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Advances in Machine Learning for High-Throughput Plant Phenotyping: Techniques, Applications, and Opportunities

Nishchal Sharma[1], Dr. Harish Chand[2]
[1]*Department of Computer Science, Govt. College Kullu*
[2]*Department of Botany, Govt. College Kullu*

Abstract: ***High-throughput plant phenotyping (HTP) has emerged as a crucial element of modern plant science and crop breeding, enabling the swift, large-scale, and non-invasive evaluation of plant characteristics. The integration of machine learning (ML), particularly deep learning approaches, has transformed HTP by automating feature extraction, improving predictive accuracy, and enabling thorough analysis under diverse environmental conditions. This review compiles the latest advancements in ML-based phenotyping, covering traditional algorithms, convolutional neural networks, transformer models, and innovative 3D reconstruction techniques. It investigates advanced phenotyping technologies, encompassing controlled-environment systems, field robotics, and UAV-driven imaging, along with novel instruments such as ChronoRoot 2.0 and PhenoAssistant. The conversation includes uses in yield forecasting, stress identification, trait measurement, and weed differentiation. Additionally, it examines significant issues like dataset constraints, interpretability of models, and scalability, while suggesting future paths that involve multimodal integration, open data standards, explainable AI, and affordable phenotyping methods. This synthesis is designed to help researchers leverage ML for phenotyping processes, thereby promoting precision agriculture and accelerating breeding initiatives***

Keywords: Deep learning; Plant phenotyping; High-throughput phenotyping; Precision agriculture; Image analysis; Root phenotyping; UAV imaging; Explainable AI; 3D plant modeling; Computer vision; Crop breeding.

I. INTRODUCTION

The world stands at a critical juncture, facing the dual pressures of a rapidly growing population and a changing climate. Projections indicate that the human population will reach 10 billion by 2050, necessitating a 35-56% increase in food production compared to 2010 levels. This challenge is further exacerbated by climate change, which has led to a rise in the frequency and intensity of abiotic stresses, such as drought, high temperatures, and flooding. These conditions severely hinder plant growth and survival, making the development of resilient crops a global imperative.

Traditional plant breeding, which has long been the foundation of crop improvement, often selects for desirable traits under optimal growing conditions. This approach, however, is frequently insufficient for identifying genotypes that harbor stress-tolerance genes, as these traits are often quantitative and controlled by multiple genes with complex genotype-by-environment (G×E) interactions. The need to rapidly develop new crop varieties that can withstand these adverse conditions has driven the search for more advanced and efficient methodologies in agricultural research.

Historically, a major obstacle in this pursuit has been the "phenotyping bottleneck." Traditional phenotyping, which involves the manual measurement of plant characteristics like height, leaf count, and biomass, is a costly, laborious, and time-consuming process. This slow pace of data acquisition has prevented phenotyping from keeping pace with the rapid advancements in genotyping technologies, leading to a significant disparity between the volume of genomic and phenotypic data available to researchers. The problem is not just the slow data collection itself; even when high-throughput technologies are adopted, they produce massive, complex datasets that can "impede the inference from those datasets". This two-phase bottleneck highlights a fundamental problem: the challenge is not only in acquiring data but also in efficiently and intelligently processing it to extract meaningful conclusions.

High-Throughput Plant Phenotyping (HTPP) has emerged as a transformative solution to this problem. HTPP involves the application of a variety of tools, ranging from ground-based imaging to aerial platforms like Unmanned Aerial Vehicles (UAVs) and remote sensing, to phenotype plants in a non-destructive, non-invasive, and rapid manner.

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However, the successful adoption of HTPP is inextricably linked to the field of machine learning (ML). Machine learning and deep learning provide the necessary interdisciplinary approaches for data analysis, utilizing principles from probability, statistics, classification, regression, and neural networks to extract useful information from the vast datasets generated by HTPP platforms. These techniques enable the feature extraction, identification, classification, and prediction criteria needed to turn raw data into actionable knowledge for plant breeding and pathology. This review aims to clarify the state-of-the-art of digital plant phenotyping, providing an overview of the machine learning techniques, their practical applications, and future research perspectives.

