Optimizing Indoor Farming: Deep Learning for Predicting Plant Growth under LED Light Treatments

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Abstract—**Indoor farming has emerged as a rapidly growing industry that harnesses controlled environmental conditions to cultivate crops. A key component of indoor farming is the utilization of LED lighting, which serves as the primary source of light for plant growth. In this study, our objective is to optimize indoor farming practices through the application of deep learning techniques, specifically by predicting the growth of plants under different LED light treatments in controlled agricultural environments. To achieve this goal, we employed existing machine learning methods and proposed a novel deep learning approach that incorporates the effects of LED light spectrum on plant growth to estimate plant biomass. Our deep learning model, BioNet, utilizes 1D convolutional neural network (CNN) to extract spatial features from the light spectrum data. Through extensive experimentation and analysis, we demonstrate that our deep learning method outperforms other conventional methods, showcasing its potential to enhance our understanding of the impact of LED light on plant growth.**

Our research provides valuable insights into optimizing indoor farming by uncovering the relationship between LED light treatments and plant biomass. BioNet serves as a valuable tool for farmers, enabling informed decisions on LED light selection, leading to improved efficiency and productivity in indoor farming. This study contributes to advancing indoor farming techniques through deep learning, opening new avenues for exploration and highlighting potential improvements in the field.

Index Terms—**Plant biomass prediction, Deep learning, Light treatment, Indoor farming.**

I. INTRODUCTION

Indoor farming, also known as vertical farming or controlled environment agriculture, offers numerous advantages over traditional farming methods. With indoor farming, crop production can continue year-round, regardless of weather conditions. This controlled environment also provides ideal growing conditions, resulting in higher crop yields compared to traditional farming. Additionally, indoor farming uses significantly less water and reduces the need for chemical pesticides, making it more environmentally friendly. By reducing land use and transportation costs, indoor farming can be a viable option for urban areas. Lastly, indoor farming systems can be designed to be energy-efficient, further reducing the carbon footprint of agriculture. Overall, indoor farming provides a promising solution for sustainable food production.

LED (Light Emitting Diode) lighting is an essential component of indoor farming, providing the primary source of light for plant growth [1]. The LED light spectrum can have a significant impact on plant growth in indoor farming environments. Plants require specific wavelengths of light for photosynthesis, which is the process by which they convert light energy into chemical energy for growth and development. LED lights offer the advantage of allowing for precise control of the light spectrum, enabling growers to optimize plant growth by providing the appropriate wavelengths of light. For example, blue light (400-500 nm) is essential for vegetative growth, while red light (600-700 nm) is crucial for flowering and fruiting [2], [3]. In addition to blue and red light, other wavelengths can also affect plant growth. For instance, green light (500-600 nm) can penetrate deeper into the canopy, improving light absorption, and enhancing plant growth [4]. Similarly, far-red light (700-800 nm) can influence plant growth by triggering plant responses such as leaf expansion, and the timing of flowering [5]. Hence, It is critical to understand the impact of LED light treatment on plant growth and to optimize the conditions for maximum crop yield. In this study, we aim to investigate the effects of LED light treatment on the growth of choy sum, a popular leafy vegetable, in indoor farming environments.

The field of plant growth prediction commonly relies on machine learning techniques [6], [7], with limited utilization of deep learning models. To bridge this gap, our study aims to assess the performance of various machine learning methods, including XGBoost, NGBoost, CatBoost, and LightGBM, in predicting the growth of choy sum under different LED light treatments. In addition, we propose a novel deep learning model called BioNet, which leverages a 1D Convolutional Neural Network (1D CNN) to extract spatial features from the light treatment data, enabling accurate plant growth prediction. Unlike existing methods that primarily focus on identifying the best LED treatment based on available data, our deep learning model offers the capability to select an LED light treatment beyond the confines of available data. This is achieved by adjusting LED treatment parameters and assessing the predicted biomass for the modified treatment.

