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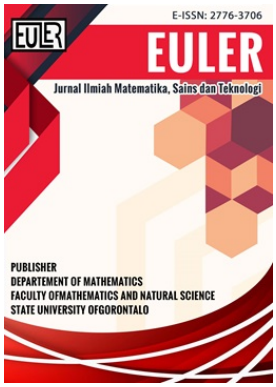

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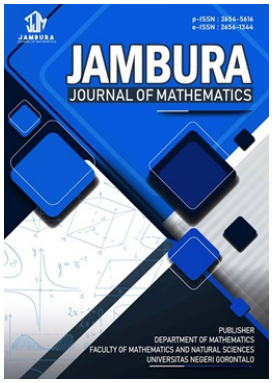

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Research Article

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Prediction of Protein Content and Glycemic Index of Local Food-Based Snack Bars Using Lagrange Polynomial Interpolation

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ABSTRACT. *Snack bars have the potential to serve as a healthy and nutritious snack alternative. One of the key factors to consider in the development of snack bars is their protein content and glycemic index. These two attributes can be predicted using the Lagrange polynomial interpolation method. In this study, predictions were carried out using Lagrange polynomial interpolation of orders 1, 2, 3, 4, and 5. The research began with the preparation of 11 snack bar formulations, followed by measurements of their protein content and glycemic index. The obtained data were then divided into two groups: the first group was used as test points for the Lagrange polynomial interpolation process, and the second group served as a benchmark for comparing the interpolation prediction results. The predicted results from the Lagrange polynomial interpolation were compared with the actual data, and the prediction accuracy was evaluated using the NRMSE value. The results showed that Lagrange polynomial interpolation of orders 1, 2, 3, 4, and 5 was effective in predicting the protein content and glycemic index of the snack bars. Furthermore, the NRMSE values indicated that second-order Lagrange interpolation provided the highest prediction accuracy, with the smallest NRMSE values: 0.08244 for protein content prediction and 0.06798 for glycemic index prediction.*

1. Introduction

The demand for functional food products has increased in line with growing public awareness of the importance of a healthy diet. Two key parameters often used to indicate the functionality of a food product are protein content and glycemic index (GI). Protein is an essential macronutrient that plays a critical role in tissue development and repair, supporting muscle maintenance and overall physiological function [1]. Meanwhile, the GI reflects the speed at which blood glucose levels rise following food consumption, and low-GI foods have been shown to be beneficial for weight management and the prevention of metabolic diseases such as type 2 diabetes [2].

Pigeon pea (*Cajanus cajan*), a locally available legume, has been recognized for its rich composition of protein, fiber, minerals, and phytochemicals, highlighting its potential as a functional food ingredient and a promising crop for improving food and nutrition security [3]. However, the development of new food formulations, such as pigeon pea–based snack bars, requires efficient evaluation of their nutritional quality and potential glycemic response. Laboratory testing for each formulation variant can be time-consuming and costly. Therefore, a reliable and efficient predictive approach is needed to accelerate the product development process.

Lagrange polynomial interpolation is one such method that is well-suited for this purpose. It is deterministic, does not require assumptions about data distribution, and can generate a polynomial curve that passes through all known data points [4]. These characteristics make it particularly suitable for modeling the relationship between formulation composition and nutritional response, especially when working with small datasets that are evenly spaced. Although simple, this method holds considerable promise for early-stage formulation screening.

Interpolation methods have been widely employed across various disciplines for predictive modeling tasks, particularly when observations are limited or irregularly spaced. In the socioeconomic domain, interpolation has been utilized to forecast stock and gold prices [5–9], estimate unemployment rates [10], project population growth [11–13], and predict student enrollment figures [14]. Some studies have also applied interpolation in public service planning, such as determining optimal public transportation fares [15]. These applications demonstrate the capacity of interpolation techniques to capture and extend numerical trends based on discrete historical datasets, offering a cost-effective and accessible alternative to more complex statistical models.