II. FOUNDATIONAL CONCEPTS: BRIDGING PLANT SCIENCE AND DATA SCIENCE

The successful integration of machine learning into plant phenotyping requires a clear understanding of the core concepts from both domains. This section establishes the fundamental definitions and principles that underpin the field.

A. Defining High-Throughput Plant Phenotyping

HTPP is defined as the quantitative measurement of a plant's structural and functional characteristics, or phenotypes. These phenotypes, such as plant height, leaf count, and biomass, are the observable result of the complex interplay between a plant's genetic makeup and its environmental conditions. HTPP has the potential to accelerate breeding cycles by non-destructively linking phenotypic information with genomic data.

Data acquisition for HTPP is accomplished through a diverse array of platforms and sensors :

1) Platforms: These include ground-based systems like automated greenhouse gantries, field-based phenotyping carts, and robotic systems. Aerial platforms, such as UAVs, and satellite-based remote sensing are also widely used for large-scale field-level phenotyping.
2) Sensors: A variety of advanced sensors are employed to capture different aspects of the plant phenotype. These include standard RGB cameras for visible traits like color and leaf area, multispectral and hyperspectral cameras for detecting chemical signatures and subtle physiological changes beyond the human eye, thermal infrared (TIR) cameras for monitoring plant temperature and water stress, LiDAR for 3D mapping of plant structure, and fluorescence imaging to assess photosynthetic health.

B. A Primer on Machine Learning Paradigms

Machine learning (ML) is a subfield of artificial intelligence that focuses on the development of algorithms that can learn from data to perform tasks without being explicitly programmed. The models, once "trained" on a dataset, can be used to make predictions or classifications on new, unseen data. The most common ML paradigms relevant to HTPP include:

1) *Supervised Learning:* This is a task-driven approach where an algorithm learns a function that maps an input to an output based on a labeled dataset of input-output pairs. Common tasks include **classification**, which separates data into predefined classes (e.g., "healthy" vs. "diseased"), and **regression**, which fits data to predict continuous numerical values (e.g., crop yield).
2) *Unsupervised Learning:* This is a data-driven process that analyzes unlabeled datasets to identify meaningful trends, structures, or groupings without human interference. It is used for tasks like clustering to group similar data points or dimensionality reduction to simplify datasets. In HTPP, an example is using K-means clustering to segment plants from their background without labeled data.
3) *Semi-supervised Learning:* A hybrid approach that operates on both labeled and unlabeled data, which is especially useful when obtaining large volumes of labeled data is costly and time-consuming.
4) *Reinforcement Learning:* An environment-driven approach where an agent learns through a system of rewards and penalties to evaluate optimal behavior in a specific context. While less common, this paradigm has potential in tasks like training robotic systems for autonomous navigation or selective harvesting.

C. The Evolving Definition of "Data" in HTPP

A crucial aspect of modern HTPP is the shift in how "data" is defined. Historically, the focus was on extracting simple, hand-engineered features from images. However, the most advanced applications have moved towards a comprehensive data fusion approach. ML models are no longer limited to analyzing images; they are increasingly being used to integrate heterogeneous, high-dimensional datasets to build a holistic understanding of plant biology. This trend is exemplified by the development of integrated multi-omics and AI frameworks. These frameworks combine data from multiple '-omics' layers, such as genomics (DNA), transcriptomics (RNA), proteomics (proteins), and metabolomics (metabolites), with phenotypic and environmental data.

This approach seeks to model the entire G×E interaction, moving beyond surface-level phenotyping to gain a deeper, systems-biology perspective of how genetic information is processed to generate functional traits. The ability of ML algorithms to handle diverse data types that differ significantly in structure, complexity, and size is what makes this paradigm shift possible, transforming phenotyping from a passive measurement process into an active, decision-support science.

III. MACHINE LEARNING TECHNIQUES FOR HTPP: FROM CLASSICAL TO DEEP LEARNING

The application of machine learning in HTPP has evolved significantly, from classical algorithms that require manual feature engineering to advanced deep learning models that automate this process.

A. *Classical Machine Learning Algorithms*

Classical ML models represent a foundational approach that remains relevant for a variety of HTPP tasks, particularly when dealing with well-structured, tabular datasets.

