Potato plant phenotyping and characterisation utilising machine learning techniques: A state-of-the-art review and current trends

by Johnson, C.M., Estrada, J.S. and Auat Cheein, F.

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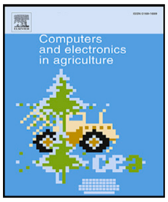

Review article

Potato plant phenotyping and characterisation utilising machine learning techniques: A state-of-the-art review and current trends

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ABSTRACT

Globally, potatoes are the fourth most produced food crop, and in the United Kingdom alone, they generated approximately £705 million in 2022. However, to achieve the United Nations (UN) Sustainable Development Goals (SDG), potato farmers need to sustainably increase yields to address the growing demand for both food and land. Crop yield can be affected by various factors, including disease, pests, and nutrient deficiencies. To tackle these challenges and optimise yields, researchers have leveraged remote sensing platforms for high-throughput non-destructive phenotyping. Data collected from these platforms can be used to develop machine learning (ML) models aimed at addressing the aforementioned issues. To summarise recent developments in ML models applied to potato plant phenotyping, a systematic review of journal articles from the last seven years was conducted. This review underscored the advantages of Deep Learning (DL) approaches and the rising trend of Convolutional Neural Network (CNN)-based architectures, while also noting the limited availability of data for training these models. This review is intended to benefit researchers and farmers by providing an up-to-date review of ML models in potato plant phenotyping.

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1. Introduction

Potatoes, as globally the fourth most produced food crop and the most produced non-cereal crop, will play a crucial role in feeding the world's growing population (Zhang et al., 2017). According to the United Nations (UN), the global population is projected to rise from 8.2 billion to 10.3 billion by the mid-2080s (United Nations Department of Economic and Social Affairs, Population Division, 2024). The combination of an increasingly unstable climate, limited land availability, and rising food demand requires farmers to optimise their yields while minimising environmental impact (Davies et al., 2009). This objective aligns with the UN Sustainable Development Goals (SDG). However, despite advancements in precision agriculture, actual crop yield is 20%–50% lower than potential yield (Prikaziuk et al., 2022).

To address these challenges, researchers are investigating various multidisciplinary approaches to maximise yield while reducing the environmental footprint of agriculture. One such approach is high-throughput, non-destructive phenotyping using remote sensing (Yang et al., 2017). The phenotype is the observable characteristics of an organism, and can be represented as the combination of the organisms genetics and its environment. High-throughput phenotyping, combined with Machine Learning (ML) algorithms, can offer valuable insights to farmers regarding the current health of their crops (Sheikh et al., 2024). This article explores modern phenotyping techniques and their application to the potato plant, as well as how researchers are leveraging remote sensing and ML to address various phenotyping applications.

A total of 100 journal articles were selected for this review from the Scopus Database, focusing on publications from the last seven years. These articles were identified through three Scopus keyword searches: "potato AND (phenotype OR phenotyping)", "potato AND (sense OR sensing)", and "potato AND (monitor OR monitoring)". The combined results were then filtered to include only articles addressing in-situ potato plant phenotyping using ML, excluding the majority of lab-based studies to provide readers with practical, in-field case studies. Articles focusing on potato tuber phenotyping rather than the plant were also excluded. The remaining articles were categorised into themes corresponding to the phenotyping tasks discussed in this review. From these themes, 100 articles were selected based on the models and methods employed, ensuring a balanced representation of each thematic category.

This review is organised as follows: Section 2 introduces phenotyping, its applications, and its challenges. Section 3 addresses the challenges surrounding potato plant phenotyping data, and Section 4 discusses the most common input features used in phenotyping models. Section 5 reviews shallow ML models employed for various potato plant phenotyping tasks, while Section 6, explores how Deep Learning (DL) models can further enhance performance in these tasks. Finally, Section 7 provides an insightful discussion and outlines potential future work, while Section 8 offers a conclusion based on the findings of this review. Fig. 1 presents an overview of the topics covered in this work.

2. Potato plant phenotyping applications

A plant's phenotype refers to its measurable characteristics, which result from the interaction between its genome and its environment (Fasoula et al., 2020). These characteristics, or traits, offer valuable insights into the plant's health, particularly in relation to biotic and abiotic stresses (Estrada et al., 2023). By examining the use of ML across various applications, this review aims to provide a more holistic view on potato plant health estimation. Fig. 2 summarises the phenotyping applications covered in this review. As shown in the diagram, disease detection is the most extensively researched phenotyping application, accounting for 29.4% of the articles, followed by yield prediction at 10.3%, and canopy assessment at 9.52%.

2.1. Biotic stress assessment

The most extensively researched phenotyping task in the reviewed literature is potato plant disease detection. This emphasis may stem from the fact that 16% of the estimated global annual crop yield is lost due to crop disease (Rashid et al., 2021), which in turn is responsible for 70—80% of global crop losses (Sharma et al., 2021). Traditionally, disease detection has been a labour-intensive task, carried out through visual inspections by farmers and experts. However, this method is prone to errors due to the variability in biological and physiological responses to infection across different cultivars (Gold et al., 2020b; Franceschini et al., 2019) and geographic location (Rashid et al., 2021; Wani et al., 2022). Moreover, plant pathologists often disagree on disease detection and severity estimation when annotating data (Mandal et al., 2023). Even when consensus is reached, some DL models can accurately classify disease patches that are missed by expert annotators (Johnson et al., 2021).

Currently, Convolutional Neural Network (CNN)-based architectures represent the state-of-the-art in disease detection (Sinshaw et al., 2022; Wani et al., 2022). Many potato leaves remain asymptomatic until advanced stages of infection. For example, Qi et al. (2023) found that up until the 12th day no lesions could be identified by the naked eye. However, asymptomatic disease detection can be achieved by building ML (Gold et al., 2020a,b) and DL (Qi et al., 2023) models that utilise the spectral reflectance in the infrared region. During early infection stages, the wavelengths of importance reside around 1000 nm and 2400 nm, with reflectance in these ranges intensifying during later infection stages. However, significant variation exists in disease response across cultivars in the early stages of infection, while greater similarity appears in later stages (Gold et al., 2020b). Therefore, it is essential to use a diverse range of cultivars in early disease detection experiments.

Once a disease is detected in the plant, estimating its severity becomes crucial. This can be done by monitoring changes in the leaf's spectral reflectance and distortions in its shape. Classification and segmentation models are commonly used to estimate disease severity (Mandal et al., 2023; Dai et al., 2022; Gao et al., 2021b). Fig. 3 highlights the most common diseases studied in this review: Potato

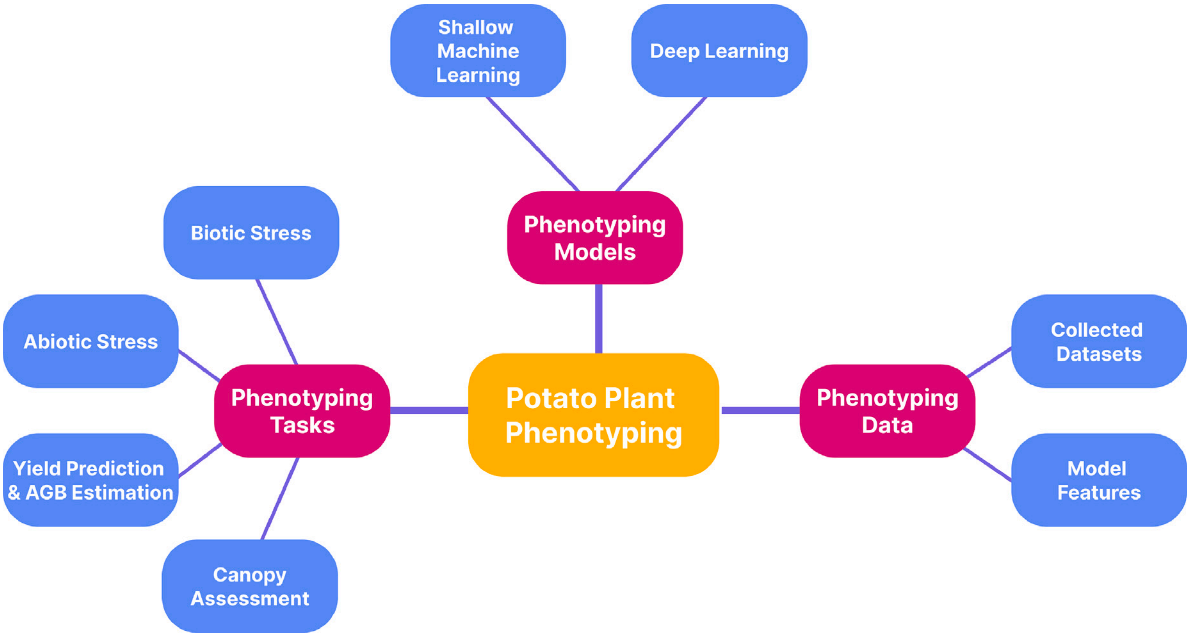

Fig. 1. The organisation and topics in this review article on potato plant phenotyping and characterisation using ML techniques.