The results of our study demonstrate that BioNet outperforms the other machine learning methods, yielding superior
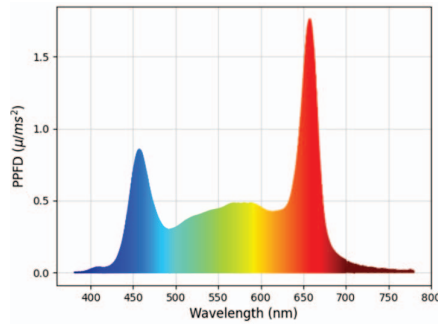
Fig. 1. Example spectrum of LED light treatment.

predictions for plant growth. By considering the entire range of light treatment rather than solely focusing on treatment intensity, our approach provide valuable insights into the impact of LED light treatment on the growth data of choy sum. Moreover, it highlights the potential of deep learning models in indoor farming applications, particularly in optimizing light treatments for enhanced plant growth.

In summary, our study contributes to the field by showcasing the efficacy of deep learning models in plant growth prediction, specifically by considering the comprehensive range of light treatment. The findings not only advance our understanding of the relationship between LED light treatment and plant growth but also underscore the potential of deep learning approaches in revolutionizing indoor farming practices.

II. LIGHT TREATMENT

A light treatment refers to the specific combination of wavelengths, intensities, and durations of light that are used for plant growth and development in indoor farming settings. The intensity of light treatment is represented using PPFD (Photosynthetic Photon Flux Density) which is a measure of the amount of light energy in the PAR (Photosynthetically Active Radiation) range that is available to plants for photosynthesis. PPFD is expressed in units of micromoles of photons per square meter per second ($\mu mol/m^2 s$), and it indicates the number of photons that fall on a given area of plants per second. An instance of a light spectrum with a PPFD of approximately 145 $\mu mol/m^2 s$ (where the total PPFD is the integral under the curve) is illustrated in Figure 1. The spectrum spans in the wavelength range of 380-780 nm.

III. PLANT GROWTH DATA

In our study, we utilized plant growth data obtained from choy sum plants. To capture this data, we employed the use of a PlantEye sensor [8], which is a specialized device designed to measure various aspects of plant growth. The sensor combines imaging and light measurement techniques to gather comprehensive information about the plants under observation. It is capable of measuring parameters such as plant biomass (in digital form), leaf area, and plant height.

The PlantEye sensor operates by utilizing multiple wavelengths of light to create a 3D model of the plant. By

considering height and 3D leaf area, PlantEye calculates the digital biomass of the plant, assuming a regular body shape for the plant and determining its volume accordingly.

In our study, the primary focus was on investigating the relationship between light treatment and plant biomass. Therefore, we maintained consistency in other growth factors such as temperature, humidity, soil pH values, and duration of light exposure throughout the experimental setup. By controlling these variables, we aimed to isolate the impact of light treatment on plant growth and biomass.

To explore the effects of different light treatments, we conducted experiments using a total of 41 distinct light treatments. The total Photosynthetic Photon Flux Density (PPFD) for these treatments varied between 100 and 300 $\mu mol/m^2 s$. For most light treatments, we had six plant saplings under observation. However, for a few specific light treatments, we utilized three plant saplings instead. The treatment data included information about the PPFD corresponding to each wavelength within the range of 380-780 nm.

During the experiment, plant measurements were captured every second day over a period of 15 days. This allowed us to observe the growth of the choy sum plants under different light treatments and track their biomass changes over time. The growth data collection process was carried out consistently across all light treatments, ensuring that the observations were reliable and comparable. A visual representation of the growth data collected under different light treatments is presented in Figure 2.
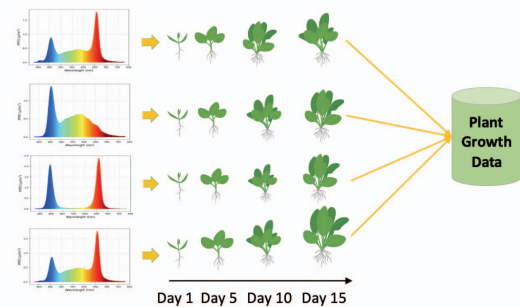

Fig. 2. Plant growth data over 15 days were collected in controlled environment while treating with different light spectra.

