ReproPheno and ReproPhenoNet: A Large-Scale Multimodal Benchmark Dataset and Deep Learning Framework for Reproductive-Stage Plant Phenotyping*

Sanjan Baitalik[1†], Rajashik Datta[2†], Utsho Banerjee[3], Rajarshi Karmakar[4], Vincent Stoerger[5], Himadri Nath Saha[8], Sruti Das Choudhury[6,7]

[1]Department of Computer Science & Engineering, Institute of Engineering & Management, Kolkata, West Bengal, India
[2]Department of Computer Science & Engineering (AI), Institute of Engineering & Management, Kolkata, West Bengal, India
[3]Department of Computer Science & Engineering (IoT), Institute of Engineering & Management, Kolkata, West Bengal, India
[4]Department of Computer Science & Engineering, University of Engineering & Management, Kolkata, West Bengal, India
[5]Agricultural Research Division, University of Nebraska-Lincoln, NE, United States
[6]School of Natural Resources, University of Nebraska-Lincoln, NE, United States
[7]School of Computing, University of Nebraska-Lincoln, NE, United States
[8]Department of Computer Science, SNEC, University of Calcutta, Kolkata, India
Sanjan.Baitalik2022@iem.edu.in, Rajashik.Datta2022@iem.edu.in, Utsho.Banerjee2022@iem.edu.in, Rajarshi.Karmakar2022@uem.edu.in, vstoerger2@unl.edu, contactathimadri@gmail.com, S.D.Choudhury@unl.edu

Abstract

High-throughput plant phenotyping is an emerging interdisciplinary field of research that lies at the intersection of computer vision, plant science, artificial intelligence, data analytics and visualization, and genomics. To develop novel algorithms that advance image-based high-throughput plant phenotyping research with an aim of precision farming and global food security, the publication of benchmark datasets is indispensable. Thus, this paper introduces ReproPheno, a large-scale, open-source dataset comprising multi-view image sequences of plants spanning their entire life cycle captured using three modalities of cameras, i.e., visible light, fluorescent, and hyperspectral, within the LemnaTec Scanalyzer 3D high-throughput plant phenotyping facility. By enabling comprehensive analysis across multiple sensing modalities and temporal scales, this dataset opens the door to several novel research directions in computer vision, including multimodal co-segmentation, hyperspectral dataset distillation, and 3D model reconstruction of living organisms with growing architectural complexity. Furthermore, the paper presents ReproPhenoNet, a novel algorithm that uses You Only Look Once (YOLO) deep neural-network-based object detector to detect flowers and fruits from visible light and hyperspectral image sequences, respectively. These detections form the foundation for the quantitative computation of reproductive-stage plant phenotypes.

Code — https://github.com/sanjanbaitalik/ReproPhenoNet
Datasets — https://plantvision.unl.edu/unl-plant-phenotyping-datasets/

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†These authors contributed equally.

Introduction

High-throughput plant phenotyping involves large-scale, non-invasive, rapid, and standardized assessments of plant phenotypes, the observable expression of a plant's traits, resulting from the interaction between the genotype and the environment (Das Choudhury et al. 2018). With advancements in imaging technologies and data acquisition systems, phenotyping has evolved into a data-intensive field, producing multimodal, multiview, time-series datasets that require the power of computer vision, artificial intelligence, data analytics and visualization techniques to extract meaningful insights which are key to improving crop resilience, yield, and adaptability (Li et al. 2024). To develop and evaluate new algorithms, and perform uniform comparisons with the competing state-of-the-art methods, public availability of benchmark datasets adhering to FAIR principles (Findability, Accessibility, Interoperability and Reusability) is crucial (Wilkinson et al. 2016). The high-throughput phenotyping system at UNL can uniquely enhance our understanding of plants' life processes by capturing plants' imagery at different life stages and in various modalities to generate massive datasets (Clarke et al. 2024). Our previous works released several benchmark datasets, but they are small and targeted, e.g., UNL-Component Plant Phenotyping for morphological analysis of maize structures ((Das Choudhury et al. 2018)), FlowerPheno for flower phenotyping ((Das Choudhury et al. 2022)) and UNL-3D Plant Phenotyping ((Das Choudhury et al. 2020)) Datasets, which typically involve a single image modality. To promote Artificial Intelligence (AI) research in agriculture, we introduce a large-scale, open-source benchmark dataset called University of Nebraska-Lincoln ReproPheno (UNL-ReproPheno) dataset. This first of its kind dataset consisting of multimodal, multi-view and temporal images of plants maturing to developing flowers and fruits, have been publicly released with the intention of advancing reproductive-stage phenotyping research based on computer vision and artificial intelligence techniques. The paper introduces a novel ReproPheno algorithm that uses YOLO deep neural networks to detect flowers from visible light image sequences and fruits from low resolution hyperspectral imagery. The paper also presents an in-depth discussion on the broader implications of the UNL-ReproPheno Dataset, underscoring its pioneering novelty and potential to serve as a foundational benchmark for advancing image-based research in several unresolved phenotyping challenges. Figure 1 shows the block diagram for ReproPhenoNet.

