with objection detection, multi-instance segmentation can accurately describe the edges of the objects and provide more detailed information. Before 2016, deep learning was not yet popular, and researchers usually used traditional image processing methods to segment different instance objects of plant organs. As shown in Fig. 3(a), plants are first extracted from the background (stage A: pre-processing), and then fruits (Fu et al., 2019; Grift et al., 2017) or leaves (Agapito et al., 2015; Yin et al., 2014) are segmented individually by a

series of image processing and pattern recognition approaches (stage B: specific strategy). Pape and Klukas (Fig. 3(a)(1)) employed 3D histograms of LAB color space (reduce the negative impacts of illumination variability) to segment foreground from background for top view images of rosette plants and estimated test pixels by using interpolation in the training data (Agapito et al., 2015). Then, the leaves center points and split points were extracted by applying morphological operations and the Euclidean distance map. Finally, the individual leaves were separated by using the region growing algorithm to generate the final instance segmentation map. A study (Fig. 3(a)(2)) applied a superpixel-based unsupervised approach, which extracts the region of interest (ROI, foreground) by utilizing the simple seeded region growing in superpixel space from the LAB color map (Scharr et al., 2016). Then, superpixels with centroids were identified by computing the distance map over the ROI and finding local maxima. In a final step, the individual leaves were divided by using the watershed transform with the extracted seeds. Another study (Fig. 3(a)(3)) applied a template matching method based on the chamfer matching algorithm to segment plant from the background, which employs the empirical threshold to select foreground candidates for template matching on the LAB image (Scharr et al., 2016). The above methods effectively segment and counted leaves, while achieved satisfactory results in the *LSC-2014*. However, the major drawbacks of these approaches are the manual design of feature extractors and the empirical selection of parameters.

In order to solve the above problems, researchers tried to utilize deep learning to separate and count organs (Table 1). According to the recent submissions of the competition, methods based on deep learning gradually replace traditional image processing. Deep learning is a data-driven approach, so model training (such as Mask RCNN (He et al., 2017), YOLACT (Bolya et al., 2019), PointRend (Kirillov et al., 2020), BlendMask (Chen et al., 2020), etc.) usually requires lots of images with pixel-level annotation. Yet, many studies faced the challenge lacking of available training data, while data annotation at the pixel level is expensive. In general, synthesizing leaf images is a crucial way to augment data, mainly including graphical modeling (Kuznichenov et al., 2019; Mündermann et al., 2005; Prusinkiewicz and Lindenmayer, 2012; Ubbens et al., 2018; Ward et al., 2018) and generative adversarial networks (GANs) (Valerio Giuffrida et al., 2017; Zhu et al., 2018). Graphical modeling employs mathematical models to generate chains of elements representing plant parts (e.g., stems, leaves, fruits) based on a set of predefined plant growth rules or functions, such as L-systems. Graphical modeling can adjust the size, orientation, and color of the organs to some extent, but the synthetic data still lack texture and geometry information on the leaf surface, which may lead to the poor performance of trained models. GANs automatically learn and compensate for differences between synthetic and real-world data, which can effectively generate organ texture and geometry. A study utilized conditional GANs to produce images of Arabidopsis leaves. Zhu et al. generated plant masks in a structured manner and then fed into the conditional GANs as input (Fig. 3(b)). These synthesized mask images served as a condition to the generator and combine the real images for training generator and discriminator. The results showed that the method based on GANs can produce leaf texture and achieve the best performance in *LSC* and *LCC*. However, the model is difficult to train because of the Nash equilibrium, which requires professional experiences in model tuning. In addition to CNN, recurrent neural networks (RNNs) are also effective methods for segmenting plant organs. A study (Fig. 3(b)) proposed an end-to-end model by combining convolution LSTM and spatial inhibition module, which sequentially finds objects and their segmentations one at a time (Romera-Paredes and Torr, 2016). To deal with the problem of the possible ordering of individual instances in the image, they designed a principled loss function based on pixel distances to object positions. This is a pioneering work, which provides an important direction for future research.

2.1.2.2. Counting based on regression. Regression is a simple and direct approach to count fruits or leaves in plant images. Researchers pose fruit/leaf counting as a nonlinear regression problem, which directly estimates the count without segmenting individual organ instances. Compared with segmentation and detection, regression is usually more efficient than identifying each leaf and simpler than generating masks for individual leaf instances. A study adopted a support vector regression model to predict the number of leaves, which transforms the original RGB images into a log-polar coordinate system before a set of features is learned and extracted in an unsupervised manner (Giuffrida et al., 2015). Unlike the above study, lots of researches replaced the last layer (such as softmax) of some classic CNNs with a single neuron for predicting the number of plant organs. For example, Aich and Stavness used simple data augmentation strategies and re-trained the VGGNet architecture as a regression model for leaf counting (Aich and Stavness, 2017). Dobrescu et al. removed the last layer of ResNet-50 intended for classification, flattening the network and adding two fully connected layers followed by ReLU activations for predicting leaf numeric values (Dobrescu et al., 2017). Rahnemoonfar and Sheppard redesigned the Inception-ResNet module with the ability to skip connections between layers for tomato counting (Rahnemoonfar and Sheppard, 2017). Itzhaky et al. proposed a regression model based on feature pyramid network (FPN) improving multi-scale leaf detection accuracy (Itzhaky et al., 2019). On the one hand, CNN as direct regression can learn from the training images without the need for manual design or professional knowledge of various plant species. On the other hand, methods based on regression only calculate the total number of leaves per plant, and cannot provide explicit spatial location information.

With the rapid development of imaging technologies, the researches on plants are no longer limited to RGB images. A study provided a general framework for leaf counting, which can calculate the number of leaves from multi-modal 2D images, including visible light, fluorescence, and near-infrared (Giuffrida et al., 2018). The framework is composed of multiple modal branches (i.e., ResNet-50) to extract leaf features. The fusion part combines these features together to retain the most useful information in each mode, while the regression part takes the fusion information and leaf count as a nonlinear regression relationship. Many visual tasks (such as counting) gradually focus on considering the association, integration, and transformation of multi-domain data in order to improve the model result and solve more practical problems. Sapoukhina et al. studied the transfer of knowledge for leaf segmentation learned from RGB imaging to fluorescence imaging, which demonstrated the existing annotated dataset in RGB could be applied to learn to segment leaves in fluorescence images by a simple RGB to gray conversion (N Sapoukhina et al., 2019). They considered these results could be extended in leaf counting as a regression. In summary, domain adaptation is a worthy direction that can transfer the existing knowledge to other unfamiliar areas to compensate for the necessarily non-perfect match between simulation and reality.

2.2. Plant below-ground organ phenotyping: Root system architecture

2.2.1. Root imaging

Root is the vegetative organ of plant, generally located under the surface of the earth. They are responsible for supporting plants, water and nutrients uptake, working with vessels to transport water and nutrients to plants (Ozel and Freire, 2016), and changing the physical and chemical properties of the rhizosphere by infiltrating large quantities of low and high molecular weight metabolites into the soil (Delory et al., 2016). In addition, there are many microorganisms interacting with the root system in the rhizosphere as well, which can stimulate the growth and activities of microorganisms, thus affecting the regulation of soil organic matter decomposition, contributing to the stability of soil aggregates, preventing soil erosion and having a positive impact on plant health (Hinsinger et al., 2009).

Quantification and visualization of plant root structure architecture (RSA) can help us understand plant growth dynamics and yield characteristics, locate QTLs (Topp et al., 2013), select good traits, and improve crop varieties (Cichy et al., 2009). However, RSA is difficult to be quantified because they are not only complex in morphology, but also grow naturally in the opaque and complex soil media. Once the root growth environment is destroyed, the results of root analysis will inevitably be affected. In addition to RSA, a large number of biological, physical, and chemical processes occur near the root surface in the rhizosphere, affecting the transport and utilization of water, nutrients, and gases (Ahmed et al., 2016; Naveed et al., 2017). Soil density, matric potential, and surfactant releasing from roots interacting with other substances would determine the mechanical properties of the rhizosphere and affect rates of root elongation and branching. It remains an important challenge for the quantitative determination of the amount of exposure between roots and soil components to better define the interaction between roots and soil structure and the heterogeneous distribution of many nutrients (Goh et al., 2016). Generally, the effective techniques for screening a large number of plant root traits are mainly divided into optical recording in non-soil medium and non-invasive measurement in soil medium according to the different growing conditions, both of which have advantages and disadvantages in studying root traits.