To ensure consistent scaling and facilitate biomass prediction within a range of 0 to 1, the training data was normalized by dividing each biomass value by the maximum biomass observed in the dataset.

IV. MACHINE LEARNING METHODS

In this section we describe different machine learning methods we use to predict the biomass of the plant under a given light treatment. We mainly focus on gradient boosting algorithms as they are known for their ability to handle complex data structures, high-dimensional data, and noisy data. The basic idea behind gradient boosting is to iteratively add new weak models to the ensemble, each one correcting

the errors made by the previous models. At each iteration, the algorithm calculates the gradient of the loss function with respect to the predictions of the current model. It then fits a new model to the negative gradient of the loss function, which is equivalent to fitting a model to the residuals of the previous model. This process continues until the ensemble achieves the desired accuracy or until a maximum number of iterations is reached.

A. XGBoost

XGBoost (Extreme Gradient Boosting) [9] is a popular machine learning algorithm used for both classification and regression tasks. It is a type of boosting algorithm that combines multiple weak learners (usually decision trees) to create a more accurate model. XGBoost uses a gradient boosting framework to iteratively improve the predictions by minimizing a specific loss function. It also incorporates a regularization technique to prevent overfitting and provides several hyperparameters that can be tuned to optimize the model's performance. XGBoost is known for its speed and scalability, making it a popular choice for a variety of machine learning tasks, including classification, regression, and ranking.

B. LightGBM

LightGBM [10] a gradient boosting framework developed by Microsoft that is designed to be efficient and scalable for large datasets. It uses a novel technique called Gradient-based One-Side Sampling (GOSS) to speed up the training process by reducing the number of samples used for each iteration of the boosting algorithm. LightGBM also includes other optimizations such as histogram-based gradient boosting and leaf-wise tree growth.

C. CatBoost

CatBoost [11] a gradient boosting framework developed by Yandex that is designed to handle categorical features more effectively than other gradient boosting frameworks. It uses a novel technique called ordered boosting, which takes into account the natural order of categorical features to improve accuracy. CatBoost also includes other optimizations such as gradient-based feature selection and symmetric tree construction. These techniques enable CatBoost to achieve better accuracy than other gradient boosting frameworks on datasets with categorical features.

D. NGBoost

NGBoost (Natural Gradient Boosting) [12] is a recent gradient boosting framework that uses a probabilistic framework to estimate predictive distributions rather than point estimates. This allows NGBoost to model uncertainty in predictions, which is useful in applications such as anomaly detection, time series forecasting, and personalized medicine. NGBoost uses a natural gradient descent algorithm to optimize the parameters of the predictive distribution, which results in faster convergence and better accuracy than other gradient boosting frameworks.

V. BioNet

As PPFD of wavelengths in the entire wavelength range (380-780 nm in our case) is treated as the feature of the light treatment, these fatures can be correlated, especially for neighbouring wavelengths. This is because neighboring wavelengths can still contain similar spectral information and contribute to similar biological responses. While gradient boosting algorithms can handle correlated features to some extent, it is generally better for the features to be as independent as possible. This is because correlated features can lead to overfitting and cause the model to be less generalizable to new data. Hence, we propose BioNet, which uses 1D CNN to extract spatial features of the light spectrum.
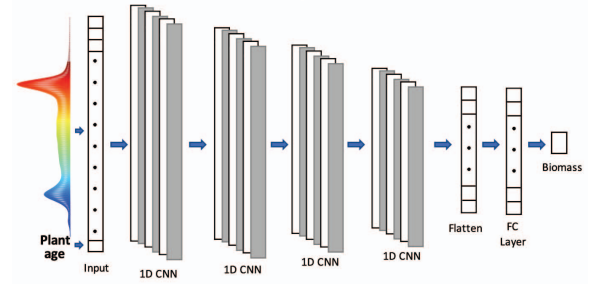

Fig. 3. Architecture of BioNet.