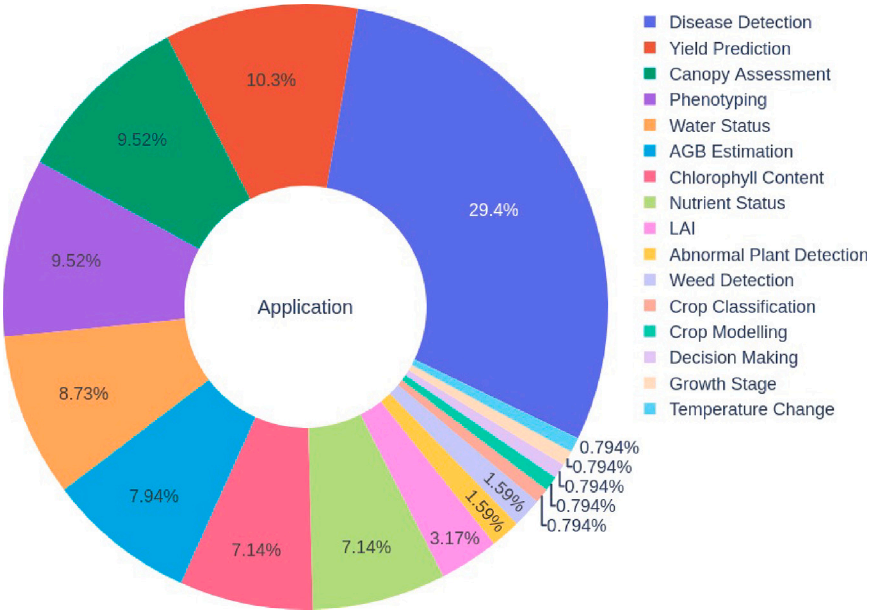

Fig. 2. The percentage of journal articles focusing on each phenotyping application, according to the literature review.

Early Blight (PEB), Potato Late Blight (PLB), Phoma Blight, Potato Virus Y (PVY) and Verticillium Wilt (VW). While Fig. 4 displays examples of PEB, PLB and healthy potato leaves in the field.

2.2. *Abiotic stress assessment*

Climate change has led to longer, more frequent and severe droughts, putting food security at risk (Aneley et al., 2022). Although potatoes are among the most water-efficient crops, producing the highest number of calories per unit of water (Elsayed et al., 2021), they are highly sensitive to water (Sun et al., 2022; Musse et al., 2021; Elsayed et al., 2021) and nutrient (Yang et al., 2021) stress due to their shallow root systems. This shallow root system, combined with the common practice of planting in coarse soil, results in poor nitrogen use efficiency (Sun et al., 2022). As a consequence, farmers often apply excessive amounts of nitrogen, which not only increases costs but also has harmful effects on the crop and the environment (Yang et al., 2021; Alkhaled et al., 2023). Water stress can also reduce the crop's photosynthetic rate and nutrient uptake (Duarte-Carvajalino et al., 2021; Elsayed et al., 2021; Peng et al., 2021a), ultimately leading to reduced yields (Romero et al., 2017; Aneley et al., 2022). Fortunately, water stress can be detected the same day as the onset of stress (Duarte-Carvajalino et al., 2021). Given the water sensitivity of potato plants, it is important to monitor them for signs of water stress and to provide remedial actions, such as irrigation, when necessary.

Reducing the impact of drought on potato crops can also be achieved through breeding programs. The main bottleneck in these programs is the time required for phenotyping (Aneley et al., 2022), as researchers need to test each crop under a range of drought conditions (Li

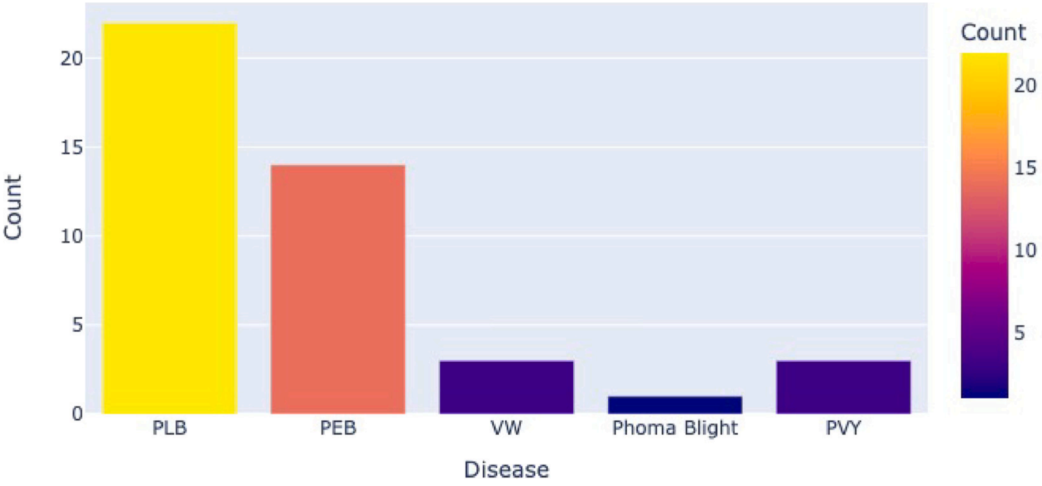

Fig. 3. The number of journal articles in the review focused on each potato plant disease. In this figure, the following diseases are displayed: Potato Late Blight (PLB), Potato Early Blight (PEB), Verticillium Wilt (VW), Phoma Blight, and Potato Virus Y (PVY).

Fig. 4. This figure shows in the left image healthy potato leaves, in the middle potato early blight, and on the right potato late blight.
Source: This figure has been taken from Li et al. (2022).

et al., 2019a). To address this bottleneck, researchers have explored using canopy traits to determine drought tolerance (Aneley et al., 2022). Traits such as yield stability (Aneley et al., 2022), stability of leaf greenness, senescence delay (Li et al., 2019a), and leaf mass (Boguszewska-Mańkowska et al., 2022) are all indicators of a crop's drought tolerance. In contrast, when determining the nutritional requirements of different cultivars, researchers use foliar ionomes (Coulibali et al., 2020). While crop traits and nutritional requirements are cultivar-specific (Liu et al., 2021; Alkhaled et al., 2023), grouping new cultivars into ionomic groups can reduce costs associated with expensive fertiliser trials (Coulibali et al., 2020).

2.3. *Yield prediction and above ground biomass estimation*

Accurate yield predictions at early growth stages could help mitigate food insecurity by enabling all stakeholders in the potato production pipeline to plan more effectively (Kuradusenge et al., 2023). The difficulty in potato yield prediction arises from the fact that the potato crop grows underground. As a result, researchers often focus on a related task, above-ground biomass (AGB) estimation, which serves as a proxy for yield (Li et al., 2020b). Yield and AGB can be influenced by factors such as planting density (Mhango et al., 2021), irrigation, and fertilisation schedules (Peng et al., 2021b). Therefore, it is crucial to vary these parameters during experiments aimed at AGB estimation and yield prediction. These tasks are commonly approached in research using UAVs to collect spectral measurements (Liu et al., 2022d; Li et al., 2020b, 2021b; Mhango et al., 2022). Using spectral data for these tasks presents challenges because the wavelengths of importance vary across growth stages (Yang et al., 2021). Additionally, temporal challenges arise when estimating AGB after canopy closure due to issues such as occlusion (Yang et al., 2023), which often leads to models underestimating AGB (Luo et al., 2022). Crop height is a commonly used feature to aid in AGB estimation (Sun et al., 2022; Li et al., 2020b; Luo et al., 2022; Liu et al., 2022b), as the height of the main stem contributes significantly to the AGB, making these values likely to be correlated (Liu et al., 2022e).

2.4. *Canopy assessment*

Canopy assessment plays a crucial role in every phenotypic task discussed in this section since the potato crop grows underground. Potato emergence rate, uniformity and canopy cover are well-researched topics as they significantly influence field management (Sun et al., 2022; Li et al., 2019b). Researchers rely on various parameters for phenotyping, with canopy characteristics being the most common (Colwell et al., 2021; Abdelbaki et al., 2021). Canopy architecture, for example, affects light interception and the plant's overall functioning (Colwell et al., 2021). When assessing canopy characteristics, it is important to account for genotype and environmental variations, as both have been shown to influence traits such as emergence rate and canopy coverage (Li et al., 2019b). Additionally, these canopy traits can be affected by other factors, including seed quality and nutrient deficiencies (Sun et al., 2022).

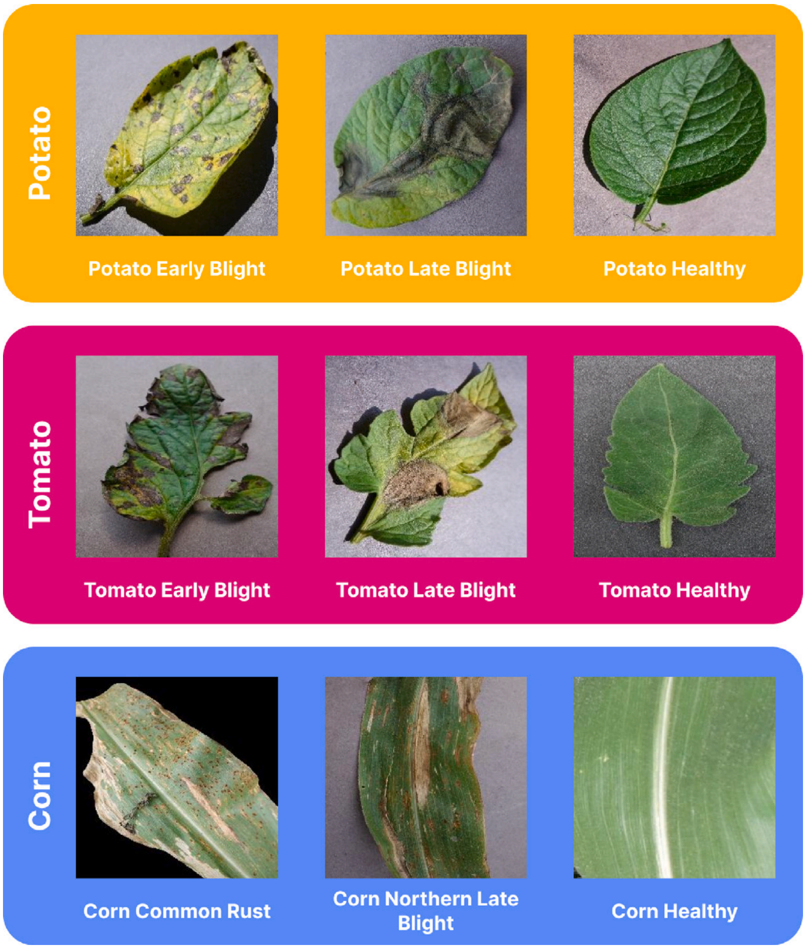

Fig. 5. Example images taken from the PlantVillage dataset collected by Hughes and Salathé (2015).