1) *Support Vector Machines (SVMs):* SVMs are supervised learning algorithms that are highly effective for both classification and regression tasks by identifying an optimal "hyperplane" that best separates data into different classes. They can handle both linearly separable and non-linear data through the use of a "kernel trick". SVMs have been extensively used in HTPP for biotic and abiotic stress phenotyping and for classifying plant diseases based on image data.
2) *Random Forests (RFs):* An ensemble learning method, Random Forest combines multiple decision trees, each trained on a random subset of the data, to make a final prediction through a voting process. This approach is effective at capturing complex, non-linear patterns and reducing the variance of a single decision tree, leading to higher accuracy. RFs have demonstrated high accuracy in plant disease detection and are considered a top-performing model for crop yield prediction. A notable advantage of RFs is their ability to provide a feature importance ranking, which helps researchers understand which variables are most influential in a model's prediction.
3) *Unsupervised Techniques:* In cases where labeled data is unavailable, unsupervised algorithms are crucial. Clustering algorithms like K-means and Expectation-Maximization (EM) have been used to perform plant and leaf segmentation from complex backgrounds. These algorithms group data points based on similarities, enabling the automatic extraction of plant structures without the need for time-consuming manual annotation.

The choice between these algorithms depends on the specific problem, dataset characteristics, and computational resources available. Table 1 provides a comparative overview of key classical machine learning algorithms used in HTPP.

IV. REVIEW OF LITERATURE

The paper [1] argues that the global adoption of high-throughput phenotyping (HTPP) will depend on its demonstrated value to end-users, particularly plant breeders, in terms of genetic gains for the resources invested. For less developed countries, where public sector breeding is dominant, the development of low-cost and easy-to-handle tools, such as those using RGB images, is considered essential. To fully leverage advances in phenotyping and molecular technologies, the document notes that significant progress is required in environmental characterization and data management. It suggests that breeders need to collaborate with climate scientists and crop modelers to address the challenges posed by climate change. This interdisciplinary approach is seen as crucial for identifying key breeding traits and understanding complex stress factor interactions. Furthermore, the text states that trait phenotyping and crop growth models are evolving to provide breeders with mechanistic information about plant adaptation. This allows for the more precise selection of cultivars suited to a target environment. The use of big data is anticipated to help refine geospatial targeting and address the complex genotype × environment × management (G×E×M) interaction. Finally, as public breeding efforts become more networked, the need for standardized methods, from data collection to analysis and sharing, is emphasized as a critical next step.

In a study [2] on barley, a non-destructive high-throughput phenotyping platform was used to map Quantitative Trait Loci (QTL) for vegetative drought stress responses. Several QTL were identified where an exotic Hsp allele had a positive effect on trait performance. In particular, the introgression line S42IL-121 demonstrated improved growth under drought conditions, consistent with previous field experiments, making it a potentially valuable candidate for further breeding. The researchers also detected several QTL where the Hsp allele had a negative effect on performance, with two specifically related to water use efficiency being noted for further investigation. Future work is planned to fine-map the QTL regions of S42IL-121 and other lines using high-resolution progeny to ultimately clone the genes responsible for the observed effects.

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The paper describing [3] sequencing of three Brassica crop genomes has enabled the creation of advanced breeding tools, including a high-throughput genotyping array for *Brassica napus*. Genetic mapping in *B. napus* is complex due to its polyploid genome, requiring robust sequence-based markers to study traits controlled by multiple loci. The described SNP array was developed through a stringent design pipeline to minimize errors from genome duplication and allopolyploidy, ensuring high genome specificity. Approximately 74% of the assays were derived from a SNP pipeline optimized to exclude paralogous sequences, and 81% of these SNPs produced genome-specific clustering patterns. This performance surpasses similar arrays for wheat. While the strict criteria reduced available SNPs by 99%, some multi-copy SNP assays were included to maintain genome-wide marker density.