2.2.1.1. Non-soil medium measurement. Cultivating roots in the open air is the fastest way to measure root phenotype (Wan et al., 2019; White et al., 2009; Zheng et al., 2019). By planting seeds on wet paper in a petri dish and then taking photos with a digital camera a few days later, the number of roots and morphological characteristics can be screened. The advantage of this method is simple and rapid imaging, but the effect of petri dish size and seed orientation limits the validity and rigor of RSA measurement. Aeroponic system (Lakhiar et al., 2018; Q. Li et al., 2018), hydroponic system (Herklotz et al., 2010; Kawasaki et al., 2018), and agar plate system (Armengaud et al., 2009; Atkinson et al., 2019; Manschadi et al., 2008) facilitate the growth of larger root systems and the measurement of root architectural components. This method enables the monitoring of root growth and morphological changes without background interference. Combining with the rapid imaging system (digital camera) can make high-throughput quantitative measurements of root number, length and diameter of plants within a few minutes. The non-soil medium method overcomes the problem of root visibility but cannot represent the plant's natural environment. For instance, the root length of dwarf wheat lines grown on agar plates increased by about 40% compared with wild-type and semi-dwarf lines, but decreased by 24–33% in sandy loam with abundant water (Manschadi et al., 2008). This difference indicates that there is a significant interaction between soil environment and genotype while the simulated non-soil environment cannot replace the real soil environment.

2.2.1.2. Soil medium measurement. A common method for studying plant roots in soil is root washing (Chapae et al., 2019; Jones et al., 2019), however, it often leads to root fragmentation and loss of spatial distribution information of roots. Another method is using non-invasive imaging technology to make 3D non-invasive measurements of roots growing in the soil. In addition to the number and length of roots, angle distribution can also be obtained. The approach has benefited from advances in other useful imaging techniques, including magnetic resonance imaging (MRI) and computed tomography (CT). MRI (Csurka et al., 2013; Mawodza et al., 2020; van Dusschoten et al., 2016) can display samples placed in a strong static magnetic field directly without any loss, which is limited by the presence of paramagnetic elements (i.e. Fe^{2+} , Fe^{3+} , Mn^{2+} , and Cu^{2+}). Root interactions may lead to interference, especially for roots less than 1 mm in diameter (Delory et al., 2017). CT (Wasson et al., 2019) can also non-invasively produce the growth of plant roots in the natural soil

environment and observe the surrounding soil matrix and related pore volume providing higher spatial resolution, which is helpful for studying the specific details of fine roots and the diameter of fine roots. While the major limitation of this technique is the overlap of X-ray attenuation values between organic matter in plant roots and soil, as well as the variation of X-ray attenuation caused by water retained in roots and stored in soil pores (Mairhofer et al., 2012). MRI (Csurka et al., 2013) provides roots with higher resolution than CT, and it can achieve strong root-soil contrast. Since CT and MRI can collect complementary information, the combination of the two models can generate more possibilities, for instance, analyzing root characteristics in different soil structures or soil moisture could be achieved (Metzner et al., 2015).

2.2.2. Root phenotyping

It would be challenging to analyze these data effectively and accurately followed by collecting a large number of pictures of plant roots. The methods of root phenotyping based on computer vision mainly include root segmentation, root reconstruction and root phenotype extraction. Root segmentation is the separation of root and non-root substances. Different from roots in non-soil media, roots in soil media are difficult to be separated. In order to improve the segmentation effect and root reconstruction performance, post-processing methods, including morphological operations (erosion, expansion, etc.) and component filtration, are often required (Xu et al., 2018). After segmentation and post-processing, the next step is to extract 2D or 3D RSA, depending on the researcher's interest and purpose. The premise of obtaining the 3D root phenotype is the reasonable and accurate reconstruction of root structure. There are two main methods of root reconstruction: image-based 3D reconstruction and CT scan-based 3D reconstruction. First of all, image-based 3D reconstruction is used for root imaging in non-soil media or soil media after washing. Digital camera is used as a sensor to obtain 2D images, and then several continuous images are spliced and stitched. There are generally two modes of operation. One is to place multiple digital cameras around the root (Brown and Lowe, 2007; Han and Kuo, 2018), while another method is to fix a single digital camera in front of the root and use electric devices (such as servo motor, steering gear, etc.) to rotate the root (Clark et al., 2011; Zheng et al., 2011). 3D reconstruction based on CT scan (Mairhofer et al., 2012; Tracy et al., 2012) for root imaging in soil medium, in which X-ray beam is projected through the target part of the sample through multiple arrays around the sample, and then a cross-section image or matrix is reconstructed. Each non-invasive "slice" consists of a set of pixels that describe the X-ray attenuation coefficient of the voxel of the scanned object (Perret et al., 2007). The output of the CT scanner uses the CT number matrix represented by the Hounsfield unit, which can generate a 3D reconstruction of the root distribution by performing multiple consecutive CT scans of the same root.

2.2.2.1. Phenotyping based on CT and MRI. Soil/root segmentation is one of the most challenging computer vision problems in plant science and soil/root monitoring is crucial for quantitative evaluation of root development. Threshold-based segmentation methods are simple and useful in most soil/root segmentation problems. For instance, a study made use of X-ray CT acquisition to the root images and histograms of the maple and chestnut tree in the sandy clay and split the roots by using the global threshold method (Pierret et al., 1999). For the fine roots, applying directly threshold-based methods often leads to misclassification and discontinuous representation. To solve this issue, a study estimated the global threshold with the Otsu's method and refined the global threshold locally around each pixel with the adaptive threshold algorithm to improve the segmentation effect of the fine roots (Bucksch et al., 2014). A study attempted to solve the above problems by applying nonlinear diffusion filter and morphological connectivity algorithm, which can detect the primary root and some thin lateral roots (Kaestner et al., 2006). However, the study was conducted in a

homogeneous sandy matrix with low water content, which is a benefit for imaging but not a good representation of field conditions. Another study utilized binary threshold technology to separate the roots of chickpeas growing in fine sand, mark the pores filled with air and water while marking the root material (Perret et al., 2007). Then the geometric filtering method was adopted to detect and eliminate the broken voxels and flood filling algorithm was used to extract the roots in 3D. However, the filter cannot eliminate gaps because attenuation values between the root and the air are similar.

The overlapping attenuation value of root material and soil environment is the core of the root/soil segmentation problem under CT image: the method only considering attenuation value and the simple threshold method is difficult to identify root material accurately. To solve the problem more easily, further understanding or assumptions about the appearance of plant roots in CT data are needed. One way to introduce the prior knowledge of roots into the segmentation process is to divide voxel data in the CT data set into horizontal plane slices to simulate the physical slices of the soil. If the slices are sorted from top to bottom and shown as video, these root areas would appear to move, besides, their shape, size, and motion would reflect the geometry of the root. Tracking the motion of 2D regions is represented by the image sequence of 2D attenuation values, which increases the possibility of extracting RSA from CT data (Mooney et al., 2012). In general, the tracking algorithm can be divided into two categories: top-down (model-driven) and bottom-up (data-driven). Top-down and bottom-up define different data or information processing strategies (Xu et al., 2018). In the top-down approach (French et al., 2009; Kaestner et al., 2006; Mairhofer et al., 2012), object representation is built based on previously available data to control the detection of other objects of the same class, and this process is to search for elements matching a certain model of the target object or class in the incoming data. Moreover, the top-down method is sensitive to the changes of noise points and contrasts and has high requirements for image quality. While in the bottom-up approach (Armengaud et al., 2009), criteria based on local images are used to define and continuously refine groups of pixels that may belong to the same category, which is usually implemented as a predefined process consisting of multiple processing steps. If there are some biases in each process, these errors could be accumulated, in which interactive error correction tools are often introduced to solve these problems (Han et al., 2008), but manual correction is time-consuming since misclassified objects are usually small and often distributed throughout a dataset. Tracy et al. proposed the method based on assigning probability functions called RootViz, which can eliminate the subjectivity of identifying root pixels in noisy images and realize detailed visualization of root structure in situ (Tracy et al., 2012). Mairhofer et al. presented a more automated tracking approach based on the level set segmentation called Roottrak (Mairhofer et al., 2012). The level set segmentation method identified the root node of the tag and constructed the initial appearance model, showing great potential in overcoming the limitations related to phase overlap in the histogram of attenuation values.