3. Potato datasets

One of the major challenges in developing ML models for potato phenotyping is the lack of task-specific public datasets. Since phenotyping is influenced by both environmental conditions and genotype variations, datasets should be sufficiently diverse to capture these factors. Researchers have observed regional (Dai et al., 2022; Rashid et al., 2021) and cultivar differences (Gold et al., 2020b; Sinshaw et al., 2022) in disease detection, prompting many to collect their own datasets tailored to specific environments and genotypes. Some of these datasets are listed in Table 1.

Table 1 provides a subset of datasets used for potato phenotyping tasks. One noteworthy example is the PlantVillage dataset, collected by Hughes and Salathé (Hughes and Salathé, 2015) in the USA and Switzerland. This dataset contains RGB images of diseased plant leaves from 14 different crops, captured in a lab-based environment. It has been widely used for disease detection, classification, and segmentation tasks (Saleem et al., 2022; Ikeda et al., 2021; Gold et al., 2020a,b; Sharma et al., 2021; Belgiu et al., 2021; Van De Vijver et al., 2022). Fig. 5 shows examples of images from this dataset. The main advantage of the PlantVillage dataset is its standardisation (Lamba et al., 2022; Saleem et al., 2022; Ikeda et al., 2021), which allows researchers to compare model performance and establish benchmarks for state-of-the-art models.

Various remote sensing platforms and sensors have been used in the reviewed articles to collect these datasets. Since previous reviews regarding potato plant phenotyping have covered the types, advantages, and disadvantages of each well, see Sun et al. (2022) and Gao et al. (2021a), this review will simply provide an update. Fig. 6 shows the distribution of remote sensing platforms across the reviewed articles. With ground-based remote sensing being the most prolific followed by UAV

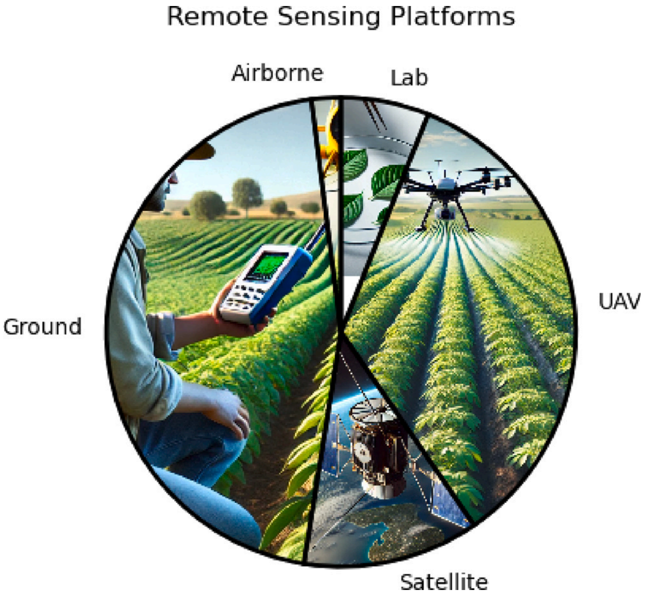

Fig. 6. Different remote sensing platforms used in the review alongside the number of lab-based phenotyping articles, most of which use the PlantVillage dataset.

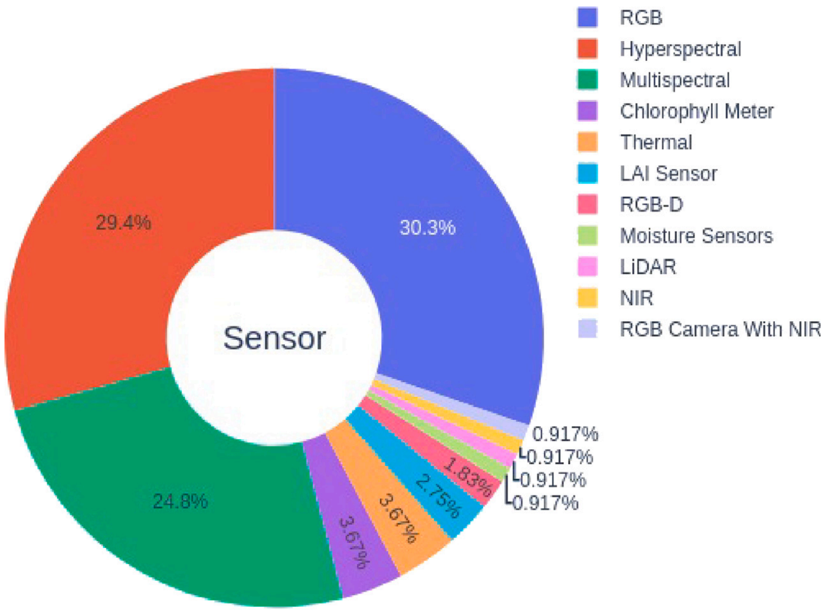

Fig. 7. The percentage of journal articles that used each sensor to perform potato plant phenotyping, according to the literature review.

and then satellite. Fig. 7 shows the distribution of sensors across the reviewed articles, while Fig. 8 shows the combinations of phenotyping tasks and sensors. The top three sensors used in the reviewed articles in order are RGB, hyperspectral and multispectral. However, this is largely task dependent as phenotyping tasks such as yield prediction and AGB estimation favour multispectral and hyperspectral cameras over RGB cameras.

3.1. Data augmentation

Data augmentation is used to artificially increase the number of samples for training ML models and has been shown to improve performance (Gold et al., 2020a; Rashid et al., 2021). The data augmentation methods used in ML articles, to overcome the lack of data, vary from simple image manipulation to Generative Adversarial Networks (GANs). Common image manipulation methods include rotation (Shoaib et al., 2022; Anim-Ayeko et al., 2023; Zhao et al., 2022b; Khan et al., 2020; Li et al., 2022; Rashid et al., 2021; Polder et al., 2019; Dai et al., 2022; Butte et al., 2021), scaling (Shoaib et al., 2022; Zhao et al., 2022b; Gao et al., 2021b; Li et al., 2022; Dai et al., 2022), blurring (Anim-Ayeko et al., 2023; Khan et al., 2020; Rashid et al., 2021), cropping (Shoaib et al., 2022; Anim-Ayeko et al., 2023; Gao et al., 2021b; Butte et al., 2021), flipping (both horizontal and vertical) (Gao et al., 2021b; Khan et al., 2020; Rashid et al., 2021; Polder et al., 2019), and colour alteration (Shoaib et al., 2022). These methods introduce noise into the images, simulating the variability that would naturally occur in the field. Many researchers apply random augmentation values within plausible ranges to maintain the realism of the data (Li et al., 2022; Rashid et al., 2021).

Data augmentation has also been achieved in the review by two DL models: GANs (Lamba et al., 2022) and Neural Style Transfer (NST) (Shoaib et al., 2022). GANs employ two networks: a generator and a discriminator. The generator adds noise to the data in an attempt to create realistic samples, while the discriminator distinguishes between real and generated data. By setting the two networks against each other, the resulting data produced by the generator can be realistic enough to use as training data (Shoaib et al., 2022). NST, on the other hand, works by combining two images, a content image and a style image, producing the content image in the style of the other image. Both GANs and NST have been applied to disease detection tasks, particularly in training models using the PlantVillage dataset (Lamba et al., 2022; Shoaib et al., 2022).

3.2. Data preprocessing

Data preprocessing can significantly enhance the performance, generalisability, and robustness of ML models (Van De Vijver et al., 2020; Liu et al., 2021). Preprocessing involves cleaning the data by removing, altering, and filling in missing values (Apat et al., 2022). The main goal of preprocessing is to reduce noise that could impair model performance, such as segmenting plant information from background interference (Aneley et al., 2022; Elsayed et al., 2021). Common noise-reduction techniques include Savitzky–Golay smoothing, often used to minimise baseline drift (Van De Vijver et al., 2020; Appeltans et al., 2021; Zhao et al., 2022a; Liu et al., 2021, 2022d); background removal using manual masking of soil and weeds (Abdelbaki et al., 2021) or Otsu thresholding (Li et al., 2020b, 2019b); geometric, radiometric, and atmospheric calibration for UAV and satellite data (Liu et al., 2021; Li et al., 2021a; Qi et al., 2023); and trimming the highest and lowest regions of hyperspectral data (Appeltans et al., 2021) to account for the fingerprint spectrum phenomenon (Liu et al., 2020).