Testing across diverse *B. napus* cultivars showed high polymorphism rates, with only 3.5% monomorphic loci. The array successfully generated dense SNP maps, with loci physically anchored to diploid progenitor genomes, though some ambiguities remained due to homoeologous recombination and short SNP region alignment issues. Additionally, the array demonstrated utility for genetic analysis in *B. oleracea* and *B. rapa*, offering tens of thousands of polymorphic markers for each. Marker coverage was relatively high—approximately one marker every 15 kb—though biased toward the A genome. Physical and genetic maps showed good collinearity, with some rearrangements possibly reflecting post-polyploidization chromosomal changes. Despite not targeting functional SNPs, 34.4% of loci fell within annotated genes. The Brassica 60K Infinium array is a valuable resource for genome-wide association studies (GWAS) and quantitative trait locus (QTL) mapping, with SNP spacing suitable for the linkage disequilibrium patterns in *B. napus*. Its applicability to *B. napus* and its progenitors extends its utility across the full crossing range of these species, supporting breeding efforts to capture and utilize wider allelic diversity for crop improvement.

The study [4] highlights that, despite significant advances in sequencing technologies for genotyping, the absence of rapid, accurate, and reproducible phenotyping platforms has limited the ability to predict desirable crop traits through genetic analysis. To address this, researchers evaluated the effectiveness of unmanned aircraft system (UAS)-based high-throughput phenotyping for supporting molecular marker development in spinach (*Spinacia oleracea* L.). Using a UAS equipped with a red–green–blue sensor, they captured aerial images of 284 spinach accessions over the crop cycle. The processed images were used to create orthomosaic and digital surface models for estimating canopy cover, canopy volume, and excess greenness index, while bolting time was recorded manually. Genome-wide association studies (GWAS) with a SNP panel generated by ddRADseq identified 99 SNPs significantly linked to growth traits, some of which were located in transcription factor and stress-response genes potentially involved in plant growth and development. The findings demonstrate the potential of integrating aerial imaging with genomic analysis to enhance marker development and establish a foundation for UAS-based high-throughput phenotyping in spinach molecular breeding.

Recent computer vision research has increasingly focused on high-throughput plant phenotyping to measure plant attributes more rapidly and accurately than traditional manual methods. In this study [5], researchers developed a method to quantify two key yield-related traits—stalk count and stalk width—important for crops such as sorghum, sugarcane, corn, and maize. Unlike earlier approaches that relied solely on object detection or dense image segmentation, the proposed pipeline combines both techniques to extract accurate measurements for these traits. Data were collected using the "Robotanist," a ground-based robot equipped with a high-resolution stereo imager, in experimental sorghum plots. The extracted data were validated against independent assessments by two human evaluators, with comparisons made for both accuracy and efficiency. The method achieved an R^2 correlation of 0.88 for stalk count and a mean absolute error of 2.77 mm for stalk width (average width: 14.354 mm), while being 30 times faster for stalk count measurement and 270 times faster for stalk width measurement compared to manual evaluation. Temporal variations in plant morphological and functional traits, shaped by genotype and environmental factors, significantly influence crop development, yield, and quality. High-throughput image-based plant phenotyping enables precise measurement of these traits across large plant populations in short timeframes, eliminating labor-intensive manual methods while allowing non-destructive, repeated assessments throughout the plant lifecycle. This interdisciplinary field integrates computer science, biology, remote sensing, statistics, and genomics to connect complex phenotypes with genetic expression, addressing agricultural challenges related to food security, resource scarcity, and climate change.

The study [6] argue that the plants exhibit dynamic changes in structure, such as phyllotaxy adjustments for optimal light capture, along with growth patterns that create self-occlusion and overlapping leaves—factors that complicate image analysis. Additional challenges include variable lighting, cluttered backgrounds, and shifting camera zoom. Current computer vision methods primarily target structural and morphological traits in 2D and 3D; however, physiological and event-based phenotypes, such as photosynthetic activity under stress, carbohydrate distribution, leaf emergence timing, and fruit or flower development, offer deeper insights into plant adaptation strategies.

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The study introduces a taxonomy extending beyond structural traits to encompass physiological and temporal phenotypes, advocating for the use of diverse imaging modalities and mechanisms. A general computational framework for image-based plant phenotyping is proposed, alongside a review of current methods, future prospects, and the importance of benchmark datasets for standardized evaluation.

The review examines convolutional neural network (CNN)–based approaches for image-based plant phenotyping, outlining their advantages and limitations across different phenotyping tasks. These methods have shown strong potential in addressing complex challenges in the field, with certain end-to-end CNN architectures significantly streamlining the extraction of phenotypic traits from images. Such advancements enhance data processing efficiency and support broader improvements in plant phenotyping applications.