2.2.2.2. Phenotyping based on RGB. CT and MRI require specialized equipment, which are expensive and take a long time to image. In contrast, digital cameras are much cheaper, faster and more accessible. Generally, there are three application scenarios for digital camera imaging: roots in non-soil-transparent media (Han and Kuo, 2018), roots after washing (Bucksch et al., 2014), and roots in soil-filled root canals (Chen et al., 2019a). Certainly, each method is not perfect and has its limitations. For example, non-soil-transparent media cannot completely replace the natural environment; roots in the soil media will be damaged after washing; rhizotrons artificially restrict the direction of root growth to two dimensions and the observation results are limited to the boundary surface and so on.

The above threshold-based methods can also segment the root in RGB images easily and quickly (Clark et al., 2013; Zheng et al., 2011).

For further improving threshold segmentation method accuracy, Han and Kuo combined CNN with Otsu's method to segment the roots from the background (Han and Kuo, 2018). The whole image is segmented into multiple over-lapping patches by using a sliding window from the top-left corner to the bottom-right corner of the images, and the CNN classifier is developed to judge whether the patches contain roots, so as to remove the background well. Finally, the image is binarized by Otsu's method and the binarized sub-images are combined to form a contour. Experimental results showed that the developed system was 98.3%, 97.6%, and 93.3% accurate regarding the primary root length, total root length, and root volume. Although the accuracy of this multi-stage processing method is improved, the process is tedious and the optimization is difficult. To solve this issue, several studies reported the use of end-to-end CNN architecture based on encoder-decoder to segment roots from root images. A study drew on the idea of U-Net and proposed an end-to-end image segmentation framework to successfully separate the roots of chickpeas from the soil (Chen et al., 2019b). The CNN performs better than the current level in many image processing and analysis tasks, but the method requires lots of sample images and manual labeling steps. Targeting for this problem, Atanbori et al. successfully applied conditional GAN to generate the synthetic images of roots, expand the dataset of cassava roots, and effectively improve the accuracy of root segmentation and counting (Atanbori et al., 2019). Chen et al. considered the problem as an image inpainting process that recovers and fills gaps from disconnected root segments in the roots visualized system (Chen et al., 2019a). The adversarial module was trained in an adversarial way to facilitate the model to produce more accurate results. The adversarial mechanisms encourage the local discriminator to obtain local high-quality inpainting results and the global discriminator to produce inpainting results with a global root view. Experimental results showed that, compared with other patch-based CNN methods, training the model on a synthetic root data achieved a 72% improvement of recovering accuracy in real chickpea root images. Applying GAN to generate synthetic images might be a potential way to train models for many CNN-based approaches and applications that lack of annotated data.

3. Whole plant phenotyping

Plant is a sophisticated organism with multiple organs operating cooperatively, so that the plant should be analyzed as a whole. A separate analysis of plant organs will break up the internal relationship of plants, which is impossible to obtain a comprehensive and objective phenotypic understanding. Generally, it is not enough to analyze the phenotype of the entire plant from a single picture or a single perspective. Most methods aim to acquire the 3D geometry as complete as possible, which requires geometric modeling of the entire aerial part of the plant. In addition, phenotypes composed of structurally and physiologically related features would influence each other at multiple levels. Changes in plant physiological characteristics will cause changes in plant structural characteristics. At the same time, plant structural characteristics can relatively reflect the physiological state of the plant body, promoting the study of plant stress.

Whole plant phenotyping is mainly discussed below from 3D phenotyping and plant stress. Section 3.1 mainly introduces the research of plant 3D phenotyping and several 3D imaging techniques used in plant phenotypic measurement. A processing pipeline based on point cloud data is proposed. At last, the 3D image segmentation algorithm will be discussed. Section 3.2 summarizes the basic types of plant stress and commonly used imaging techniques, introduces their respective development processes from two directions of RGB and hyperspectral images, and then discusses several common image analysis algorithms and applications.

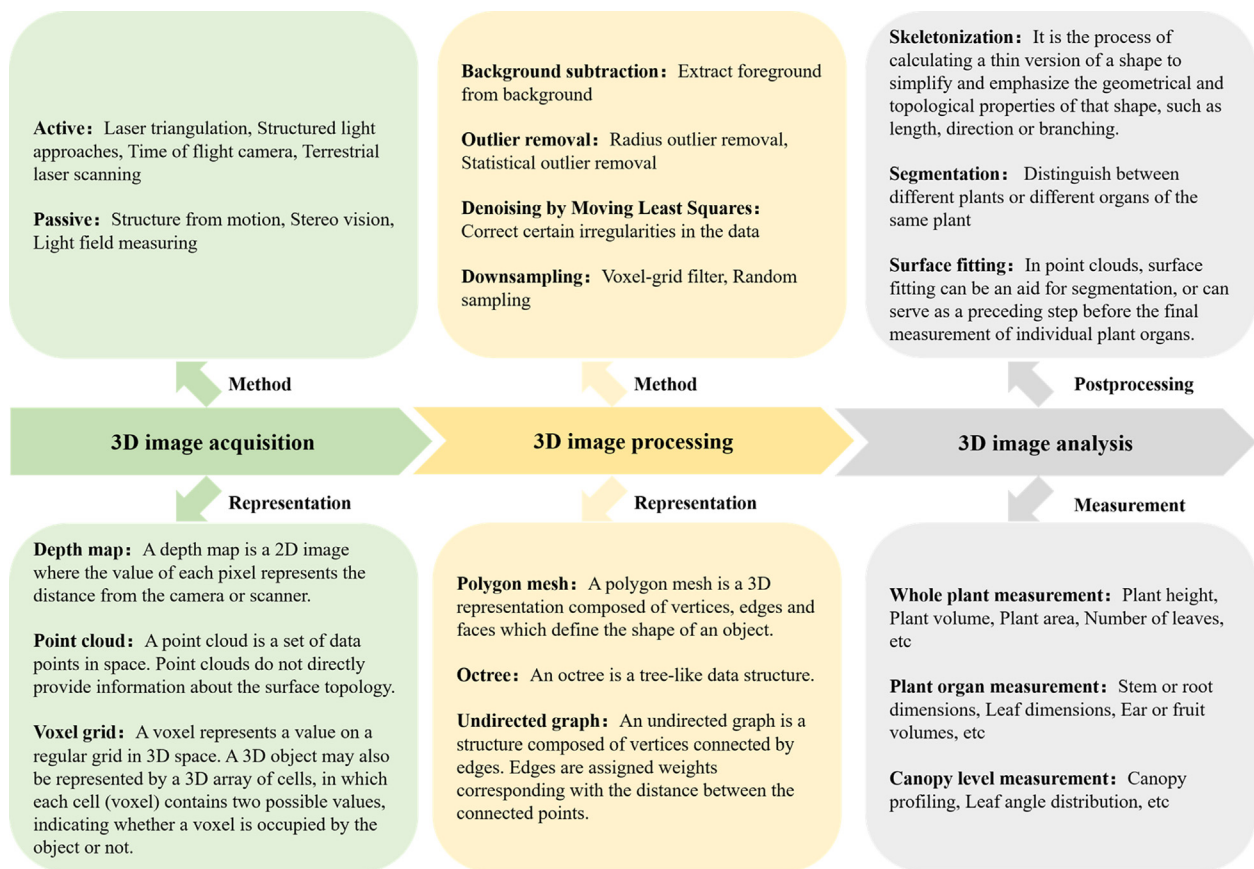


Fig. 4. The pipeline of 3D plant phenotyping.

3.1. 3D phenotyping

Over the past three decades, 3D measurements of plant phenotypes have made rapid progress. Compared with the 2D vision, it avoids the lack of depth information, which can generate accurate coordinates and distance estimates, and also can give the precise orientation of objects, making it easier to estimate plant morphology, growth, and biomass (Vandenberghe et al., 2018). Due to the complexity of plant structure and the diversity within species, lots of problems may be encountered in the processing and analysis of 3D phenotypes, thus it's necessary to design a set of diverse tools. In general,

typical processing and analysis steps for 3D plant phenotyping involve 3D image acquisition, 3D image preprocessing, and 3D image analysis, as shown in Fig. 4.

There are various technologies for obtaining 3D images or depth information, which can be roughly divided into active and passive methods. Active methods require sensors from active light emitters to obtain 3D data, while passive methods essentially only rely on ambient light. Active measurement technology can be divided into two categories, one is a system based on triangulation and the other is a system based on time of flight (ToF) measurement. The former includes laser triangulation (LT) and structured light approaches (SL), the latter mainly includes terrestrial laser scanning (TLS) and ToF cameras. In addition, stereo vision technique, light field measuring (LF) and structure from motion (SfM) belong to passive measurement technology. Different imaging technologies have their own characteristics, so researchers usually choose the appropriate imaging way based on the specific application scenario and task. All the 3d imaging technologies reviewed for various phenotyping applications are summarized in Table 2. Therefore, researchers could quickly compare and choose 3D imaging methods to solve particular problems in their applications.