This review supports the findings of Wani et al. (2022), confirming that the most widely used preprocessing method in plant disease detection is the conversion of RGB images to HSV colour space, as it is akin to human vision (Lazarević et al., 2022; Elsayed et al., 2021; Johnson et al., 2021). However, Johnson et al. (2021) tested the ability of five colour spaces in the detection of disease patches and infected leaves, and found HSL to be superior to HSV. This article also concluded that the correct choice of colour space can improve both performance and inference time.

4. Model features

Not all data collected contributes effectively to accomplishing the desired phenological task. Certain data will introduce noise, hindering the ML model's ability to identify patterns and learn to perform the task accurately. As a result, only beneficial features must be used during model training. This section will briefly discuss the three main categories of features encountered during the review: spectral, spatial, and textural. Finally, this section concludes with the methods used to perform feature selection.

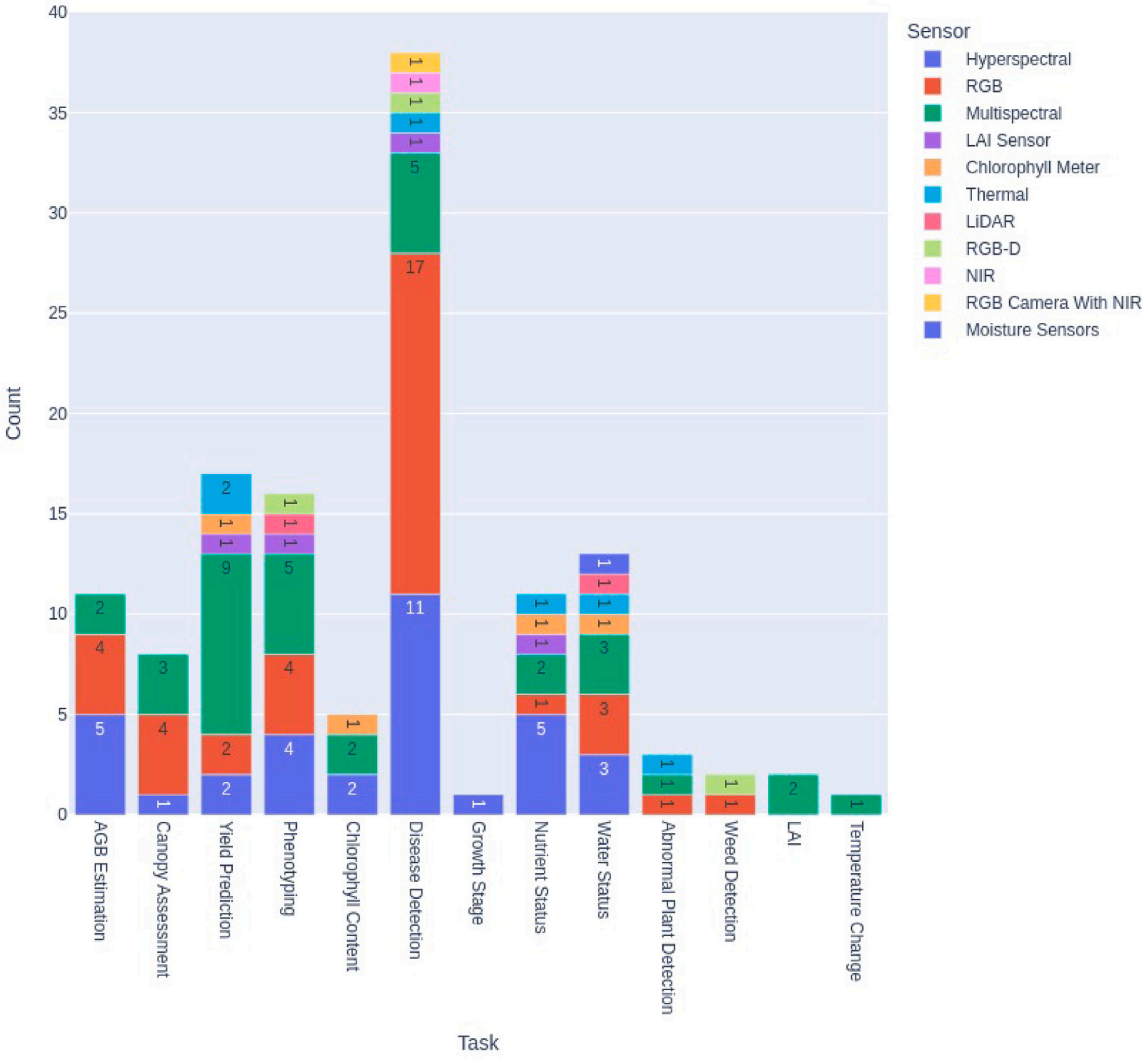

Fig. 8. Phenotyping task on the *x*-axis and the number of articles focusing on each task is included on the *y*-axis, which is also further broken down by sensor type. The task breakdown varies from Fig. 2 as some papers use multiple sensors.

4.1. Spectral features

Vegetation Indices (VIs), or Spectral Indices (SIs), are transformations of two or more spectral bands used to represent certain vegetative properties or characteristics. VIs have been used in disease identification (Duarte-Carvajalino et al., 2018), phenotyping (Romero et al., 2017), and nitrogen status estimation (Liu et al., 2021; Peng et al., 2021a). They can reduce interference from factors such as soil, illumination, and atmospheric conditions (Li et al., 2020a), through methods like relative VIs (Luo et al., 2020).

VIs are widely studied, especially in yield prediction and AGB estimation (Li et al., 2020b; Liu et al., 2022e,b; Li et al., 2021b; Mukiibi et al., 2024). Most studies rely on well-established VIs (Li et al., 2020a; Liu et al., 2022d,a), while some optimise or create new VIs (Yang et al., 2021). For example, Pasqualotto et al. (2018) proposed new VIs to estimate Canopy Water Content (CWC), leading to the creation of the Water Absorption Area Index (WAAI) and the Depth Water Index (DWI). Other spectral features used in AGB estimation include spectral-position features, such as the absorption valley depth, width, and area (Liu et al., 2022d). Some articles even attempt to utilise the full spectrum of information for AGB estimation; however, this approach has not yet shown improvements in performance (Yang et al., 2021; Li et al., 2020b). Feature selection plays a critical role in improving the robustness of AGB estimation models, but the method used to select these features significantly impacts their effectiveness. For instance, Luo et al. (2022) found that RReliefF selected features based on their correlation with the AGB value, whereas RF-OOB selected complementary features that reduced the underestimation of AGB caused by the growth stage effect. This underscores the importance of selecting the most relevant spectral data for accurate AGB estimation.

VI have demonstrated excellent performance in AGB estimation, even outperforming features such as crop height (Li et al., 2020b). However, they do have some serious shortcomings. VIs experience spectral saturation under high canopy coverage when the AGB is large due to the growth stage effect (Liu et al., 2022b,c). Additionally, the correlation between AGB and VIs fluctuates with the growth stage, increasing and then decreasing with maturity (Liu et al., 2022a). Furthermore, no single VI performs consistently well across all growth stages (Liu et al., 2022e). To mitigate these shortcomings, combining spectral information with other features often proves beneficial.

4.2. Spatial features

Crop height can be calculated by subtracting the ground Digital Elevation Model from a Digital Surface Model (Sun et al., 2022;

Table 1
A subset of the datasets collected and used in the review. In the Dataset column '–' means the article did not name the dataset they collected. The data points column pertains to only potato data points. And '–' in the Data Points column means the number of potato data points is not provided in the article.

Dataset	Paper	Task	Data points
PlantVillage	Ahmad et al. (2020), Anim-Ayeko et al. (2023) and Lamba et al. (2022)	Disease	2152
NZDLPlantDisease-v2	Saleem et al. (2022)	Disease	–
NZDLPlantDisease-v1	Saleem et al. (2022)	Disease	–
DeepWeeds	Saleem et al. (2022)	Weeds	–
PBD-IM	Dai et al. (2022)	Disease	4546
–	Duarte-Carvajalino et al. (2018)	Disease	748,071
–	Gold et al. (2020a)	Disease	2039
–	Gold et al. (2020b)	Disease	1330
–	Fenu and Malloci (2021)	Disease	1074
PLD	Rashid et al. (2021)	Disease	4062
Tarnab farm data	Khan et al. (2020)	Disease	5652
–	Mhango et al. (2021)	Plant Density	828,000
–	Yang et al. (2023)	AGB estimation	2000
–	Mandal et al. (2023)	Disease	1000
–	Johnson et al. (2021)	Disease	1840
–	Van De Vijver et al. (2020)	Disease	1500*
–	Butte et al. (2021)	Water status	1560
–	Abbas et al. (2020)	Tuber Yield	479
–	Abdelbaki et al. (2021)	Canopy Characteristics	–
–	Abukmeil et al. (2022)	Chemical Composition	4800
–	Afzaal et al. (2021)	Disease	5199
–	Appeltans et al. (2021)	Disease	–
–	Coulibali et al. (2020)	Yield/chemical composition	–
–	Couture et al. (2018)	Disease	–
–	d'Andrimont et al. (2022)	Classification + Phenological stage	–
–	Duarte-Carvajalino et al. (2021)	Water Stress	116
–	Fernández et al. (2020)	Disease	225
–	Franceschini et al. (2017)	Disease	–
–	Gao et al. (2021b)	Disease	2100
–	Gómez et al. (2019)	Yield Prediction	44
–	Griffel et al. (2018)	Disease	242
–	Leon et al. (2021)	Disease/Water Status	–
–	Li et al. (2019b)	Canopy Characteristics	473
–	Li et al. (2022)	Disease	500
–	Liu et al. (2020)	Chlorophyll/Growth stage	314
–	Liu et al. (2022e)	AGB estimation	144
–	Lizarazo et al. (2023)	Disease	200
–	Mhango et al. (2022)	Count stem number	500
–	Pipia et al. (2019)	LAI estimation	97