The paper [7] highlights three main future research directions. First, there is a need to expand the availability of labeled datasets tailored to agricultural contexts, as existing public datasets like ImageNet and MS COCO are not optimized for such applications—particularly for postharvest quality assessment involving diverse imaging modalities and limited sample sizes. Second, the development of a customizable deep learning framework could facilitate the integration of emerging DL techniques, offering unified interfaces for model integration, visualization tools for interpretability, and reinforcement learning for performance improvement. Dissemination of these tools and techniques could be supported through educational initiatives and training programs. Third, further research should focus on CNN architectures capable of direct processing of 3D and multimodal data, enabling tasks such as skeleton extraction, branch-pattern classification, and analysis of plant development. The study [8] presents a modular, end-to-end system for yield estimation in apple orchards, aiming to identify the most effective fruit detection and counting methods for this application. A novel semantic segmentation–based technique for fruit detection and counting is introduced and evaluated through an extensive comparative analysis against multiple state-of-the-art approaches. This work is the first to conduct a direct, head-to-head comparison of various fruit detection and counting methods using the same datasets. Findings reveal that, for fruit detection, a semisupervised method based on Gaussian Mixture Models outperforms deep learning–based methods in most datasets. However, for fruit counting, deep learning approaches achieve superior performance across all datasets. By combining the strengths of both methods, the proposed system attains yield estimation accuracies between 95.56% and 97.83%.

The study [9] explores the use of convolutional neural networks (CNNs) to estimate wheat ear density from nadir high–spatial–resolution RGB images, offering a faster alternative to tedious and inefficient manual counting. Two approaches were evaluated: the state-of-the-art Faster R-CNN object detector and the TasselNet local count regression network. Both methods achieved strong performance (rRMSE $\approx$ 6%) when tested under conditions similar to model calibration. Faster R-CNN demonstrated greater robustness when applied to datasets collected at later growth stages, where ears and backgrounds appeared differently due to higher plant maturity. The optimal spatial resolution for Faster R-CNN was approximately 0.3 mm, enabling image acquisition from UAV platforms for high-throughput phenotyping of large-scale experiments. Comparisons with in-situ manual counts showed reasonable agreement despite small sampling areas. Furthermore, both Faster R-CNN and manual counting achieved high and comparable heritability ($H^2 \approx 85\%$), indicating that high-resolution RGB imagery–based ear density estimation could effectively replace traditional counting methods.

The research [10] introduces a UAV-based high-throughput phenotyping technique for automated monitoring and assessment of individual citrus trees using high-resolution multispectral imagery. The approach employs a deep learning–driven machine vision algorithm to accurately detect individual trees in aerial maps and integrates an NDVI-based image segmentation method to delineate tree canopies of varying shapes. Tested over a large and complex 14-acre orchard with diverse tree sizes, the method achieved exceptional accuracy—99.8% overall (99.9% precision, 99.7% recall) for tree detection and 94.2% accuracy (100% precision, 89.1% recall) for identifying tree gaps. Individual canopy area estimation reached 85.5% accuracy compared to manual measurements of 20 trees, though the algorithm's measurements were found to be more accurate and consistent than traditional rectangular canopy estimates. Given the rising adoption of UAV imaging in agriculture, this method demonstrates significant potential to streamline orchard management by providing precise, scalable, and reliable canopy and gap detection for the researchers, organizations, stakeholder and field managers.

This study [11] presents a convolutional neural network (CNN) model, based on the AlexNet architecture, for hyperspectral image–based detection of pesticide residues on apples. Using a dataset of 6,144 images across four types of hyperspectral pesticide residues, the CNN achieved an average recognition rate of 95.35% for single-band images and a true positive detection rate of 99.09% on the test set, with no overlap between training and testing data—demonstrating strong generalizability. For image preprocessing, the Otsu segmentation algorithm was applied to generate binary images of the region of interest (ROI) in apples. A roundness-based analysis of these binary images was used to create effective ROI masks, successfully eliminating irrelevant regions.

When compared to traditional methods such as Support Vector Machines (SVM) and k-Nearest Neighbors (KNN), the CNN showed advantages in speed and robustness. However, detection errors were more likely when hyperspectral images from the same band had similar appearances. The authors suggest that future improvements could focus on increasing the number of specific feature parameters in convolution kernels to enhance feature extraction, thereby improving classification accuracy for visually similar hyperspectral images.