The morphological parameters of the whole plant or even a single

organ can be captured by 3D scanning to describe the plant size, shape and development. From the aspect of the complexity of description, we divide the traits into non-complex and complex traits. Among them, the traits of the whole plant are described as non-complex traits and those at the organ level are called complex traits because the description of complex traits requires identification and segmentation of plant organs in advance. Non-complex traits include plant height, width, volume measurement, rough leaf area estimation, etc. Complex traits describe the exact leaf area, stem length, internode distance, fruit count, fruit volume, etc. Due to continuous changes of plants over time, we can repeatedly measure and analyze these traits at specific time intervals to extract time-lapse features of the plant, such as leaf surface development, leaf movement and field maps showing growth in different locations. Since time can be described as an extra dimension, time-lapse features are called 4D features (Paulus, 2019).

2D images can be uniformly represented by a regular grid of pixels, but 3D images have multiple representations, such as the depth-based, voxel-based, point-cloud-based, and mesh-based representation. The performance of various programs depends on representation to a great degree and there is no unique representation working for all applications. Taking point cloud as an example, we introduce the processing pipeline of the 3D point cloud (Fig. 5). Firstly, the original point cloud data are preliminarily segmented to obtain the ROI. Then, applying background subtraction, outlier removal, denoising by moving least squares, and down-sampling usually cleans and preprocesses ROI data. Next, non-complex traits can be estimated based on the current point cloud parameters. For instance, plant height, plant width, plant volume can be calculated by 3D coordinate system transformation and numerical calculation. Total leaf area and slope can also be estimated by plane fitting and mesh algorithms. In order to extract more complex trait parameters, hand-designed feature extractors can be used to encode surface structures, extract 3D features and realize the

Table 2
Summary of 3D imaging techniques successfully used to plant phenotyping.

Type	Name	Major component	Principle	Resolution	Output	Advantages	Disadvantages
Active	Laser triangulation	Laser & CCD camera & lens	Pairing the laser light source with the camera to capture the 3D data. Based on fixed angular offset of the camera and the laser position, the linear distance between the detection surface and the camera can be deduced to determine the distance or height information of the object.	< mm	XYZ(I)	(1) High measurement accuracy at close range (2) High resolution (3) Low cost (4) Relatively insensitive to the effects of lighting conditions or surface textures	(1) Serious mistakes in large distance (2) Difficult to scan transparent or reflective surfaces correctly (3) No color information (4) Heavy computing
	Structured light	camera & projector	A series of known patterns are sequentially projected onto the object, and the pattern will be deformed due to the geometry. Then the camera is used to observe the object from different directions. By analyzing the distortion of the observed pattern and the width of each stripe, depth information can be extracted.	< mm	XYZI(RGB)	(1) High accuracy (2) Fast scanning speed (3) High resolution in a certain rang	(1) Susceptible to ambient light interference (2) Poor outdoor experience (3) Accuracy will decrease as the measurement distance increases.
	Time of flight	Time of flight camera	The sensor continuously sends light pulses to the target, receives the light returned from the object and obtains the distance of the target by detecting the flight (round trip) time of the light pulse.	mm	XYZ(I)	(1) The small size of the camera is easy to install. (2) Short measurement time (3) Wide measurement range (4) Less effect from ambient light (5) No need for scanning equipment to assist in work	(1) Expensive (2) Difficult to handle shiny surfaces
Passive	Terrestrial laser scanning	Terrestrial laser scanner	Time of flight or a phase shift approach	cm	XYZ(I/RGB)	(1) Wide measurement range (2) High accuracy	(1) Expensive (2) Time-consuming
	Structure from motion	RGB cameras	Cameras capture a series of 2D images at different points around the scene to estimate the 3D structure, including camera calibration, image point measurement, 3D point cloud generation, surface generation, and texture mapping.	mm	XYZRGB	(1) Low cost (2) Wide measurement range (3) High resolution (4) Mature algorithm	(1) The measurement equipment needs to move continuously. (2) Complicated operation (3) Time-consuming (4) Poor stability
	Stereo vision	RGB cameras	Cameras capture the same scene with a pair of cameras and calculate the depth using triangulation based on the disparity of each pixel.	cm	XYZRGB(I)	(1) Simple to use (2) Low cost (3) High accuracy	(1) Limited imaging range (2) Low imaging quality (3) Heavy computing (4) Poor real-time performance

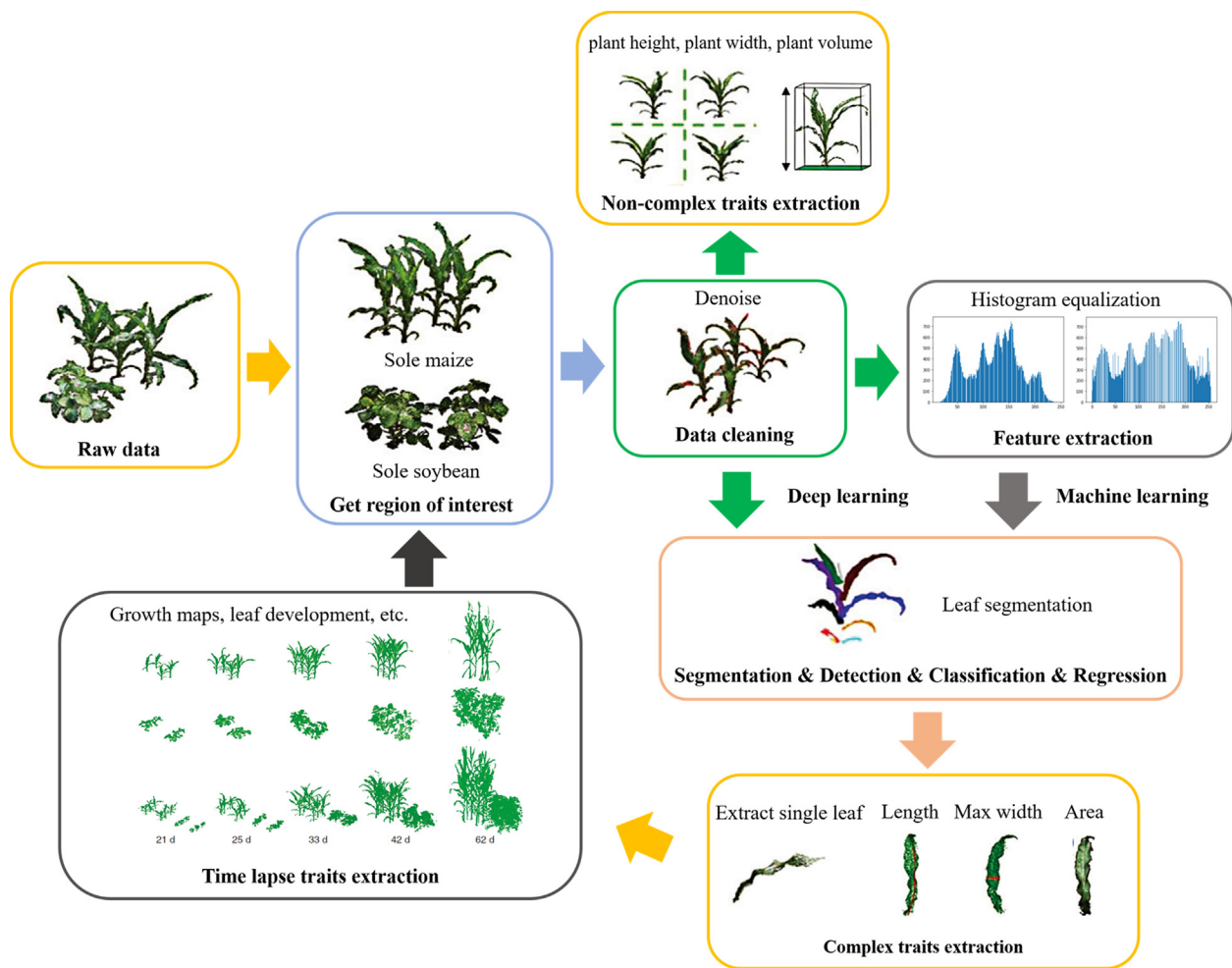


Fig. 5. A 3D plant point cloud processing pipeline. Figures were reproduced from (Zhu et al., 2020).

classification, segmentation, and detection by machine learning algorithms (e.g., support vector machine, random forest, k-means clustering). In addition to traditional machine learning methods, CNN can also be employed to automatically extract image features and complete end-to-end data processing by designing reasonable network structures. Finally, repeated measurements can calculate plant developmental growth parameters over time, such as growth curves at the level of plant and organ. The circadian cycle can be observed and compared to daily growth, because 3D devices are able to distinguish between growth and movement (Dornbusch et al., 2012; Herrero-Huerta et al., 2018). Besides, since growth is a direct indicator of stress, high-precision 3D measuring equipment is ideal for measuring 3D shape changes to detect the stress (Omasa et al., 2007).