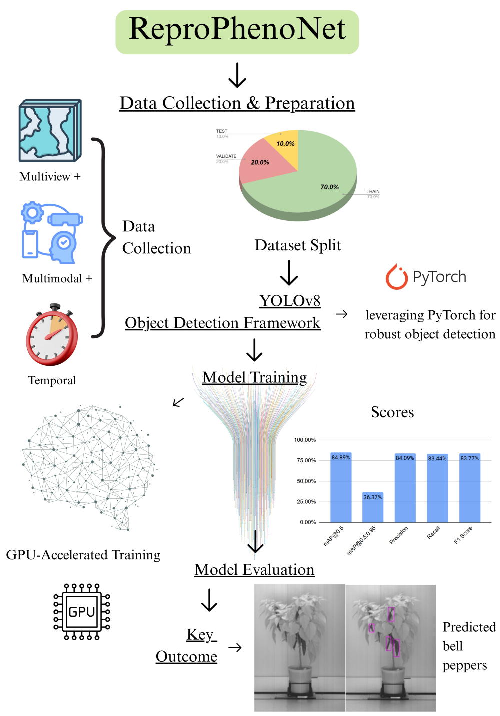

Figure 1: Block diagram of ReproPhenoNet.

UNL-ReproPheno Dataset

Imaging setup

The University of Nebraska-Lincoln (UNL) is equipped with LemnaTec Scanalyzer 3D high throughput plant phenotyping platform (HTP3). In a HTP3, the images of the plants are captured at regular intervals (typically once daily) by cameras in various modalities, e.g., visible light, infrared, fluorescent and hyperspectral, for a significant growth period (Das Choudhury and Samal 2020). Each imaging chamber has a rotating lifter for up to 360 side view images. Each plant is placed in a metallic carrier on an automated conveyor belt that moves the plants from the greenhouse to the four imaging chambers successively for capturing images in different modalities. The specifications of the cameras and detailed descriptions of the HTP3 can be found in Das Choudhury et al.(2018). The average time interval between a plant entering into and exiting from each of the first three imaging chambers for capturing 10 side view images is approximately 1 min 50 s. Since a hyperspectral camera typically captures a scene in hundreds of bands at a narrow interval over a broad range of the spectrum, its image capturing time is significantly higher than that of the other imaging modalities.

Dataset organization

UNL-ReproPheno dataset consists of two subsets: (a) FlowerPheno and FruitPheno. FlowePheno consists of multiview image sequences of six flowering plants captured using three camera modalities, i.e., visible light, hyperspectral and fluorescent (see Table 3 for details). Fruitpheno consists of multiview image sequences of okra, cucumber and six species of peppers captured using the same three camera modalities (see Table 1 for details). Fluorescent images were captured using four side views, i.e.,0°, 72°, 144° and 216°, and a top view. Hyperspectral images were captured using a single side view, i.e., 90°. Visible light images were captured using 10 side views, i.e., 0°, 36°, 72°, 90°, 108°, 144°, 216°, 252°, 288°, 324°, and a top view. The size of the dataset is approximately 6 TB.