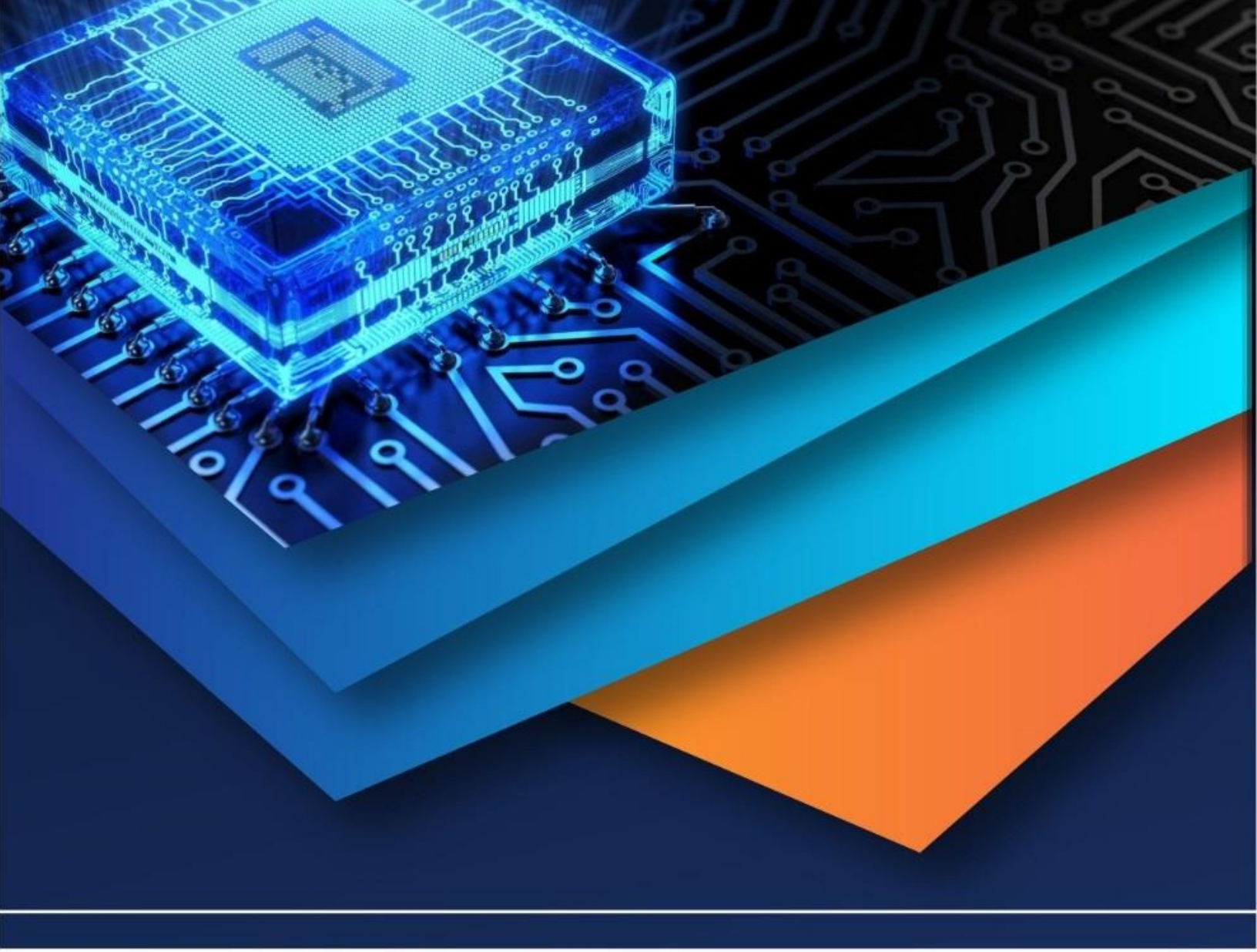
V. CONCLUSION

Across the reviewed studies, it is evident that modern computer vision and deep learning methods are revolutionizing agricultural monitoring, yield estimation, and quality assessment. Applications such as fruit detection and counting, wheat ear density estimation, citrus tree canopy mapping, and hyperspectral pesticide residue detection consistently demonstrate that AI-driven approaches can outperform traditional manual and statistical methods in both accuracy and efficiency. Techniques ranging from object detection (e.g., Faster R-CNN) and semantic segmentation to specialized architectures (e.g., TasselNet, AlexNet) have proven effective under diverse conditions, with accuracies often exceeding 90% and, in some cases, achieving near-perfect detection. Furthermore, UAV-based multispectral and RGB imaging platforms provide scalable, high-throughput data acquisition, enabling large-scale phenotyping and orchard management with minimal human labor. While certain challenges remain—such as robustness under varying environmental conditions, spectral similarity between classes, and the need for extensive labeled datasets—the integration of optimized preprocessing methods (e.g., Otsu segmentation, NDVI-based canopy delineation) and model-specific improvements can mitigate these limitations. Collectively, these findings reinforce the role of AI-powered image analysis as a transformative tool for precision agriculture. By enabling accurate, rapid, and non-destructive assessment of crop traits, these technologies not only enhance decision-making for breeders and growers but also contribute to sustainability by optimizing resource use and reducing waste. Future research should focus on improving model generalizability, automating pipeline integration, and extending applicability across crops, geographies, and environmental scenarios.

REFERENCES

[1] J. L. Araus, S. C. Kefauver, M. Zaman-Allah, M. S. Olsen, and J. E. Cairns, “Translating High-Throughput Phenotyping into Genetic Gain”, Accessed: Aug. 11, 2025. [Online]. Available: https://www.cell.com/trends/plant-science/abstract/S1360-1385(18)30020-7