Franceschini et al., 2017; Luo et al., 2022), with LiDAR being the most accurate sensor for measuring crop height (Sun et al., 2022). Crop height generally peaks at the tuber bulking stage, followed by a decrease until it reaches senescence (Liu et al., 2022e), and is impacted by factors such as weeds (Colwell et al., 2021), temperature, cultivar (Lazarević et al., 2022), and severe water stress (Musse et al., 2021). Crop height is an important and frequently used feature in AGB estimation (Sun et al., 2022; Li et al., 2020b; Luo et al., 2022; Liu et al., 2022b), as it is correlated with AGB (Liu et al., 2022e,c; Mourad et al., 2020). This correlation arises because the height of the main stem accounts for the majority of the plant's AGB (Liu et al., 2022e). In addition, combining crop height with multi-resolution texture features has been used successfully to address the underestimation issue caused by the growth stage effect when using VIs for AGB estimation (Liu et al., 2022c).

Yield is also influenced by various factors, prompting researchers to incorporate additional features to improve model predictions. For instance, yield is impacted by soil moisture content (SMC) (Paudel et al., 2021), therefore an increased ground slope has been shown to negatively impact yield, thus researchers use it as a feature for yield prediction (Abbas et al., 2020). SMC can also be impacted by leaf traits, such as leaf area and average leaf angle, increasing temperatures can reduce both of these leaf traits, resulting in an increase in light penetration and a reduction in SMC, making these traits useful features for yield prediction (Lazarević et al., 2022).

4.3. Textural features

Texture features are often used to enhance model performance across multiple growth stages (Liu et al., 2022e,c), addressing limitations commonly encountered with spectral features like VIs (Liu et al., 2022c; Li et al., 2021b; Liu et al., 2022b). The two most frequently used types of texture features in the review are grey-level co-occurrence matrix (GLCM) (Yang et al., 2022; Liu et al., 2022e) and Gabor-based approaches (Liu et al., 2022c).

4.4. Feature selection

Feature selection can significantly improve model performance compared to models that utilise all available variables (Gómez et al., 2019), as not all variables contribute positively to the target task (Qi et al., 2023). Identifying the variables that capture the most variation in the target value is often an effective approach for feature selection. In the review, variance and feature importance were assessed using methods such as Principal Component Analysis (PCA) (Franceschini et al., 2019), Variable Importance Projection (Zhou et al., 2022), Stepwise Multiple Linear Regression (SMLR) (Elsayed et al., 2021), and the mean decrease in impurity and accuracy (Li et al., 2021b). Feature selection can also reduce storage and computational complexity, which can be a problem in plant phenotyping. For example, Appeltans et al.

(2021) demonstrated that by reducing the number of spectral bands in their model from 174 to just 2, they could significantly decrease storage complexity with only a slight reduction in classification accuracy, from 99.83% to 99.48%.

In AGB estimation, one of the most effective feature selection methods identified was RReliefF (Li et al., 2020b; Luo et al., 2022). Feature selection not only improved model performance but also enhanced model robustness (Luo et al., 2022). Other noteworthy feature selection methods include SIFT and FLANN (Franceschini et al., 2019), WR Sum Test (Apat et al., 2022), Recursive Feature Elimination (Yang et al., 2022), Continuous Wavelet Transforms (CWT) (Zhao et al., 2022a; Liu et al., 2020), Moving Window Partial Least Squares (MWPLS) (Liu et al., 2022d), Monte Carlo Uninformative-Variable Elimination (MC-UVE) (Liu et al., 2022d), and Random Leapfrog (Liu et al., 2022d, 2020).

5. Machine learning models

ML is an umbrella term that encompasses a variety of statistical models. There are four types of ML models: supervised, semi-supervised, unsupervised and reinforcement learning. This review focuses on supervised and unsupervised models, as they are the most prolific in the literature. Additionally, this review distinguishes between shallow ML models and DL models, with this section exploring the application of shallow ML models in potato plant phenotyping. For a more comprehensive subset of the ML models deployed across different phenotyping tasks, please refer to Appendix.

5.1. Supervised learning

Supervised learning algorithms utilise labelled data to detect patterns and predict desired outcomes. These algorithms encompass a wide range of models, including regression and classification. Regression models have been applied to tasks such as nitrogen status estimation (Zhou et al., 2022; Alkhaled et al., 2023) and yield prediction (Kuradusenge et al., 2023). Alkhaled et al. (2023) categorise regression models into parametric and nonparametric regression models. Nonparametric models are further divided into linear and nonlinear approaches. Linear nonparametric regression includes methods like PCA, PLSR, OLSR, PCR, and MLR, while nonlinear nonparametric regression contains SVR, GPR, RF, and ANN. Their study reports that 58% of research focuses on parametric regression, 22% on nonlinear nonparametric regression, and 20% on linear nonparametric regression.

A common linear nonparametric regression model used in potato plant phenotyping is Partial Least Square Regression (PLSR), which typically utilises the full spectrum of data without feature selection (Li et al., 2020a; Liu et al., 2021; Li et al., 2020b). In this review, PLSR has performed well in tasks such as chlorophyll content estimation (Li et al., 2020a), nitrogen concentration estimation (Liu et al., 2021), and AGB estimation (Liu et al., 2022d). However, Random Forest (RF) has outperformed the PLSR model in both yield prediction (Li et al., 2020b) and AGB estimation (Luo et al., 2022; Li et al., 2020b). RF can also be used for classification tasks, such as grouping cultivars into low- or high-yield productivity classes (Coulibali et al., 2020). Despite its strengths, RF performance declines when data is scarce (Liu et al., 2022b). A related approach often used in phenotyping is gradient boosting decision trees (GBDT) (Boguszewska-Mańkowska et al., 2022; Duarte-Carvajalino et al., 2021; Paudel et al., 2021). Both RF and GBDT are examples of ensemble models.

Support Vector Machine (SVM) is another versatile model that can be used for both classification and regression, including tasks like growth stage classification (Liu et al., 2020) and yield prediction (Abbas et al., 2020; Li et al., 2021b). Li et al. (2021b) used SVM to predict yield from UAV-based multispectral images and cultivar information, outperforming their RF regression model in this case. However, SVMs struggles with unbalanced datasets. To address this, Griffel et al. (2018) implemented a class-weighted SVM to improve PVY detection using hyperspectral spectroradiometer data. They tested weights ranging from 0.2 to 1 and found that a class weight of 0.8 produced the best performance with visible spectrum data.

One of the key challenges in classification tasks is determining the appropriate number of classes. Typically, in this review, reducing the number of classes improves model performance (Leon et al., 2021; Van De Vijver et al., 2020; Johnson et al., 2021). Most experiments attempt a two class problem, distinguishing diseased leaves from healthy ones (Khan et al., 2020; Afzaal et al., 2021; Van De Vijver et al., 2020). A notable exception is Johnson et al. (2021), who differentiated between the potato blight and background classes. After two class experiments, class designations depend on the task. For example, Afzaal et al. (2021) conducted experiments with two, four, and six classes to classify diseased and healthy leaves based on growth stages. Johnson et al. (2021) used a four class system, categorising images as blight disease patches, infected leaves, healthy leaves, or background. Van De Vijver et al. (2020) conducted a three class experiment, using healthy, PEB-infected, and soil classes. Expanding from a two class system often involved adding a soil or background class. Classification can also be performed hierarchically, as seen in Khan et al. (2020), where the first step involves binary classification of diseased or healthy leaves, followed by a second classifier to identify the specific disease in infected leaves.

5.2. Unsupervised learning

Unlike supervised learning, unsupervised learning models do not require human-labelled data and instead learn patterns from unlabelled data. The most common form of unsupervised learning found in this review is K-means clustering (Mishra et al., 2020; Mhango et al., 2022; Belgiu et al., 2021). For example, Mhango et al. (2022) used K-means clustering to segment meristems from the background when counting the number of potato stems in the field. In contrast, Mishra et al. (2020) employed the Calinski–Harabasz index to determine the optimal number of clusters for extracting biophysical features, though this approach did not perform well. Another unsupervised learning model used to perform background removal is the Gaussian Mixture Model (GMM) (Yang et al., 2022), which establishes the spectral threshold for removal based on the intersection between soil and leaf reflectance.

6. Deep learning models

DL is a prominent subset of ML that has garnered significant attention for its state-of-the-art performance in areas such as computer vision (CV) (Wang et al., 2023; Srivastava and Sharma, 2023), natural language processing (NLP) (Borgeaud et al., 2022; Lourie et al., 2021), and robotics (Ye et al., 2021; Shao et al., 2023). However, due to the limited availability and variability of publicly available datasets (Wani et al., 2022), some authors, including Ahmad et al. (2020), are sceptical about the effectiveness of DL models for potato plant phenotyping tasks. Despite these concerns, several studies have successfully applied DL architectures, often outperforming traditional shallow ML models and even human experts (Johnson et al., 2021). This section will explore these findings in greater detail.