We represent the light treatment as a vector $\boldsymbol{x} \in \mathbb{R}^N$, where $\boldsymbol{x} = [x_1, x_2, \ldots, x_N]$ denotes N consecutive wavelengths, and x_i corresponds to the PPFD of the ith wavelength. Figure 3 shows a high level overview of BioNet. As we are interested in predicting the plant biomass based on its age (in days) and light treatment used, age of the plant is also an input to the network. BioNet is a parameterized function F_θ which maps the light treatment $\boldsymbol{x}$ and age a to the biomass of the plant, i.e. $F_\theta(\boldsymbol{x}, a) = \hat{y}$, where $\hat{y}$ is the predicted biomass. It consists of four 1D CNN layers followed by a fully connected layer that connects to the output layer responsible for estimating the biomass. We also incorporate dropout and batch normalization layers to enhance the model's performance and generalization. The intermediate layers utilize the ReLU activation function, which introduces non-linearity to the network and enables better representation learning. On the other hand, we employ the sigmoid activation function on the final output layer to ensure that the predicted biomass yield falls within the range of [0, 1]. It is important to note that BioNet is trained using normalized values of biomass.

To train BioNet, we utilize the mean squared error (MSE) loss and the Adam optimizer [13]. The loss value is computed as follows, where y_i represents the ground truth biomass value, $\hat{y}_i$ represents the predicted biomass, and n is the batch size:

$$\mathcal{L}_\theta = \frac{1}{n} \sum_{i=1}^{n} (y_i - \hat{y}_i)^2 \tag{1}$$

VI. Experiments and Results

This section provides a detailed discussion of our experimental setup and results. Among the 41 light treatments, we utilized the growth data from 25 light treatments for training purposes, while 8 light treatments were used for testing purposes. The remaining 8 light treatments were used exclusively for validation.

A. Hyperparameters

We conducted an exclusive hyperparameter search for both the machine learning methods and the proposed deep learning method. To obtain the optimal parameters, we utilized the GridSearchCV [14]. The search for learning rates was performed between 1e-1 and 1e-3, and the optimal learning rates were found to be 1e-2 for XGBoost, 5e-2 for LightGBM, 1e-2 for CatBoost, and 5e-2 for NGBoost. In the case of the deep learning method, we used a learning rate of 5e-3 after searching between 1e-2 and 1e-4. The batch size for training was 256, and we trained the models for 300 epochs. We trained the deep learning models using 100 different seeds and ultimately chose the model that provided the least validation error.

B. Evaluation

In our work, we used several evaluation metrics to assess the performance of our machine learning models and deep learning method. These metrics included Root Mean Squared Error (RMSE), Mean Absolute Error (MAE), and R-squared (R^2). RMSE is a measure of the difference between predicted and actual values, with lower RMSE indicating better model performance. MAE is another measure of the difference between predicted and actual values, but it is less sensitive to outliers than RMSE. R^2, on the other hand, measures the proportion of variance in the target variable that is explained by the model. They are mathematically expressed as provided in Equations 2-4

$$RMSE = \sqrt{\frac{\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}{n}} \quad (2)$$

$$MAE = \frac{1}{n}\sum_{i=1}^{n}|y_i - \hat{y}_i| \quad (3)$$

$$R^2 = 1 - \frac{\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}{\sum_{i=1}^{n}(y_i - \bar{y}_i)^2} \quad (4)$$

Where, $y, \hat{y}$ and $\bar{y}$ represent ground truth value, predicted value and mean of y values respectively. n is the number of samples in the test data. In summary, RMSE and MAE measure the accuracy of the predictions made by the model. On the other hand, R^2, quantifies the goodness of fit of a model to the data. It takes values between 0 and 1, where a higher value indicates a stronger fit between the model and the data.

In our experiments, we used these metrics to evaluate and compare the performance of different models and methods, and to choose the best performing model for our use case.

Metric	XGBoost	LightGBM	CatBoost	NGBoost	BioNet
R^2	0.723	0.723	0.756	0.638	**0.787**
RMSE	0.039	0.039	0.036	0.044	**0.034**
MAE	0.027	0.021	0.025	0.023	**0.019**

TABLE I
PERFORMANCES OF MACHINE LEARNING AND DEEP LEARNING METHODS.