Broader impact

The broader impact of the dataset is discussed below:

Multimodal cosegmentation: Co-segmentation emulates the human visual system by identifying common objects that repeatedly appear across a set of images (Rother et al. 2006). Since its inception in 2006 (Rother et al. 2006), numerous innovative approaches have been developed (Russell et al. 2006); however, the majority of these methods have focused exclusively on a single imaging modality, typically RGB imagery (Tsai, Zhong, and Yang 2016). Co-segmentation using multimodal image sequences with varying spatial and spectral resolutions remains largely unexplored, presenting a promising direction for future research using our UNL-ReproPheno dataset.

Event phenotyping: The timing of important events in the life cycle of a plant, e.g., emergence of col-eoptile from the surface of the soil, emergence of leaves, flowers and fruits, and their growth characteristics regulated by genotype and environment provide crucial information about a plant's vigor, and is denoted as the event-based phenotypes (Lowe, Harrison, and French 2017; Couture et al. 2016). ReproPhenoNet dataset holds a great deal of potential to promote event phenotyping research, e.g., transition timing detection from the vegetative stage to reproductive stage by the emergence of first fruit and reporting total number of fruits present in the plant on a day. Most pepper fruits initially appear as green, and then gradually transition through yellow and orange colors, before they finally mature to red. Automatic determination of time interval during which a pepper changes its color completely, is an important event phenotype of economic importance (Meki et al. 2023; Banerjee et al. 2020; Wendel, Underwood, and Walsh 2018).

Dataset distillation: Over the past several years, deep learning has achieved tremendous success in various research fields, e.g., computer vision, natural language processing, smart agriculture, robotics and automation. The success of deep learning is attributed to the massive datasets used to train the deep neural networks. The collection, storage, pre-processing, and transmission of the excessively large amount of data cause significant challenges, further at the expense of enormous computational complexity. To alleviate these shortcomings, dataset distillation, also known as dataset condensation has been introduced which aims to derive a much smaller dataset comprising of synthetic samples from the large-scale dataset such that the models trained on it have comparable performance to those trained on the original dataset (Huang et al. 2024). Hyperspectral cameras typically capture a scene in hundreds of bands covering a broad range of wavelengths at very narrow intervals that enable a detailed analysis of the spectral characteristics of the materials. While visible light images contain only three bands, red, green, and blue, hyperspectral imagery consists of hundreds of adjacent narrow bands, thus providing the opportunity to capture salient information manifested at specific bands, often not identifiable in visible spectra. Despite the usefulness, one obvious limiting factor of hyperspectral imagery is data redundancy, i.e., not all bands are equally informative for a specific application. Thus, dataset distillation holds significant relevance in the domain of hyperspectral image analysis.

3D object reconstruction from hyperspectral image sequences: Our previous work on 3D voxel-grid plant model reconstruction from multiple side view images to compute 3D phenotypes received much attention as the first ever attempt for large-scale fully automatic 3D reconstruction of objects with ribbon-like structures (maize plants) where the distance between the object and the camera is significantly larger (5.5 m) compared to the state-of-the methods (Das Choudhury et al. 2020). Although numerous research methods have been developed for 3D reconstruction using multi-view RGB images, reconstructing 3D models from low-resolution hyperspectral image sequences is yet to be explored.

4D phenotyping: Plants are living organisms whose architectural complexity increases with time due to continuous emergence of new organs, e.g., leaves, fruits and flowers. Since the images of UNL-ReproPheno dataset were obtained at regular time intervals over the plant's life cycle, the dataset holds tremendous potential for temporal plant phenotyping analysis to study the variation of phenotypes regulated by genotypes as a function of time (Li et al. 2024). With exponential growth of computing power and storage capacity, neural-network based time series analysis of living organisms could be investigated using our dataset, and thus, conducting pioneer research on 4D phenotyping analysis (3D model reconstruction with time as the 4th dimension) by exploiting multi-view feature of the dataset.