6.1. Disease detection

Segmentation models, such as YOLOv5, are commonly used in DL architectures for disease detection. One example is the Potato leaf Disease Detection Convolution Neural Network (PDDCNN) (Rashid et al., 2021), which combines YOLOv5 with a CNN-based model to test the hypothesis that diseases vary based on geographical location. Another model, DA-ActNN-YOLOv5, also utilises a YOLOv5 backbone to detect PEB and PLB, while incorporating an ActNN module to compress model parameters (Dai et al., 2022).

Similarly, Shoaib et al. (2022) developed the Context-Aware CNN (CANet), which segments and classifies crop leaf disease lesions and estimates the plant's survival chances. CANet performs background removal through semantic segmentation, then feeds the extracted features into a 3D CNN to classify leaves as healthy, PLB-infected, or PEB-infected. Finally, a linear regression model predicts the plant's survival chances by estimating the number of days it has left to live.

Zhao et al. (2022b) aimed to detect a range of diseases in potatoes, corn, and tomatoes using the PlantVillage dataset. Their model, RIC-Net, integrates a Convolution Block Attention Module (CBAM) into an RI-Net architecture. CBAM is a lightweight, modular CNN that combines spatial and channel attention mechanisms. The model also includes a weighting operation to enhance the importance of disease-related information. RIC-Net, with the weighting operation, achieved the best performance among the seven models tested, closely followed by Xception. When using Inception models, the authors realised that sometimes global features are required while other times fine-grained features are required. As a result, they experimented with different kernel sizes in RIC-Net, finding the optimum to be of size three. They also used various filter sizes to perform convolution and max-pooling at the same level, widening the model rather than deepening it, an approach that helps avoid the computational expense and overfitting typical of very deep networks.

Hyperspectral data, provides both spectral and spatial information, which several authors believe is underutilised in current disease detection models (Qi et al., 2023; Shi et al., 2022; Van De Vijver et al., 2020). Qi et al. (2023) proposed the PLB-2D-3D-A model for detecting PLB, combining spatial features extracted using a 2D-CNN with spatial–spectral features from a 3D-CNN. These features are then combined using the AttentionBlock and SE-ResNet attention mechanisms. Van De Vijver et al. (2020) incorporated spectral and spatial characteristics using a decision tree, while Shi et al. (2022) leveraged the hierarchical structure of spectral–spatial features in their model, CropdocNet, to better capture the relationship between these features and potato plant diseases. Shi et al. (2022) believe that previous papers have failed to model the part-to-whole relationship of spectral-spatial features. CropdocNet uses 1D and 3D convolution blocks to extract spectral–spatial features, which are processed through a hierarchical class-capsule structure, followed by a decoder. Increasing the depth of the 1D and 3D convolution layers and the number of capsule features improved classification accuracy. They proved statistically that their model outperforms RF, SVM, and a 3D-CNN model, correctly identifying soil patches which the other models misclassified as PLB.

Transformers models have attracted significant attention across various DL research fields (Brohan et al., 2023; Junayed et al., 2022; Chowdhery et al., 2022) including potato plant phenotyping. These phenotyping articles focus mainly on disease detection by combining Vision Transformer (ViT) and CNN architectures. Notable examples include PLDPNet (Arshad et al., 2023), MDSCIRNet (Catal Reis and Turk, 2024), and EfficientRMT-Net (Shaheed et al., 2023). This hybrid approach leverages the complementary strengths of CNNs and ViTs, enabling the models to effectively utilise both local and global information (Arshad et al., 2023).

6.2. Early disease detection

Early detection of disease is critical to minimise its negative impact on crops. This can be accomplished during the asymptomatic phase using multispectral and hyperspectral cameras (Qi et al., 2023; Appeltans et al., 2021; Van De Vijver et al., 2022). Qi et al. (2023) proposed an interesting DL model for early disease detection called PLB-2D-3D-A, which utilises a 2D-CNN to extract spatial information and a 3D-CNN to extract spatial–spectral information. The aim of the experiment was to leverage hyperspectral data to detect PLB before visible lesions could be identified by an expert. The model achieved its best performance using data from day 12, when the lesions first became visible, with an F1 score of 0.864. Interestingly, the second best performance was achieved using data from the first day of data collection, with an F1 score of 0.796. Suggesting that there is not a linear relationship between disease detection and days after infection.

6.2.1. Disease severity estimation

Disease severity can be calculated using various methods, with common approaches including changes in leaf colour, distortion of leaf shape, and counting the number of lesions or infected pixels (Mandal et al., 2023; Gao et al., 2021b; Dai et al., 2022) to compute the percentage of disease in the leaf or image (Duarte-Carvajalino et al., 2018; Mandal et al., 2023). The ultimate goal is to classify a leaf, plant, or canopy into a disease severity class. Disease severity estimation has been achieved through segmentation and classification models, regression models could also be applied, although no articles in the review utilised this approach.

Direct classification of disease severity was achieved by Mandal et al. (2023) using the Inception v3 model and RGB image data. This model classified leaves into six severity classes based on the percentage of infection. Conversely, Li et al. (2022) approached the task by splitting it into instance segmentation and semantic segmentation, where instance segmentation refers to identifying individual leaves and semantic segmentation refers to detecting the diseased areas. For instance segmentation, they employed ResNet-50 and ResNet-101, finding that ResNet-101 achieved the best performance, while ResNet-50 offered faster inference times. For semantic segmentation, they tested UNet, PSPNet, and DeepLabV3+, with UNet delivering the highest mean Intersection over Union (MIoU) and Average Pixel Accuracy (MPA) scores. While DeepLabV3+ missed some important feature information as the disease spots can be small.

Lesion segmentation was also explored by Gao et al. (2021b), who used an encoder–decoder architecture based on SegNet to segment PLB lesions in ground-based RGB images of 775 genotypes. They compare their model against a baseline Fully Convolutional Network (FCN) and three other models: Convolutional K-means, PSPNet, and DeepLab. All models, except for Convolutional K-means, outperformed the baseline model, with SegNet achieving the highest performance. The authors also set a threshold for maximum lesion size to avoid misclassifying shadows on leaves as lesions.

Finally, Van De Vijver et al. (2022) used UNet for PEB lesion segmentation. In their study, they hypothesised that a high-resolution camera is essential for detecting PEB, as the features are often small and difficult to identify.

6.3. AGB estimation and yield prediction

Yang et al. (2023) aim to develop a low-cost method for estimating AGB using UAV-based data and an RGB camera. They propose a model called DenseNet-potato, which calculates the number and total area of detection boxes. This is achieved through the use of feature pyramids and a feature fusion network that extracts features at four scales, with a Soft-IoU layer used to assess the reliability of the detection boxes. The authors claim that RetinaNet is the state-of-the-art for leaf segmentation, despite its poor performance with overlapping leaves. To address the issue of overlapping leaves, they employ a mixture of Gaussian approach to merge and filter detection boxes. While their model performs satisfactorily on highly dense canopies with small leaves, it struggles with illumination changes and tends to underestimate AGB.

Mhango et al. (2022) estimate potato plant density by counting the number of stems in the field after canopy consolidation using a UAV. They implement a Faster R-CNN model to perform segmentation and classification of the segmented regions. The Faster R-CNN network is built on a VGG-16 backbone and includes a Region Proposal Network (RPN). Faster R-CNN uses anchor boxes to define bounding boxes, which are then refined by regression. When compared to another image analysis algorithm, Faster R-CNN, achieved top performance in localisation, precision, and IoU. However, the model predicted more consistently sized bounding boxes, which is less desirable as meristems vary in size. Although meristem count does not directly correspond to stem count, the Faster R-CNN model showed better-than-human performance for this task. Mhango et al. (2021), also used the Faster R-CNN model to estimate potato plant density from UAV and Satellite data.

6.4. Canopy assessment

Oishi et al. (2021) detect abnormal potatoes at growth stages, before canopy closure, by dividing the task into segmentation and classification components. They use the YOLO-v3 and Faster R-CNN for leaf segmentation, and Explainable Classifiable Latent Features-Class-Specific (ECLF-CS) model for classification. ECLF-CS utilises a variational autoencoder (VAE), that, once trained, can classify potatoes as either diseased or healthy as well as generate diseased and healthy images. The study found that for the segmentation task, Faster R-CNN outperformed YOLO-v3. Faster R-CNN also proved more robust to changes in illumination, whereas YOLO-v3 became more robust to illumination variation through preprocessing.

6.5. Explainable Artificial Intelligence (xAI)

DL models are often viewed as black-box models, and explainable artificial intelligence (xAI) seeks to demystify the inner workings of these models. One approach to this is analysing activation maps (Sharma et al., 2021), as demonstrated by Anim-Ayeko et al. (2023), who generated saliency maps to identify the key features their ResNet model used for disease classification. Their analysis revealed that the shape and outline of the leaf were not significant features for the model, while the specific areas where blight lesions typically occur were crucial for accurate classification.

6.6. Transfer learning

In this review, researchers frequently used transfer learning to address the challenges posed by limited data when training DL models (Saleem et al., 2022; Johnson et al., 2021; Butte et al., 2021; Oishi et al., 2021). The most commonly used datasets for pretraining these models were PlantVillage (Hughes and Salathé, 2015) and Microsoft's Common Objects in Context (COCO) dataset (Lin et al., 2015). Saleem et al. (2022) and Dai et al. (2022) found that the choice of pretraining dataset had a significant impact on the model's performance, highlighting the importance of careful dataset selection. However, pretraining does not always lead to improved performance. For example, Afzaal et al. (2021) found that fine-tuning GoogleNet after pretraining actually reduced its performance, leading them to train the model from scratch instead. When fine-tuning, it is not necessary to update the weights of the entire network; a common approach is to adjust only the top layers using the target dataset, which can reduce the time needed for fine-tuning (Mandal et al., 2023).