C. Results

Table I presents a comprehensive comparison of evaluation metrics. Additionally, line plots illustrating the predicted values against the ground truth values of the test data are included for each method in Figure 4. These line plots provide insights into the prediction accuracy relative to the actual values. As mentioned previously, our test data consisted of growth data from 8 different light treatments, with either six or three plant samples under each treatment. Each point on the x-axis of the plots represents a data point, with the blue value on the corresponding y-axis being the ground truth value and the red value being the predicted value. The data points are organized based on light treatment, and within each light treatment, they are further sorted by plant samples. The data points for each plant begin from day 0 and continue up to the day of harvest. As a result, the decrease in the value along the x-axis indicates that the data point corresponds to the day 0 of the subsequent plant in the test data set. Since the input for each model consists of the light treatment spectrum and plant age, the predicted biomass for each plant sample under the same light treatment is expected to be the same, as can be seen in the plots. However, in reality, the biomass may vary for each plant even if they are grown under the same conditions. To address this variance in the ground truth values, one workaround is to train the model with the average biomass of each plant under the same light treatment. However, this approach may reduce the amount of training data, and we observed that it also reduced the training performance in our experiments.

While the performance of all the methods is comparable, BioNet demonstrates superior performance across all metrics, achieving an RMSE of 0.034, MAE of 0.019, and R^2 value of 0.787. XGBoost and LightGBM exhibit similar performances, with an RMSE of 0.039 and R^2 of 0.723. However, LightGBM outperforms XGBoost in terms of MAE, with an MAE of 0.021 compared to 0.027 for XGBoost. One notable difference between the two models is that XGBoost tends to overpredict biomass values when the plant is very small (around 2-3 days old), while LightGBM tends to overestimate final biomass values (around 15 days old). On the other hand, CatBoost tends to overpredict biomass values for younger plants, but underpredicts for older plants. As a result, the R^2 value for CatBoost (0.756) is relatively high, but the MAE is also high at 0.025. Among all the methods, NGBoost exhibits the poorest performance, as it tends to overpredict biomass for older plants. The corresponding RMSE, MAE, and R^2 values for NGBoost are 0.044, 0.023, and 0.638, respectively. The superiority of BioNet, proposed in this study, can be attributed to its capability to extract spatial features from the
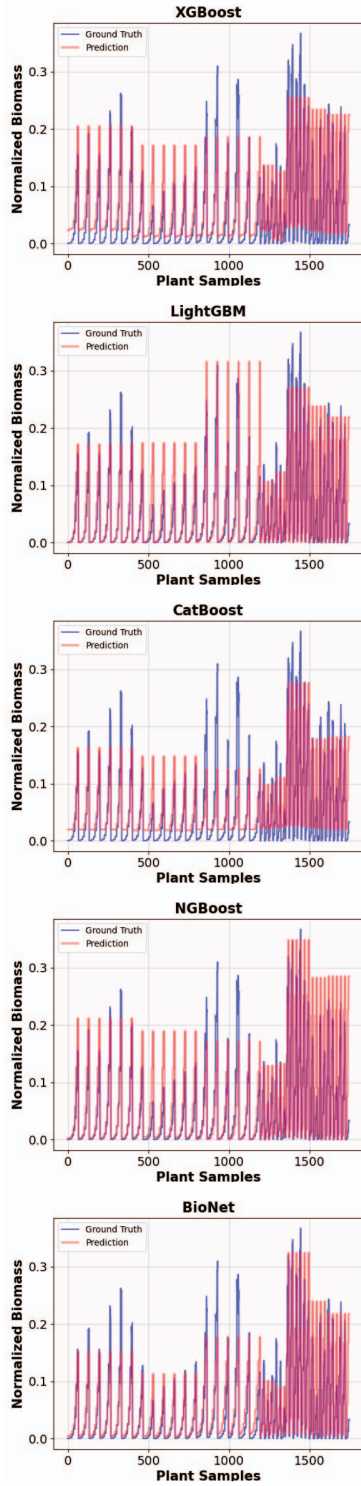
Fig. 4. Comparison of RMSE, MAE and R^2 values for various methods. We also show how each method predicted the biomass as compared to the ground truth values. Best viewed in color.

light spectrum.