3D point cloud of plants contains abundant phenotypic features, and automatically segmenting these data is helpful to phenotyping. However, the complex plant spatial structure requires a higher performance of the segmentation and detection algorithm. Leaf segmentation is the most difficult among segmentation tasks. Plant leaves are usually distributed in clusters, sometimes severely overlapping in the images. Therefore, it is still a great challenge to automatically segment each individual leaf from a dense plant canopy for phenotyping. There are three types of segmentation methods commonly used in 3D point clouds, model-based methods, clustering-based methods, and region-growing-based methods. Common model-based methods include Hough transform and random sample consensus (RANSAC). The point clouds of sunflower and sorghum were obtained from a multi-view imaging system, while segmentation and classification were performed using the RANSAC-based segmentation, then segmented leaf area was measured

(Gélaré et al., 2017). The method based on model fitting is not affected by noise and abnormal data but the segmentation quality is greatly affected by the characteristics of the pixels, which is not suitable for large-scale data segmentation. A study used the density-based spatial clustering of applications with noise (DBSCAN) algorithm to cluster the central area points of the leaves of the point cloud of *Ehretia macrophylla*, *crape myrtle* and *Fatsia japonica* trees, obtaining the corresponding central point on the surface of each leaf (Xu et al., 2019). The method based on clustering features is more robust and does not need to find points or areas, however, continuous boundary points cannot be detected by this method and need to be refined after segmentation. Segmentation methods based on region growing are widely used in 3D point cloud segmentation. For instance, the region growing is used to segment leaves from 3D cotton reconstructed by stereo vision (Paprocki et al., 2012) and leaf segmentation on the 3D tulips can be reconstructed by TLS, and the morphological characteristics of the leaves were described (Koma et al., 2018). A study applied facet over-segmentation on the point cloud of ornamental plants in the greenhouse, and single-leaf segmentation was achieved by the facet region growing method (D. Li et al., 2018). Guo and Xu made use of multi-view stereo vision systems to generate point clouds for common crops, and the leaves were segmented by a region growing method based on fully connected conditional random field (Guo and Xu, 2017). Duan et al. proposed a region growing method based on octree search, which segmented the point cloud into data sub-blocks and then refined the incomplete data blocks (Duan et al., 2016). The 3D wheat organs were successfully segmented and the reconstructed phenotypic parameters such as leaf number, leaf height, leaf length, and leaf angle were

extracted from the wheat point cloud. Although the segmentation method based on region growing is simple to implement, it is poor in robustness and calculation time influenced by various evaluation criteria.

Deep learning is proven to be a powerful tool to build models for 3D image processing, such as 3D-R2N2 (Choy et al., 2016), PointNet (Qi et al., 2017), PV-RCNN (Shi et al., 2019), etc. However, it is still at the early stage to apply 3D deep learning to plant phenotyping, and few studies directly utilize CNN to reconstruct or segment 3D images, which main reasons are as follows: 1) Lacking training data with annotation. 3D images of plants are more complex than cities, roads, rooms, etc., so image annotation is expensive and difficult. 2) Lacking available learning material. Currently, there are many oral presentations on 3D deep learning, but systematic explanations and code demonstrations are less, which is unfriendly to researchers who have just learned the rudiments or non-computational professionals. 3) Lacking reliable software or tools. Because 3D images of plants are large, we need more efficient data compression and model optimization algorithms to reduce network training and inference time. In summary, 3D plant phenotyping is a promising and challenging development direction, which requires the joint efforts of researchers.

3.2. Plant stress phenotyping

Plants need to cope with a constantly changing environment, including stressful environments that are not conducive to plant growth and development. These adverse environments include biotic stresses (such as pathogen infection and grazing by herbivores) and abiotic stresses (such as drought, high temperature, cold damage, nutritional deficiencies, salt damage, and toxic metals including aluminum, arsenic, and cadmium in the soil). It will provide opportunities for early intervention to control the spread of infections or change plant management practices before the entire crop becomes infected or damaged. Plant phenotypic changes (such as leaf curl, leaf, and stem color changes, root distribution, etc.) always reflect the type of plant stress and damage. Plant stress phenotyping would provide information for the selection of accession lines with high-stress resistance and guide plant breeding efforts.

In order to improve the study of whole-plant physiological performance and stress phenotyping, more high-throughput and high-resolution automated phenotyping platforms for phenotypic data collection have been widely developed. Depending on the application scenario, phenotyping facilities and systems can generally be classified as controllable-environment-based and field-based platforms (Fig. 6). The former includes XYZ camera movement systems (e.g., Phenovator (Flood et al., 2016)), conveyor scanners (e.g., LemnaTec Scanalyzer 3D (Choudhury et al., 2016)), robotic systems (e.g., Enviratron (Bao et al., 2019), human-like robot (Atefi et al., 2019)). The latter includes fixed frameworks (e.g., cable-suspended systems (Bai et al., 2019), gantry systems (Virlet et al., 2017)) and mobile frameworks (e.g., manually operated carts (Bai et al., 2016; Shafiekhani et al., 2017), tractor-based vehicles (Deery et al., 2014), field robotics (Underwood et al., 2017), unmanned aerial vehicles (Chapman et al., 2014)). Each platform has its own advantages and limitations, so platform design should be combined with specific phenotyping task requirements. For instance, XYZ camera movement systems are characterized by automation, high-throughput, and high precision, but it is not flexible enough and has only one single imaging view (top view, suitable for rosettes). Robotic systems are flexible and multi angle measurement, however, it has lower measurement throughput and requires high accuracy position sensors and tracing algorithms. There are many advantages on tractor-based platforms, including simple design, flexibility, and low-cost. On the other hand, some limiting factors also exist, including compaction in soil and mechanical damage to crops. Unmanned aerial vehicles are portable, low-cost, and suitable for tall crops, but would be limited by measurement duration and accuracy. Fixed field-based frameworks

have high stability and precision, while it is only suitable for a prearranged field, and the construction cost is expensive.

In recent years, many non-invasive imaging techniques have been developed for the detection of plant stress, including visible-light imaging, hyperspectral imaging, multispectral imaging, infrared imaging, and fluorescence imaging. These advanced imaging techniques are integrated on phenotyping platforms to capture multi-modal plant traits. For example, plant sensors onboard NU-Spidercam (Bai et al., 2019) include a four-band RGB-NIR (multispectral) camera, a thermal IR camera, a 3D scanning LiDAR, and a VNIR portable spectrometer. Phenotypic data collection is the first step in plant phenotyping. For high-throughput phenotyping platforms, large amounts of data can be generated in a short time. Therefore, researchers should consider how to quickly analyze high dimensional data and effectively extract phenotypic traits from raw data (Fig. 7).

3.2.1. Plant stress phenotyping based on visible-light imaging

Visible-light imaging is the most direct way to obtain plant images and a large number of plant pictures can be easily collected by digital cameras or smartphones. From the computer vision perspective, plant stress phenotyping based on RGB images can be categorized into the following tasks: image classification, detection, and segmentation (semantic or instance). Plant stress classification is the most basic phenotyping task, which identifies the type of stress and assigns a label to each image. In the early days, traditional image processing and machine learning methods have achieved good results in plant stress classification. People can extract the color features, texture features, or edge features of an image, and then use k-nearest neighbors (KNN), support vector machine (SVM), principal component analysis (PCA), probabilistic neural network, etc. to classify image and finally use cross-validation to evaluate the classification effect (Kadir et al., 2012; Kaur, 2016; Kumar et al., 2011). Recently, some annotated image datasets and challenges for plant stress classification (such as the *Plant Pathology 2020* (<https://www.kaggle.com/c/plant-pathology-2020-fgvc7>), *PlantVillage* (<https://plantvillage.psu.edu/>), etc.) accelerated the evolution of deep learning for stress phenotyping, which even gradually replaces traditional methods (Table 3). Several CNN architectures on the *PlantVillage* dataset achieved accuracies to 99%, such as 99.35% GoogLeNet (Mohanty et al., 2016), 99.66% ResNet-101 (Too et al., 2019). With the development of various open-source deep learning libraries and platforms (PyTorch, TensorFlow, Caffe, Paddlepaddles, Keras, Theno, MXNet, CNTK, etc.), classic CNNs have been implemented using above libraries, so people can quickly develop or train CNN models after annotating their own data. These favorable factors greatly promote the application of CNN in plant stress identification. For example, a study trained and assessed several specific CNN architectures (AlexNet, VGGNet, GoogLeNet), then achieved the best 99.53% accuracy on VGGNet (Ferentinos, 2018). By applying useful training tricks (e.g., transfer learning, hyper-parameter tuning, super-resolution, data augmentation, etc.), the accuracy of CNNs was improved to 93% in plant stress classification and various datasets, far surpassing other methods (Cruz et al., 2017; Ramcharan et al., 2017; Yamamoto et al., 2017).