7. Discussion

Potato plant phenotyping covers a broad range of applications, from disease detection to yield prediction. However, across all applications, the lack of variation in field data limits the practical usability of many models. Notably, several articles collect data from only a single cultivar under ideal, cloud-free, sunny conditions (Liu et al., 2020; Luo et al., 2020). Since phenotyping is influenced by both environmental factors and the genotype, varying both will significantly improve the generalisability of models. The research community could address this issue by promoting a more open-source approach to data sharing in potato plant phenotyping. Fostering a more inclusive and constructive research environment by allowing researchers to contribute without the need for expensive sensors or access to farmland. By compiling larger, more diverse datasets from multiple regions and cultivars, the complexity and robustness of models would improve, while simultaneously enabling the establishment of state-of-the-art models and facilitating comparisons across studies.

Another challenge involving the effective comparison of research articles, is the lack of baseline and benchmark models, especially when presenting new models. Baseline and benchmark models allow the reader to contextualise the proposed model's results, generating a community of work that can build upon previous research. Certain articles present baseline models however few provide sufficiently complex benchmark models. This may be due to the lack of clarity regarding state-of-the-art models for the majority of phenotyping tasks.

The review highlights the widespread adoption of the PlantVillage dataset, which despite its popularity, has some limitations. As Rashid et al. (2021) noted, diseases present differently based on their geographical location, yet all data in PlantVillage was collected in the USA and Switzerland. Additionally, the dataset is highly unbalanced, not only across crop types but also within individual crops. For instance, the potato class has 2152 images compared to the 18,162 tomato images. Within the potato class the disease distribution is skewed, with 1000 PEB and PLB images but only 152 healthy leaf images. Moreover, the dataset was collected under controlled, lab-based conditions with a plain backgrounds, making it difficult for models trained on this dataset to generalise to real-world scenarios with varying lighting and complex backgrounds. Some researchers have tried to replicate lab conditions in the field by placing a white sheet of paper behind leaves (Mandal et al., 2023), but this approach is not scalable.

When integrating data from multiple platforms, researchers should exercise caution. Cross-platform data collection often uses ground-based platforms as the ground truth for models built to use airborne and satellite data. For example, Franceschini et al. (2017) sought to detect PLB by combining ground and airborne hyperspectral measurements to compute VIs that can predict crop traits. While VIs computed with only visible spectrum data produced differing results between the UAV and ground-based sensors, including the NIR spectrum made the VIs comparable between both platforms. Nevertheless, integrating data from both platforms, especially in the earlier growth stages, proved challenging, and the authors suggested a transfer function may be beneficial.

VIs are valuable features for yield prediction and AGB estimation, sometimes even more so than crop height (Li et al., 2020b). However, they have significant limitations. VIs do not generalise well across growth stages (Liu et al., 2022c,e) and tend to saturate with dense canopies (Mourad et al., 2020; Yang et al., 2022). Spectral saturation in the Visible-Near Infrared (VNIR) bands during AGB estimation is referred to as the 'growth stage effect' by Liu et al. (2022b). Some attribute this drop in performance after canopy closure to occlusion (Yang et al., 2023), yet the results are the same regardless of the reason, statistical models often underestimate AGB (Luo et al., 2022).

Another factor affecting yield prediction is the distinction between commercial weight and marketable yield (Gómez et al., 2021). This difference can impact model performance, as marketable yield discards potatoes affected by disease, defects, and other disorders (Li et al., 2021b). Consequently, commercial weight and marketable yield may include noise which could propagate into the model.

In the review, the results presented by various journal articles have come under question. First, data leakage and contamination should be avoided by using different rows or harvest years for training, validation, and test sets (Polder et al., 2019). Second, it is essential that the metrics used to validate models are appropriate for the task. For example, real-time models should report inference time (Théau et al., 2020; Shoaib et al., 2022), and models designed to be deployed on edge devices, like smartphones, should be compute- and memory-efficient and the appropriate metrics should be reported. Reporting only accuracy, particularly with unbalanced datasets, is problematic and should be avoided. Third, models intended for field use should not be trained, validated, and tested solely on lab-based data (Shoaib et al., 2022). Finally, as noted by Johnson et al. (2021), their disease detection model identified diseases not annotated in the dataset. This resulted in a low precision score and a high false positive rate. Therefore, a thorough review of model results is needed to ensure such issues do not misrepresent performance.

To conduct cutting-edge research, potato plant phenotyping researchers should engage with the literature in different but tangential fields. Research published in CV, ML, and agricultural journals and conferences can provide valuable insights to ensure the field remains at the forefront of innovation. For example, transformers have shown great promise in Robotics (Brohan et al., 2023), CV (Junayed et al., 2022) and NLP research (Chowdhery et al., 2022). The integration of ViT with CNN models has been shown to achieve superior performance in the detection of potato plant disease (Arshad et al., 2023; Catal Reis and Turk, 2024). It has also been successful in other tasks such as crop-mapping (Wang et al., 2024) and weed detection (Guo et al., 2025). Consequently, further research utilising transformers may prove fruitful for a variety of potato plant phenotyping applications beyond disease detection. The ability of the transformers to identify patterns across spatial and temporal localities may be useful in time series AGB estimation and yield prediction.

Emerging chlorophyll fluorescence technologies, such as the European Space Agency's FLEX satellite, which will carry a high-resolution Fluorescence Imaging Spectrometer (FLORIS), represent exciting opportunities for plant phenotyping and health assessment. FLEX is the first satellite mission specifically designed to monitor solar-induced chlorophyll fluorescence (SIF) (Mohammed et al., 2019), offering a valuable resource for phenotyping research. Additionally, advanced instruments such as the pulse-amplitude modulation-fluorometer and SIF-fluorometer provide promising alternatives. For example, the handheld FluoWat leaf clip, used in combination with a spectrometer, can measure the full SIF emission spectrum (Van Wittenberghe et al., 2024). However, during this review, only one article discussing chlorophyll fluorescence was selected. Lazarević et al. (2022) utilised chlorophyll fluorescence, gas exchange, and multispectral data, as well as various other traits to evaluate the effects of elevated temperatures on potato morphology and physiology. Given the potential of chlorophyll fluorescence in phenotyping, a dedicated review exploring its application alongside machine learning (ML) in potato plant phenotyping would be valuable.

7.1. Future work

Future work should focus on consolidating datasets across various potato phenotyping tasks. These datasets should be collected in field conditions with sufficiently complex backgrounds to encourage researchers to move towards more realistic and applicable experimental setups. To improve the generalisability of models, dataset collection should include variations in the time of day, weather conditions, and sensor placement. Additionally, a wide range of cultivars and geographical locations should be present in the dataset.

Such consolidated datasets would enable the establishment of state-of-the-art models that can serve as benchmarks for future research. Models trained on these datasets should account for features that are effective across different crop growth stages. Features such as VIs are highly growth stage-dependent and saturate after canopy closure due to severe occlusion, greatly impacting phenotyping tasks such as AGB estimation (Mhango et al., 2021). Since AGB estimation often performs poorly with multi-growth stage data, researchers may want to consider texture features, which have been shown to generalise well across growth stages (Liu et al., 2022e). Other factors that negatively impact AGB estimation, yield prediction and canopy assessment models include leaf curl, fuzzy contours, and changes in illumination (Yang et al., 2023), in conjunction with the over- and under-estimation of models due to low and high VIs, respectively (Gómez et al., 2019; Liu et al., 2022b; Li et al., 2019b).

Finally, a more comprehensive disease detection dataset is needed, as current research primarily focuses on PLB, PEB, and VW. To ensure the full coverage of diseases which can impact potatoes, such as potato leaf roll, latent mosaic viruses, and blackleg, data on these diseases should be collected. Another area of disease detection which requires future research is detecting multiple diseases on a single leaf (Rashid et al., 2021). Currently, each leaf is assigned a single disease with bounding boxes for the identified lesions. However, in real-world conditions, crops may be affected by multiple diseases simultaneously, and models should be developed to account for this.

8. Conclusion

This review analysed 100 journal articles focused on the application of ML techniques in potato plant phenotyping and characterisation. A discussion of the main phenotyping tasks identified in this review was provided. The necessity for variation and collaboration when collating datasets was made evident in several articles. When collating these datasets, researchers should consider a combination of spatial, spectral and textural features. Currently, researchers create their own, often small, datasets, which necessitates the need for extensive data augmentation. The lack of open-source potato plant phenotyping datasets hinders the establishment of clear state-of-the-art ML models. However, both shallow ML and DL models have been used to great success in a variety of potato plant phenotyping applications. Future work should focus on consolidating sufficiently diverse in-situ datasets to better determine state-of-the-art ML models for each phenotyping task.

CRediT authorship contribution statement

Ciarán Miceal Johnson: Writing – review & editing, Writing – original draft, Methodology, Investigation, Formal analysis, Data curation. **Juan Sebastian Estrada:** Writing – original draft, Methodology, Investigation. **Fernando Auat Cheein:** Writing – review & editing, Writing – original draft, Supervision, Project administration, Conceptualization.