VII. RELATED WORK

Plant growth under various light treatments has been a popular research topic among scholars. For instance, [15] utilized four distinct light treatments to examine the growth of choy sum and established that LED light intensity and spectrum both influenced growth, with the red-blue light treatment producing the highest shoot biomass at 160 $\mu mol/m^2 s$. Meanwhile, [16] studied the effect of sole-sourced LED and mineral nutrient fertility treatment on Chinese kale and observed that plants showed superior accumulation of sulfur, boron, and zinc in the root tissue under the 10% blue/90% red LED light treatment, while iron concentrations were highest in the 40% blue/60% red LED light treatment. Another research on Chinese kale by [17] found that plants grown under fluorescent/incandescent light treatment had significantly higher shoot fresh and dry mass. [18] studied the effects of UV-A irradiation on the cultivation and quality of microgreens and found that supplementing light treatments with UV-A irradiation resulted in increased leaf area and fresh weight of the plants. In a separate study on pak choi, [19] investigated the effect of light treatments on the regulation of carotenoid levels and discovered that blue, red, and white light had varying impacts on carotenoid composition. Although all of these studies focus on examining the impact of light treatments on plant growth, they solely concentrate on the light treatments used in their respective experiments and are unable to comment on the effects of light treatments not utilized in their studies. Our work, on the other hand, centers on predicting biomass based on the light treatment used. Therefore, even if a particular light treatment has not been tested in an experiment, our model can provide insight into whether the proposed light treatment is beneficial or detrimental to the plant. This information can assist farmers in designing light treatments for their indoor farming operations.

Similar to our work, [6] developed light-time-biomass model to predict the biomass of the plant under given light treatment. However, instead of considering the entire spectrum of the light treatment, they just include intensity of the treatment in their model. The experimental light treatments they used had varying PPFD values ranging from 50-500 $\mu mol/m^2 s$. However, the ratios of PPFD for different wavelength ranges remained constant across all light treatments. In other words, they did not take into account the different light spectrums that had the same PPFD. Our experimental data showed that light treatments with similar PPFD but different spectra resulted in significantly different biomass yields. Hence, their model fails to capture any effect of light spectrum on the plant biomass. Furthermore, their model requires initial weight of the seedling under the controlled environment. In contrast to their approach, our work is centered on constructing a model that takes into account the complete spectrum of the light treatment when making predictions about biomass yield.

Various researchers have suggested the utilization of 1D CNN for spectral analysis in different contexts, such as

identifying unknown substances through Raman spectra [20], classifying microplastics using Raman spectroscopy [21], and performing hyperspectral fluorescence imaging [22], vibration-based structural damage detection in civil infrastructure [23] and diagnosing bearing faults based on non-stationary signals of rotating machinery [24]. Additionally, 1D CNN has been utilized for Electrocardiogram (ECG) beat identification [25]. In our work, we are the first to utilize 1D CNN for predicting biomass under different light treatments.

VIII. CONCLUSION

In conclusion, we present a study on predicting the biomass of choy sum plants using different machine learning techniques and proposed deep learning technique. We use spectral data of different light treatments and plant age as input features, and the biomass of the plants as the target variable. We use four machine learning models: XGBoost, LightGBM, CatBoost, and NGBoost, as well as proposed BioNet, a deep learning model.

Our experimental results showed that all the models could predict the biomass of the plants comparatively. XGBoost and LightGBM had similar performances, with LightGBM performing slightly better in terms of MAE. CatBoost had a relatively high R^2 value, but also had a high MAE due to overprediction for younger plants and underprediction for older plants. NGBoost showed promising results but required a longer training time than the other models. The proposed deep learning model, BioNet, exhibited the best performance among all the models, with an RMSE of 0.034, MAE of 0.019, and R^2 of 0.787. The model also demonstrated good generalization ability on the test data.

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