Compared with image classification, the object detection-based solutions can detect all the lesions in an image, locate each infected region, and count the number of pests and spots (Table 3). There are three representative detection architectures in the field of deep learning, namely Faster RCNN, SSD, and YOLO. These state-of-the-art methods were successfully applied to detect plant stress, locate the region of plant stress in the image, and determine the specific category of each object. For instance, a study utilized Faster RCNN and SSD to detect banana pest and disease symptoms on different parts of the banana plants using real-time field images, which achieved the best detection accuracy of 73.46% on Faster RCNN with ResNet-50 (Selvaraj et al., 2019). Fuentes et al. evaluated three main families of detectors: Faster RCNN, SSD, and region-based fully convolutional network (R-FCN),

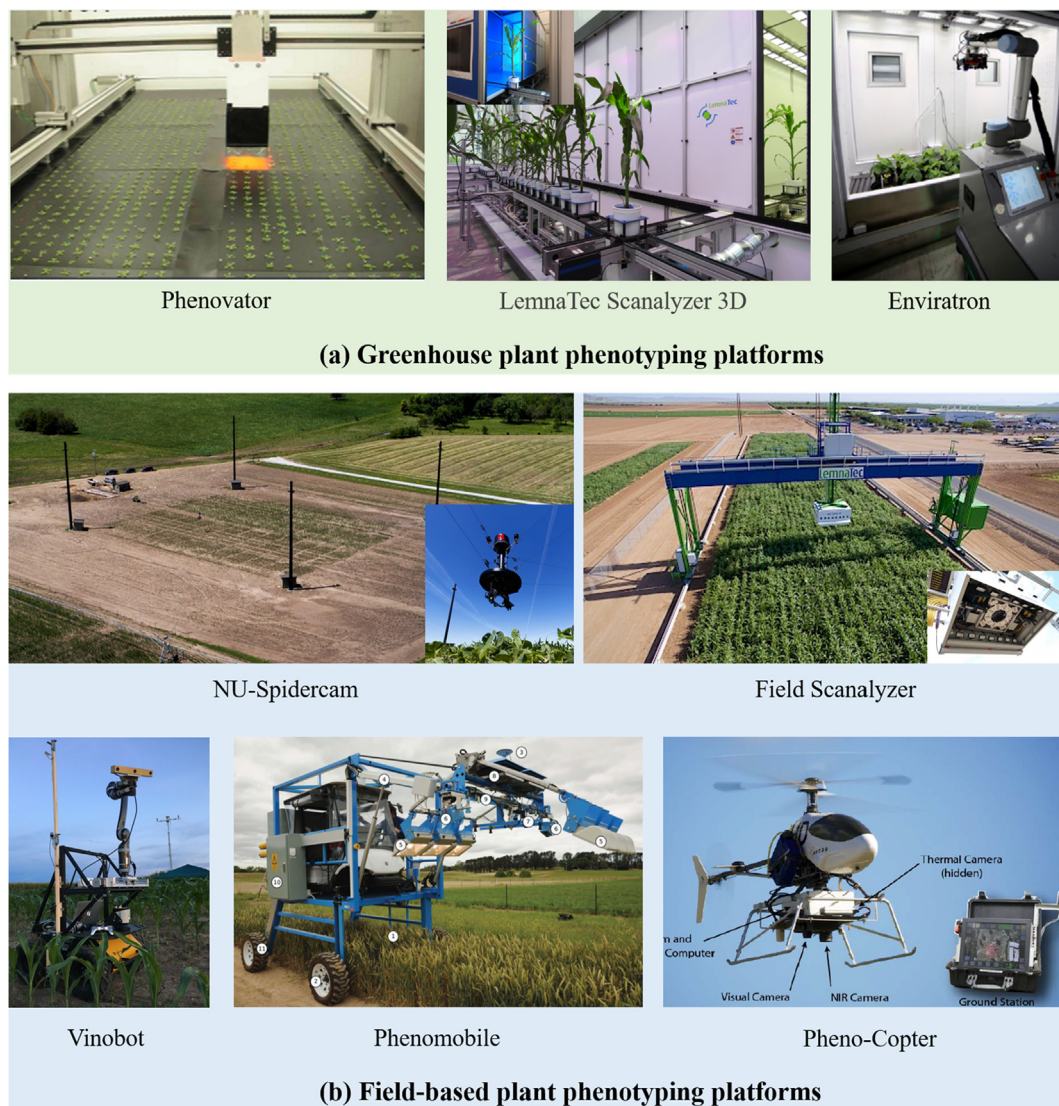


Fig. 6. High-throughput plant phenotyping platforms. (a) Greenhouse plant phenotyping platforms. (b) Field-based plant phenotyping platforms. (a) and (b) were reproduced using figures from (Bai et al., 2019; Bao et al., 2019; Chapman et al., 2014; Choudhury et al., 2016; Deery et al., 2014; Flood et al., 2016; Shafiekhani et al., 2017; Virlet et al., 2017).

which for the purpose of detecting the class and location of diseases in tomato plants (Fuentes et al., 2017). The comparative results demonstrate that R-FCN with ResNet-50 as a feature extractor achieved the best average precision of 85.98%. The segmentation-based solutions could be more useful and straightforward methods to detect stress at the pixel level, which can not only locate the infected area, but also obtain the area and shape of the disease spot (Table 3). Segmentation masks can be used to calculate infected areas and quantify stress severity. A study applied Mask RCNN to detect tomato disease types and segment the locations and shapes of infected areas. In order to obtain more abundant stress traits, detection and segmentation could be effective and important detection for future studies (Wang et al., 2019).

3.2.2. Plant stress phenotyping based on hyperspectral imaging

In addition to visible-light imaging, hyperspectral imaging is also commonly used to extract plant phenotypic information. Hyperspectral imaging can capture plant data in a wider spectral range than RGB imaging to reveal subtle stress differences among cultivars, supplementing RGB images for plant morphological measurement. In general, parametric methods cannot correctly analyze the spectral characteristics of plants under stress, such as simple or multiple regression and

functional statistics. Therefore, nonparametric methods are widely used in the hyperspectral field, including PCA, support vector regression (SVR), partial least squares regression (PLSR), cluster analysis (CA), random forest (RF), and neural network (NN). Researchers usually need to denoise and reduce the dimension for these high-dimensional data before analysis to improve the data processing speed. In the plant phenotyping, dimensionality reduction can save us a lot of time and cost within a certain range of information loss for plant phenotyping. PCA is a commonly multivariate statistical method that can select sensitive wavelengths from a large number of related variables in spectral analysis. Lu et al. performed PCA on 57 spectral indices, and finally obtained 6 principal components for disease detection of tomato leaves at different periods (Lu et al., 2018). Then, KNN was used to classify principal components with a weight coefficient of 1–30, in which the classification accuracy in tomato healthy leaves and diseased leaves is as high as 100%. Nagasubramanian et al. used genetic algorithm (GA) and SVM to select the best band for early identification of soybean anthracnose (Nagasubramanian et al., 2018). The GA-SVM method identified anthracnose in 3 days after inoculation with the rate up to 97% of classification accuracy.