ReproPhenoNet

Hyperspectral imaging is a powerful technique that captures salient information of living or non-living objects across a wide range of wavelengths, typically ranging from visible light to near infrared at hundreds of contiguous narrow intervals (Garini, Young, and McNamara 2006; Feng et al. 2019). For living objects like plants that undergo massive morphological and physiological changes over the course of time due to complex cellular activities, hyperspectral imagery has tremendous potential for vast research explorations to characterize a plant's vigor (Luo et al. 2024; Detring et al. 2024). A hyperspectral image can be represented as a three-dimensional array with two spatial dimensions, width (x) and height (y) of the image measured along the horizontal and vertical axes respectively; and a spectral dimension (λ) comprising multiple discrete and specific wavelengths or spectral bands (λ_1,λ_2,.....,λ_n), over which the data is collected. This three-dimensional representation is called a hyperspectral data cube,commonly denoted by H(x,y,λ) (Feng et al. 2019; Luo et al. 2024; Detring et al. 2024).

Since hyperspectral imaging captures a broad range of wavelengths at narrow spectral intervals, it possesses the capability to reveal subtle patterns that are not discernible in conventional RGB imagery, which is limited to three broad bands—red, green, and blue. Figure 2 illustrates this contrast through two images of the same pepper plant, acquired on the same day and from the same viewing angle but using different imaging modalities. Figure 2 (left) presents an RGB image, while Figure 2 (right) displays a representative spectral band from the hyperspectral data cube. Identifying the green peppers in the RGB image is highly challenging, even to the naked eye; however, the peppers are distinctly visible in the corresponding hyperspectral band, demonstrating the enhanced discriminative power of hyperspectral imaging.

Figure 2: RGB image of a pepper plant (left); and Hyperspectral band at wavelength 1333 nm of the same plant (right).

ReproPhenoNet is a deep-learning framework for detecting reproductive structures (flowers and fruits) from image sequences in high-throughput phenotyping platforms. It uses hyperspectral data cubes $H(x, y, \lambda)$ for fruit detection and visible light imagery for flower detection, employing YOLOv3 and YOLOv8 backbones. The system processes multi-view image sequences from vegetative to reproductive stages, computing phenotypes like emergence timing, counts, and growth trajectories of flowers and fruits. Data augmentation (e.g., flipping, scaling, contrast adjustment) enhances model robustness.

Trained on 300 labelled images from the UNL-ReproPheno dataset (sunflower, coleus, canna for flowers; bell peppers for fruits), the framework uses anchor box optimization (9 anchors) and evaluates performance with Intersection over Union (IoU), confidence scores, and precision-recall curves, achieving high accuracy across species and views. ReproPhenoNet generates reproductive status reports, supporting precision agriculture applications like yield estimation and breeding.

Algorithm: ReproPhenoNet is designed to analyze the temporal evolution of plant phenotypes, integrating data derived from flower and fruit detections to provide a comprehensive framework for reproductive-stage phenotyping. To the best of our knowledge, ReproPhenoNet successfully applies YOLO object detector for the first time on low resolution hyperspectral imagery for high-throughput phenotyping. Algorithm 1 below presents ReproPhenoNet.

Algorithm 1: Problem definition: ReproPhenoNet

Input: The multimodal image sequence of a plant (where modality is either visible or hyperspectral), i.e., $P = \alpha_{d_1}, \alpha_{d_2}, \ldots, \alpha_{d_n}$, where α_{d_i} denotes the image obtained on day d_i, n denotes the total number of imaging days, and $d_1 < d_2 < \cdots < d_n$. Furthermore, $\alpha_{d_i} = \alpha_{d_i v_1}, \alpha_{d_i v_2}, \ldots, \alpha_{d_i v_m}$, where $\alpha_{d_i v_j}$ is the j-th view (v_j) of the plant P taken on day d_i, where $d_i < d_{i+1}$ and m denotes the total number of views.

Output: To compute a set, G, of reproductive phenotypes for each image modality in the sequence, where $G = G_{d_1}, G_{d_2}, \ldots, G_{d_n}$ and G_{d_i} is the set of phenotypes for day d_i.

```
Initialize an empty set G = ∅.
for each day d_i in P = α_{d_1}, α_{d_2}, ..., α_{d_n} do
    Extract multi-view images α_{d_i} = α_{d_i v_1}, α_{d_i v_2}, ..., α_{d_i v_m}.
    Preprocess α_{d_i} to enhance spectral and spatial features (e.g., normalization, band selection).
    Apply object detection model (e.g., YOLOv8) to detect flowers and fruits in α_{d_i}.
    Compute phenotypes G_{d_i}.
    Add G_{d_i} to G.
end for
return G
```