Declaration of Generative AI and AI-assisted technologies in the writing process

During the preparation of this work the authors used DALL·E 2 in order to generate images of the various remote sensing platforms. ChatGPT 4o was also used to improve the readability of the text. After using these tools/services, the authors reviewed and edited the content as needed and take full responsibility for the content of the published article.

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Declaration of competing interest

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Table A.2
A subset of the ML models used in articles addressing potato plant disease detection.

Model	Articles
AlexNet	Khan et al. (2020)
ANN	Fenu and Malloci (2021) and Lamba et al. (2022)
CNN	Duarte-Carvajalino et al. (2018), Shi et al. (2022), Lamba et al. (2022) and Sharma et al. (2021)
Convolutional K-means	Gao et al. (2021b)
CropdocNet	Shi et al. (2022)
DA-ActNN-YOLOV5	Dai et al. (2022)
DarkNet	Khan et al. (2020)
DCDM	Khan et al. (2020)
Decision Tree	Sharma et al. (2021)
DeepLab/DeepLabV3+	Gao et al. (2021b) and Li et al. (2022)
DenseNet	Khan et al. (2020)
EfficientDet	Saleem et al. (2022)
EfficientNet	Afzaal et al. (2021)
Ensemble model (XGBoost, LightGBM)	Lizarazo et al. (2023)
Faster R-CNN	Saleem et al. (2022)
Fully Convolution Neural Network (FCN)	Polder et al. (2019) and Gao et al. (2021b)
GBC	Rodríguez Galvis et al. (2021)
GMM	Franceschini et al. (2019)
GoogleNet	Afzaal et al. (2021)
Inception-ResNetV2	Zhao et al. (2022b)
Inception V3	Mandal et al. (2023), Zhao et al. (2022b) and Li et al. (2022)
KNN	Rodríguez Galvis et al. (2021), Lamba et al. (2022) and Sharma et al. (2021)
Linear Regression	Théau et al. (2020)
Logarithmic Regression	Théau et al. (2020)
LSVC	Rodríguez Galvis et al. (2021)
Mask R-CNN	Johnson et al. (2021)
MLP	Duarte-Carvajalino et al. (2018)
Multiple Non-Linear Regression	Théau et al. (2020)
Naive Bayes	Lamba et al. (2022)
Non-Linear Regression	Théau et al. (2020)
PDDCNN	Rashid et al. (2021)
PLS-DA	Gold et al. (2020a), Van De Vijver et al. (2020), Couture et al. (2018) and Gold et al. (2020b)
PSPNet	Gao et al. (2021b) and Li et al. (2022)
Region-based Fully Convolutional Network	Saleem et al. (2022)
ResNet-50	Khan et al. (2020), Zhao et al. (2022b) and Li et al. (2022)
ResNet-101	Li et al. (2022)
RetinaNet	Saleem et al. (2022)
Random Forest	Rodríguez Galvis et al. (2021), Duarte-Carvajalino et al. (2018), Leon et al. (2021), Gold et al. (2020b), Shi et al. (2022), Lamba et al. (2022) and Sharma et al. (2021)
RI-Net	Zhao et al. (2022b)
RIC-Net	Zhao et al. (2022b)
SegNet	Gao et al. (2021b)
Single-Shot multibox Detector (SSD)	Saleem et al. (2022)
SqueezeNet	Khan et al. (2020)
SVM	Rodríguez Galvis et al. (2021), Duarte-Carvajalino et al. (2018), Van De Vijver et al. (2020), Shi et al. (2022), Lamba et al. (2022), Sharma et al. (2021), Ahmad et al. (2020), Fernández et al. (2020) and Griffel et al. (2018)
UNet	Li et al. (2022) and Van De Vijver et al. (2022)
VGG16	Afzaal et al. (2021), Khan et al. (2020) and Li et al. (2022)
Xception	Zhao et al. (2022b)

Table A.3
A subset of the ML models used in articles addressing potato plant AGB estimation and yield prediction.

Model	Article
avNNet	Gómez et al. (2019)
DenseNet-potato	Yang et al. (2023)
Decision Tree	Apat et al. (2022)
Elastic Net	Abbas et al. (2020)
Expectation-Maximisation	Apat et al. (2022)
Extreme Learning Machine	Liu et al. (2022c) and Liu et al. (2022e)
Faster Region-based CNN	Mhango et al. (2021)
Gaussian Process Regression	Liu et al. (2022d) and Liu et al. (2022b)
Generalised Linear Model	Gómez et al. (2019) and Jasim et al. (2020)
Gradient-Boosted Decision Tree	Paudel et al. (2021)
J48 Pruned Tree	Apat et al. (2022)
K-means	Apat et al. (2022)
K-NN	Abbas et al. (2020), Paudel et al. (2021) and Gómez et al. (2019)
Linear model of Fully Constrained Least Square	Luo et al. (2022)
Linear Regression	Abbas et al. (2020), Yang et al. (2023), Apat et al. (2022) and Luo et al. (2020)
Linear Regression with Backward Selection	Gómez et al. (2019)
Logistic Regression	Apat et al. (2022)
LSTM	Apat et al. (2022)
Multilayer Perceptron	Yang et al. (2023)
Multiple Linear Regression	Apat et al. (2022)
Multiple Stepwise Regression	Liu et al. (2022e)
Multivariate Adaptive Regression Splines	Gómez et al. (2019)
Naive Bayes	Apat et al. (2022)
PLSR	Liu et al. (2022d,c,a) and Luo et al. (2022)
Polynomial Regression	Kuradusenge et al. (2023)
RetinaNet	Yang et al. (2023)
Quantile Regression with LASSO penalty	Gómez et al. (2019)
REPTree	Apat et al. (2022)
Random Forest	Kuradusenge et al. (2023), Yang et al. (2021), Liu et al. (2022a,b), Li et al. (2021b), Luo et al. (2022), Gómez et al. (2021, 2019) and Apat et al. (2022)
Ridge Regression	Paudel et al. (2021)
RNN	Apat et al. (2022)
SSD	Yang et al. (2023)
SVM	Abbas et al. (2020), Kuradusenge et al. (2023), Liu et al. (2022c,b), Li et al. (2021b), Paudel et al. (2021), Luo et al. (2022), Gómez et al. (2021, 2019) and Apat et al. (2022)
YOLOv3-spp	Yang et al. (2023)

Appendix

This appendix contains a subset of the ML models and their corresponding articles for the following potato plant phenotyping applications: disease detection, yield prediction, AGB estimation, water status, nutrient status, and canopy assessment (see Tables A.2–A.5).

Data availability

No data was used for the research described in the article.

Table A.4
A subset of the ML models used in articles addressing potato plant nutritional and water status.

Model	Article
AdaBoost	Boguszewska-Mańkowska et al. (2022) and Duarte-Carvajalino et al. (2021)
ANFIS-GA	Elsayed et al. (2021)
Beta Function	Aneley et al. (2022)
CNN	Duarte-Carvajalino et al. (2021)
Decision Tree	Aneley et al. (2022)
Extra Trees	Boguszewska-Mańkowska et al. (2022)
Faster R-CNN	Butte et al. (2021)
KNN	Coulibali et al. (2020)
Linear Mixed Model	Zhou et al. (2022)
Linear Regression	Aneley et al. (2022)
Logistic Regression	Aneley et al. (2022)
Multiple Linear Regression	Abukmeil et al. (2022)
Mask R-CNN	Butte et al. (2021)
MLP	Duarte-Carvajalino et al. (2021)
Ordinary Least-Squares Regression	Liu et al. (2021)
PLSR	Zhou et al. (2022) and Liu et al. (2021)
Quadratic Discriminant Analysis	Boguszewska-Mańkowska et al. (2022)
Random Forest	Coulibali et al. (2020), Peng et al. (2021a), Boguszewska-Mańkowska et al. (2022) and Duarte-Carvajalino et al. (2021)
RetinaNet	Butte et al. (2021)
Retina-UNet-Ag	Butte et al. (2021)
Richard's Logistic Regression	Aneley et al. (2022)
Stepwise Multiple Linear Regression	Elsayed et al. (2021)
SVM	Coulibali et al. (2020) and Duarte-Carvajalino et al. (2021)
Weibull Regression	Aneley et al. (2022)
XGBoost	Boguszewska-Mańkowska et al. (2022) and Duarte-Carvajalino et al. (2021)
YOLOv3	Butte et al. (2021)

Table A.5
A subset of the ML models used in articles addressing potato plant canopy assessment.

Model	Article
CNN	Zhao et al. (2022a)
ECLF-CS	Oishi et al. (2021)
Faster R-CNN	Oishi et al. (2021)
GMM	Yang et al. (2022)
K-means	Belgiu et al. (2021)
KNN	Yang et al. (2022)
Linear Regression	Mourad et al. (2020)
Light-GBM	Yang et al. (2022)
MLR	Li et al. (2021a)
Multi-Output Gaussian Process	Pipia et al. (2019)
Partial Least Square Regression	Zhao et al. (2022a) and Yin et al. (2022)
Random Forest	Li et al. (2020a, 2021a), Yin et al. (2022) and Li et al. (2019b)
Ridge Regression	Yin et al. (2022)
Stepwise Regression	Li et al. (2020a)
SVM	Yang et al. (2022), Li et al. (2020a), Liu et al. (2020), Li et al. (2021a) and Yin et al. (2022)
YOLOv3	Oishi et al. (2021)

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