As the most promising hyperspectral data analysis tool, NN has

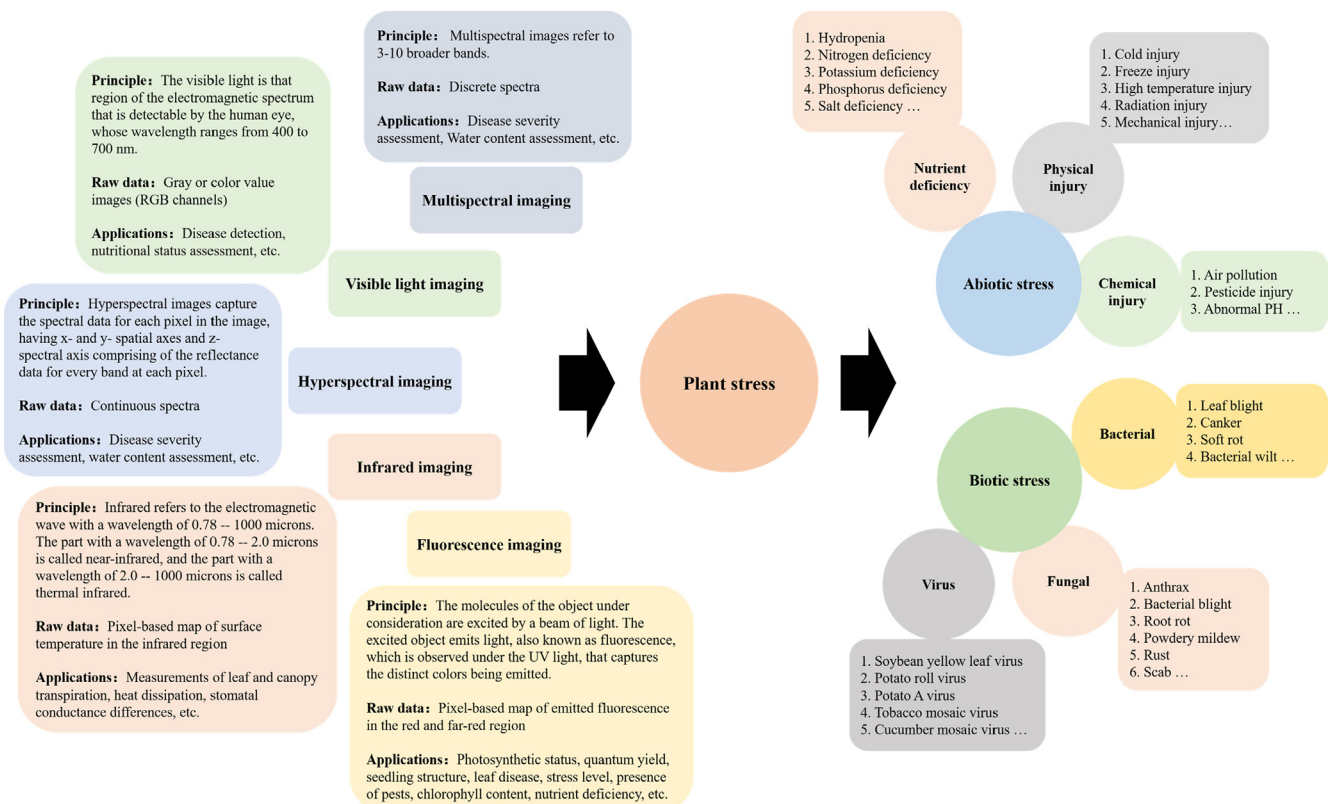


Fig. 7. Summary of plant stress and corresponding imaging techniques.

attracted increasing attention. Zhu et al. used hyperspectral imaging combined with variable selection methods and machine learning classifiers, by which tobacco mosaic virus disease was detected in a short period of time (Zhu et al., 2017). For back propagation neural network (BPNN), extreme learning machine (ELM) and least squares support vector machine (LS-SVM) models, the accuracy is as high as 95%. Jin et al. applied the DCNN classification algorithm to the pixels of the hyperspectral image to accurately identify the fusarium head blight of wheat (Jin et al., 2018). They reconstructed the pixel spectrum data into a two-dimensional data structure and proposed a hybrid neural network classification model with convolutional layers and two-way recurrent layers, showing the result of the accuracy of 74.3% for the entire test dataset. Polder et al. detected virus diseased of potato on hyperspectral images with CNN and obtained reliable precision (78%) and recall (88%) (Polder et al., 2019).

Hyperspectral imaging can not only characterize the spectral variations of field crops under drought stress or disease stress to describe morphological and physiological traits, but also quantify plant biochemical properties. PLSR can be referred as one of the most widely linear modeling techniques for predicting plant traits. Recent study utilized PLSR to predict leaf water content from the extracted plant leaf reflectance spectra (Ge et al., 2016). Ge et al. found that hyperspectral imaging allows the better resolution of water absorption bands, and PLSR modeling is highly efficient in extracting useful spectral information correlated with water content even in the presence of confounding factors and noises, demonstrating that hyperspectral imaging would be a powerful tool for the biochemical properties of entire plants. In addition to estimating water content, the technique can be extended to quantify other plant biochemical phenotypes such as nitrogen content, photo-pigment concentration, and mineral content. Moreover, a further study applied PLSR to accurately model and predict the nutrient concentrations (e.g., nitrogen, phosphorus, potassium, etc.) and water content for maize and soybean plants from their reflectance spectra (Pandey et al., 2017). This research pioneered the use of hyperspectral

imaging to detect the nutrient concentration of living plants in vivo, which is of guiding significance for plant stress phenotyping. It would inspire future studies related to plant stresses and enhance our understanding of plant growth response stresses from various perspective.

4. Challenges and perspectives

4.1. Data collection

(1) Image acquisition. Plant grows in a highly variable natural environment and the imaging is affected by many factors, such as illumination, spatial location, wind, etc. For the above reasons, high-quality imaging of the plant becomes relatively difficult, especially in the root system. Several common solutions of the root imaging show some limitations: a) Non-soil media and optical techniques lack preciseness and cannot completely represent or replace the natural environment. b) Soil media and non-invasive techniques will take a lot of time to scan samples. Besides, imaging instruments are extremely expensive, while fine roots are difficult to image as results of beam hardening and low contrast resolution. c) Soil media and optical techniques (such as root washing and rhizotrons) may cause root damage and lose the spatial distribution of the root. Also, researchers will spend considerable time in experimental preparation and sample post-processing.

(2) Imaging selection. a) 3D imaging. The performance of the 3D image reconstruction method mainly depends on the application scenario, so it's a complicated task to choose the appropriate imaging technology. Researchers should select the most suitable imaging method from these two perspectives: measurement and object. The former includes measurement time, measurement range, point cloud resolution, and cost budget. The latter includes object size, shape, texture, temperature, and accessibility. b) Stress imaging. Visible light imaging only captures changes in the plant structure and pigmentation (VIS, 400–700 nm), so some errors and practical challenges may occur

Table 3
Summary of deep learning methods in plant stress image-based phenotyping.

Vision task	Model	Descriptions	Year	Plant species	Stresses	Reference
Classification	AlexNet	AlexNet is regarded as the pioneer of deep learning. It contains 8 layers: the first five are convolutional layers, some of them followed by max-pooling layers, and the last three are fully connected layers.	2016	Apple & Cherry & Corn, etc 14	Scab & Black rot & Rust, etc 26	(Mohanty et al., 2016)
			2017	Tomato	Spider mites & Mosaic virus & Target spot, etc 9	(Brahimi et al., 2017)
			2018	Soybean	Bacterial blight & Leaf spot & Sudden death syndrome, etc 8	(Ghosal et al., 2018)
	VGGNet	Compared with AlexNet, VGGNet increases network depth (19) by utilizing small-sized (3*3) convolutional filters. In addition, it uses multi-scale training to improve performance.	2017	Apple	Black rot	(Wang et al., 2017)
			2018	Apple & Banana & Cassava, etc 25	Bacterial spot & Black rot & Sigatoka, etc 58	(Ferentinos, 2018)
	GoogLeNet	GoogLeNet applies Inception modules to increase the width and depth of CNNs for improving the capability of feature extraction and representation.	2017	Cassava	Brown streak & Mosaic & Brown leaf spot, etc 5	(Ramcharan et al., 2017)
	ResNet	Residual block and skip connection enable the training of very deep CNNs (152 layers), which can avoid vanishing gradient and network degradation.	2018	Apple	Leaf spot, Mosaic, Rust, Brown spot	(Liu et al., 2018)
			2019	Wheat	Septoria & Tan Spot & Rust	(Picon et al., 2019)
			2019	Apple & Cherry & Corn, etc 14	Scab & Black rot & Cedar rust, etc 26	(Too et al., 2019)
			2019	Apple	Alternaria leaf spot & Brown spot & Mosaic & Grey spot & Rust	(Jiang et al., 2019)
Detection	Faster RCNN	Faster RCNN is a typical two-stage framework to generate ROIs, including backbone, RPN, ROI pooling and fully connected layers.	2017	Tomato	Gray mold & Canker & Leaf mold & Plague & Leaf miner, etc 9	(Fuentes et al., 2017)
			2020	Apple	Black spot	(SARDOĞAN et al., 2020)
	SSD	SSD is a one-stage framework to regress class labels and bounding box coordinates. It allocates different anchor areas and ratios for layers to detect targets of various sizes.	2019	Banana	Wilt & Bunchy top & Black sigatoka, etc 7	(Selvaraj et al., 2019)
	YOLO v3	YOLO v3 is also a one-stage framework that uses DarkNet as the backbone. It applies conv to down-sampling, and uses feature fusion to enhance the accuracy of small target detection.	2019	Column	Pests	(Bhatt et al., 2019)
Segmentation	FCN	FCN is a typical semantic segmentation network. Fully convolutional architecture is used to train and predict classes at the pixel level in an end-to-end way.	2019	Apple	Anthracnose	(Tian et al., 2019)
			2017	Wheat	Powdery mildew & Smut & Black chaff & Stripe rust & Leaf blotch & Leaf rust	(Lu et al., 2017)
	Mask RCNN	Mask RCNN added a new mask branch based on Faster RCNN for instance segmentation.	2020	Tomato	Canker & Gray Mold & Leaf Mold, etc 9	(Nazki et al., 2020)
			2019	Tomato	Rot & Sunscald & Gray mold, etc 10	(Wang et al., 2019)