Experimental setup: The experiments were conducted on a high-performance computing system equipped with a 12th Gen Intel® Core™ i5-12400F processor, operating at 2.5 GHz with 6 cores and 12 logical processors. The system was configured with 16.0 GB of installed physical memory (RAM) and an NVIDIA GeForce RTX 3050 GPU to support efficient processing of hyperspectral image analysis and deep learning model training. The GPU was utilized with CUDA-enabled PyTorch to accelerate computational tasks.

Dataset preparation: The training dataset consists of 600 manually annotated images selected from the UNL-ReproPheno dataset to maximize diversity. Specifically, 300 visible-light images (for flower detection) were chosen from sunflower (*Helianthus annuus*), coleus (*Coleus scutellarioides*), and canna (*Canna generalis*), covering early, mid, and late flowering stages across multiple side views. The remaining 300 hyperspectral images (single 90° side view, 243 bands) were selected from bell pepper varieties (*Capsicum annuum* 'Fooled You Jalapeno' and 'NuMex Big Jim') spanning fruit initiation to maturity. Images were stratified to include approximately equal representation of early, peak, and late reproductive stages, as well as varying occlusion levels and plant densities. The dataset was split into 70% training (210 images), 20% validation (60 images), and 10% test (30 images) sets while preserving species and stage balance.

Ground-truth generation: Ground-truth bounding-box annotations for flowers and fruits were created manually using the LabelImg tool by four trained annotators. Each annotator labeled reproductive structures (flowers in visible-light images; fruits in hyperspectral images) across multiple views and growth stages. To ensure consistency and quality, the following protocol was followed:

- All 300 training images were independently annotated by at least two annotators.
- Disagreements were resolved through discussion with a senior annotator (third reviewer).
- Inter-annotator agreement was measured using Intersection over Union (IoU); only boxes with IoU > 0.7 between annotators were retained without modification.
- A final quality-control pass was performed on the entire annotation set to correct obvious errors (e.g., missed small fruits or false positives on leaves).

This process resulted in high-quality, consistent annotations suitable for training robust object detectors.

Implementation details: ReproPhenoNet was implemented in the Python programming language, leveraging libraries tailored for computer vision and machine learning tasks. Key libraries included OpenCV for image processing, TensorFlow and Keras for building and training deep learning models, Scikit-learn for additional machine learning utilities, and Ultralytics YOLOv8 (Jocher et al. 2022) for object detection. The YOLOv8n (nano) model was selected for its balance of speed and efficiency, with the option to scale to larger models if needed. The implementation focused on analyzing hyperspectral data cubes, represented as three-dimensional arrays $H(x, y, \lambda)$, where x and y denote the spatial dimensions (width and height) and λ represents the spectral dimension across multiple wavelength bands.

Training: The training process utilized 300 annotated images for each of two modalities, i.e., hyperspectral images for fruit phenotyping and visible light images for flower phenotyping. Training was performed with 100 epochs, a batch size of 16, and an input image size of 640x640 pixels, accelerated by the NVIDIA GeForce RTX 3050 GPU. The total execution time for training was approximately 3 hours.

Trained models were saved as checkpoints for subsequent evaluation and testing.

Evaluation metrics: Model performance was assessed using mean Average Precision (mAP@0.5 and mAP@0.5:0.95), precision, recall, and F1-score to evaluate segmentation and phenotyping accuracy for fruits and flowers (Meki et al. 2023). The mAP@0.5 measures precision at an IoU threshold of 0.5, while mAP@0.5:0.95 covers IoU thresholds from 0.5 to 0.95. Precision is the ratio of correct positive predictions to total positive predictions, recall is the ratio of correct positives to all actual positives, and F1-score is their harmonic mean.