[2] N. Honsdorf, T. J. March, B. Berger, M. Tester, and K. Pillen, “High-Throughput Phenotyping to Detect Drought Tolerance QTL in Wild Barley Introgression Lines”, doi: 10.1371/journal.pone.0097047.
[3] W. E. Clarke et al., “A high-density SNP genotyping array for Brassica napus and its ancestral diploid species based on optimised selection of single-locus markers in the allotetraploid genome,” Theor. Appl. Genet., vol. 129, no. 10, pp. 1887–1899, June 2016, doi: 10.1007/s00122-016-2746-7.
[4] H. O. Awika et al., “Developing Growth-Associated Molecular Markers Via High-Throughput Phenotyping in Spinach,” Plant Genome, vol. 12, no. 3, p. 190027, 2019, doi: 10.3835/plantgenome2019.03.0027.
[5] H. S. Baweja, T. Parhar, O. Mirbod, and S. Nuske, “StalkNet: A Deep Learning Pipeline for High-Throughput Measurement of Plant Stalk Count and Stalk Width,” 2017. doi: 10.1007/978-3-319-67361-5_18.
[6] S. Das Choudhury, A. Samal, and T. Awada, “Frontiers | Leveraging Image Analysis for High-Throughput Plant Phenotyping”, doi: 10.3389/fpls.2019.00508.
[7] Y. Jiang and C. Li, “Convolutional Neural Networks for Image-Based High-Throughput Plant Phenotyping: A Review,” Plant Phenomics, vol. 2020, p. 4152816, Jan. 2020, doi: 10.34133/2020/4152816.
[8] N. Häni, P. Roy, and V. Isler, “A comparative study of fruit detection and counting methods for yield mapping in apple orchards,” J. Field Robot., vol. 37, no. 2, pp. 263–282, 2020, doi: 10.1002/rob.21902.
[9] S. Madec et al., “Ear density estimation from high resolution RGB imagery using deep learning technique,” Agric. For. Meteorol., vol. 264, pp. 225–234, Jan. 2019, doi: 10.1016/j.agrformet.2018.10.013.
[10] “UAV-Based High Throughput Phenotyping in Citrus Utilizing Multispectral Imaging and Artificial Intelligence.” Accessed: Aug. 11, 2025. [Online]. Available: https://www.mdpi.com/2072-4292/11/4/410
[11] B. Jiang et al., “Fusion of machine vision technology and AlexNet-CNNs deep learning network for the detection of postharvest apple pesticide residues,” Artif. Intell. Agric., vol. 1, pp. 1–8, Mar. 2019, doi: 10.1016/j.aiia.2019.02.001.

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