in stress detection and quantification. The visible can combine near infrared (NIR, 700–1100 nm), shortwave infrared (SWIR, 1100–2500 nm) to increase the coverage of the spectrum (Ge et al., 2019). VIS–NIR–SWIR and hyperspectral imaging are promising methods to describe stress and measure chemical compositions of plants including the water content, dry matter, etc. However, the above methods are still at their beginning stage, which is difficult to effectively establish spectral libraries and collaboratively analyze multi-model data.

3D sensors show great potential for non-invasively measuring, tracking, and quantifying geometric features of plants. Further research should focus on how to best apply 3D image reconstruction techniques to measure all desired parameters and simultaneously overcome the challenges of image processing speed and cost-effectiveness for online applications. In addition, modern high-throughput phenotyping platforms and various imaging technologies have provided researchers with a large number of available images including visible light, fluorescence, near infrared, etc. Combining different imaging technologies, making full use of multi-modal data, and improving image registration will facilitate image segmentation and quantitative trait measurement, while evaluate more accurate and abundant plant phenotypes. In terms of plant phenotyping platforms, low-cost, high-throughput, portable imaging systems and facilities will become an important tool for people to quickly visualize and analyze plant traits.

4.2. Data availability

(1) Image quality. Many studies and competitions used plant image dataset with a single background. For example, the *PlantVillage* dataset contains many labeled plant leaf images from various species with different diseases, but pictures were from the controlled environment and their backgrounds are very simple. However, due to the effects of lighting, occlusion, and shadows in the natural environment, the image quality and visual perception ability will degenerate greatly. In particular, a large number of noises appear in the images, which is a huge challenge for automatically analyzing unconstrained natural images in the field. Although human visual systems can easily deal with these problems, establishing a computational model of plant phenotyping is still an open-ended question.

(2) Image annotation. Deep learning needs to learn features from sufficient annotated data, but data annotation is faced with the following challenges: a) Manual annotation sometimes requires a large amount of prior or professional domain knowledge and rich working experience. b) Data annotation is a time-consuming and laborious process, especially in object detection and image segmentation. Detection and segmentation require instance level (boxes) and pixel level annotations (masks). If lots of images are to be annotated, the workload will be massive, while efficiency and accuracy cannot be guaranteed. c) Some images lack visual cues, such as hyperspectral and thermal imaging, so it is much more difficult to label these data than RGB images.

Several future research suggestions are proposed. Firstly, the dataset should contain images in different scenarios including controlled and field environments to improve the robustness and reliability of the model. In order to discover plant diseases before the symptoms of the plant are obvious, researchers should consider the combination of hyperspectral and RGB images. Moreover, a more accurate algorithm needs to be used to judge the type of stress and calculate the number of pests, which can avoid the misuse and overuse of pesticides, thereby saving costs and preventing secondary damage. Secondly, researchers can apply crowdsourcing or artificial intelligence pre-labeling technology to improve the speed of data annotation, reduce the dependence on manpower, and save labor costs. For example, *Amazon Mechanical Turk* provides commercial services for crowdsourcing annotation to ensure that data annotation gets done quickly and accurately. Google researchers have developed a human–machine collaboration interface

called fluid annotation (Andriluka et al., 2018) that can be used to annotate the class label, delineate the contours of every object and background in an image.

4.3. Data analysis

(1) Algorithm robustness. At present, some mainstream algorithms perform well on particular datasets and most of them are only designed for specific organs or specific plant species. Due to the large differences in color, shape, size and other characteristics between different detection objects, these algorithms do not generalize well. When the dataset changes, many algorithms will be invalid, so researchers must redesign the feature extractor and readjust the hyperparameters. For stress phenotyping, the degree of plant stress changes over time. The model needs to be improved and modified to be dynamically analyzed throughout the entire cycle of stress, which is a challenge for designing a processing framework.

(2) Deep learning. Firstly, deep learning-based algorithms rely on a large number of labeled sample images, which makes it difficult to achieve excellent results in the following three scenarios: a) Training samples do not exist in some object categories. b) There are little samples in object categories. c) The sample size of different categories is extremely imbalanced. Then, some deep learning-based solutions lack prior knowledge that it is difficult to adaptively mine discriminative visual features. Moreover, the deep neural network is used as a “black box”, which cannot perform explicit reasoning and lacks interpretability. As for the problems relying on high-level logical reasoning, such as gene-phenotype association and image description, it's difficult to obtain satisfactory results by simple classification or regression methods. Finally, most of 3D point clouds still are analyzed by utilizing traditional 3D processing methods. Solutions based on deep learning have not been popularized in plant phenotyping.

The following research aspects are worthy of attention in the future. a) Plant images with complex backgrounds require effective segmentation of the foreground and background. Methods based on deep learning are very suitable for image segmentation, but image annotation becomes the major limiting factor for applying deep learning in plant phenotyping. To obviously reduce the requirements of annotated data, the following solutions were proposed and developed: On the one hand, some image generation strategies (e.g., GANs) can be applied to increase image diversity and availability. On the other hand, the dependence of models on data can be reduced by improving algorithms, such as zero sample learning, small sample learning, transfer learning, and so on. b) Most existing deep learning algorithms rely on a large number of labeled images to fit a large number of parameters for prediction, ignoring the prior knowledge of many domain associations and the intuitive understanding of decision-making processes, which limits the interpretation of model functions to a certain extent. c) CNN has a great potential in 3D reconstruction and segmentation. Some approaches by using CNN project 2D segments onto 3D representations or apply to 3D images directly. Thus, a lot of 3D processing work requires to apply CNN architectures to characterize and understand plant phenotypes directly.

5. Conclusion

In this paper, we comprehensively review solutions of plant phenotyping based on computer vision, summarize merits and limitations of imaging technologies and analysis methods from two perspectives of the plant organ and whole plant, and then provide some typical algorithm principles and processing frameworks. Through these studies, we found that image-based plant phenotyping methods show great potential in automatically phenotypic measurement and quantification. In particular, deep learning simplifies the process of extracting phenotypic features and improves plant phenotyping applications greatly.

Plant phenotyping is a complex and difficult task, which not only

needs the support of hardware systems (imaging equipment and phenotyping platforms) to capture raw data, but also the establishment of a multi-domain, multi-level, multi-scale plant phenotypic database. In addition, it is also necessary to develop the trait identification technology system and bioinformatics technology to extract information from massive omics data. In this review, we only focus on extracting phenotypes from images. Phenotyping sources and genetic analysis are still a very tough task. We must work together to solve these problems and further push forward the process. Moreover, we will collaborate with different disciplines to integrate expertise in various fields and provide technically reliable solutions of biological or agronomic significance.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

We wish to acknowledge Dr. Yu Jiang, for his constructive suggestions in the process of paper revision. This work is supported by the Science Program of Hebei "Integration and demonstration of IoT technology for vegetable quality and safety control of facilities" (No. 18047405D), and the Science & Technology Cooperation Program of Hebei "The development and demonstration of the precision control system for the aquatic vegetable planting environment based on the IoT".

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