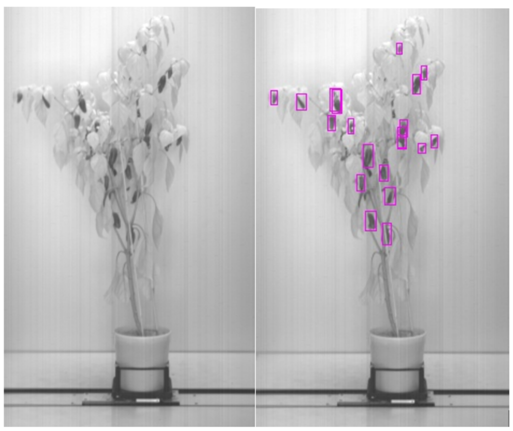

Figure 3: Illustration of pepper (*Capsicum annuum* 'Fooled You Jalapeno') detection: The original image (left); image with detected fruits (right).

Results: ReproPhenoNet effectively detects reproductive structures using hyperspectral and visible light image sequences. Figures 3 and 4 show the highly accurate results of fruit detections from hyperspectral imagery for two varieties of peppers, i.e., *Capsicum annuum* 'Fooled You Jalapeno' and *Capsicum annuum* 'NuMex Big Jim'. For flower detection, RGB images support precise identification across Blanket (*Gaillardia*) and PurpleCone (*Echinacea*), as illustrated in Figures 5 and 6. The results, paired with high mAP@0.5 and F1-scores, demonstrate the model's robustness in detecting fruits and flowers across multi-view sequences.

The trained ReproPhenoNet models were evaluated on the held-out test set using standard object-detection metrics (see Table 2). The model achieves high performance (mAP@0.5 = 84.9%) despite the low-resolution images and significant occlusion in dense canopies. Performance is slightly higher for flowers in visible-light images due to higher spatial resolution and better contrast.

Phenotype computation: The detections of flowers and fruits from the plant image sequences lead to the computations of the following novel phenotypes: (a) transition timing from the vegetative to reproductive stage with the emergence of first flower, total number of flowers and fruits present on the plant on a single day, total number of flowers bloomed in the plant for the entire life cycle, growth rate of individual

Figure 4: Illustration of pepper (*Capsicum annuum* 'NuMex Big Jim') detection: The original image (left); image with detected fruits (right).

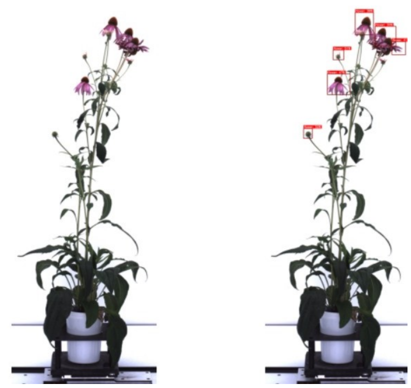

Figure 5: Illustration of flower (PurpleCone (*Echinacea*)) detection: The original image (left); image with detected flowers (right).

fruits and flowers, timing detection of ripening of fruits, etc.

Temporal phenotype extraction and validation: Detections from ReproPhenoNet are post-processed to derive biologically meaningful temporal phenotypes. For each plant and each imaging day, bounding boxes across all available views are aggregated: overlapping detections (IoU $>$ 0.3) from different views of the same structure are merged and counted as a single instance to avoid double-counting. This results in daily counts of flowers and fruits.

Figure 7 shows the temporal phenotypes for two example plants. Panel (a) shows the daily fruit count for a *Capsicum annuum* 'Fooled You Jalapeno' plant, clearly capturing fruit initiation around day 45, peak fruit load around day 70, and subsequent decline. Panel (b) shows flower count over time for a sunflower (*Helianthus annuus*), highlighting the characteristic single major flowering peak. To validate accuracy, daily counts from the automated pipeline were performed on 30 randomly selected plant-day combinations. The Pearson correlation coefficient was 0.94 for fruits and 0.97 for flowers (p ¡ 0.001), with mean absolute error of 2.1 fruits and 3.4 flowers per plant-day. These results confirm that YOLO detections reliably translate into accurate temporal reproductive phenotypes suitable for downstream genetic and physiological studies.

Table 1: ReproPheno dataset (Subset: FruitPheno)

Species	**Total plants**	**Imaging Days**	**Modality**		
			Vis	**Hyp**	**Fluor**
Capsicum annuum 'NuMex Big Jim'	20	30	Yes	Yes	Yes
Capsicum annuum 'Snackabelle'	20	30	Yes	Yes	Yes
Capsicum annuum 'Fooled You Jalapeno'	20	30	Yes	Yes	Yes
Capsicum annuum 'Cayenne'	20	30	Yes	Yes	Yes
Capsicum annuum 'Orange Spice Jalapeno'	20	30	Yes	Yes	Yes
Capsicum chinense 'Ghost'	20	30	Yes	Yes	Yes
Capsicum chinense 'Carolina Reaper'	20	30	Yes	Yes	Yes
Capsicum chinense 'Roulette Habanero'	20	30	Yes	Yes	Yes
Capsicum chinense 'Habanada Habanero'	20	30	Yes	Yes	Yes
Capsicum chinense 'Trinidad Scorpion'	20	30	Yes	Yes	Yes

Table 2: Object detection performance of ReproPhenoNet on the test set.

Modality	**Target**	**Performance**				
		mAP@0.5	**mAP@0.5:0.95**	**Precision**	**Recall**	**F1-score**
Visible light	Flowers	0.872	0.391	0.865	0.859	0.862
Hyperspectral	Fruits	0.826	0.336	0.817	0.810	0.813
Combined		0.849	0.364	0.841	0.834	0.838

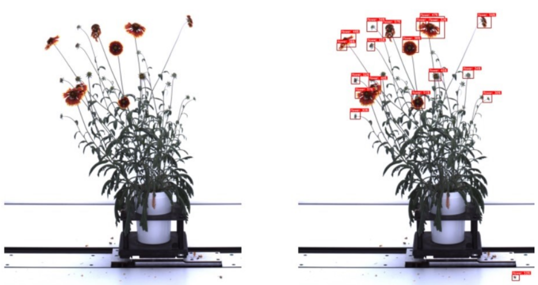

Figure 6: Illustration of flower (Blanket (*Gaillardia*)) detection: The original image (left); image with detected flowers (right).

Conclusion

The paper introduces UNL-ReproPheno, a massive, open-source dataset comprising of multiview, multimodal, and temporal images designed to advance critical research in computer vision, with a particular emphasis on application of AI for high-throughput plant phenotyping. The images were captured using LemnaTec Scanalyzer 3D HTPP facility at the UNL, USA. The paper also presents a ReproPheno algorithm that uses YOLO deep neural network-based object detection to detect flowers and fruits from visible light and hyperspectral image sequences, respectively. These detections are subsequently utilized for the quantitative analysis of reproductive-stage phenotypes, providing a robust framework for automated phenotyping research. ReproPheno uses visual inspection to manually select the particular band of hyperspectral imagery where the bell peppers are substaintially distinct from the rest of the plant, however, future work will consider atutomatic band selection for this purpose.

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Table 3: ReproPheno dataset (Subset: FlowerPheno)

Species	**Total plants**	**Imaging Days**	**Modality**		
			Vis	**Hyp**	**Fluor**
Stevia rebaudiana	10	30	Yes	Yes	Yes
Achillea millefolium	10	30	Yes	Yes	Yes
Celosia argentea	10	30	Yes	Yes	Yes
Helianthus annuus	20	30	Yes	Yes	Yes
Canna generalis	20	30	Yes	Yes	Yes
Coleus scutellarioides	20	30	Yes	Yes	Yes

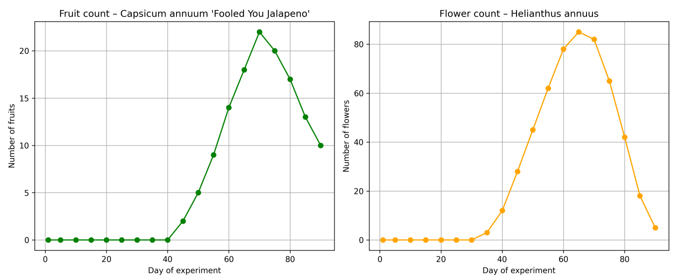

Figure 7: Computation of temporal reproductive phenotypes: (a) daily fruit count for a representative 'Fooled You Jalapeno' pepper plant; and (b) daily flower count for a representative sunflower plant.

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