In environmental and geospatial research, interpolation has been applied to generate spatially continuous estimates of parameters such as rainfall distribution [16, 17], water quality [18], surface heat distribution on photovoltaic panels [19], and air pollution levels, including ozone and particulate matter [20, 21]. These studies have shown the efficacy of both deterministic methods, such as Inverse Distance Weighting (IDW), and geostatistical approaches like Kriging, which incorporate spatial au-

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tocorrelation via variogram modeling. By reconstructing spatial fields from sparse data, these techniques have become essential in environmental monitoring and planning.

Similarly, in digital image processing and pattern recognition, interpolation has proven valuable for reconstructing and enhancing visual data. It has been used to improve image resolution [22–27] and support diagnostic systems such as white blood cell classification [28]. These applications underscore the method's ability to infer continuous values from discrete observations a principle that parallels the prediction of nutritional properties based on formulation data in food product development.

In public health and epidemiology, interpolation has been employed to model disease dynamics, including the spread and recovery of COVID-19 and HIV [29–32]. These studies validate the use of interpolation in biological systems characterized by temporal uncertainty and limited sampling frequency. These studies validate the use of interpolation in biological systems that are often characterized by temporal uncertainty, inconsistent data availability, and limited sampling frequency. By estimating missing values and constructing continuous trends from discrete case data, interpolation enables researchers to project future trajectories, assess intervention impacts, and support decision-making in real-time scenarios.

Despite its broad application, most existing studies have concentrated on technical, economic, environmental, or spatial prediction tasks. The use of interpolation to predict nutritional parameters specifically protein content and glycemic index, in snack bar formulations based on local ingredients remains relatively novel and underexplored. Its application in food product development, particularly for estimating nutritional quality across formulation variations, is still limited. This study seeks to address that gap by demonstrating how Lagrange interpolation can function as a practical and cost-effective tool for nutritional prediction during early-stage product formulation, particularly for small-scale or resource-constrained food producers. This study aims to evaluate the performance of Lagrange polynomial interpolation in predicting protein content and glycemic index in snack bars formulated with pigeon peas. Validation is performed by comparing predicted values with laboratory data using the Normalized Root Mean Square Error (NRMSE) metric. The results are expected to contribute to the development of a practical, accurate, and cost-effective predictive tool to support innovation in healthy, functional food products based on local commodities.

2. Methods

2.1. Data Collection Techniques

Several steps were implemented for data collection in this study. The first step was to determine variations in the formulation of local food-based snack bars, which were analyzed in the laboratory to determine their protein content and glycemic index. The variations in snack bar formulations were designed based on differences in the ratio between pigeon pea granules and yellow sweet potato granules in the snack bars. The next step involved preparing all the snack bar formulations that had been designed. Subsequently, laboratory testing was conducted to measure the protein content and glycemic index of each snack bar formulation. The laboratory measurement results were recorded and classified into two data groups. Part of these results served as test points for data to form the basis for developing a mathematical model using the Lagrange polynomial interpolation method. The remaining measurement results, which were not used as test points, were used for comparison with the predicted results obtained from the mathematical model during the model validation stage.

2.2. Mathematical Modelling and Prediction Results

The mathematical model is developed using the Lagrange polynomial interpolation method. The Lagrange polynomial interpolation method was selected for modeling due to its numerical efficiency and ability to represent experimental data exactly. This method does not require solving systems of linear equations, estimating derivatives, or specifying additional parameters. The interpolating polynomial is constructed directly from the data points, making the implementation computationally lightweight, particularly suitable for small to medium-sized datasets.

Mathematically, suppose there are $n+1$ data points $(x_0, y_0), (x_1,\ y_1), \ldots, (x_n, y_n)$, then according to [33], the general form of the Lagrange polynomial of order n is given in eq. (1).

$$\begin{aligned} p_n(x) &= \sum_{i=0}^{n} a_i L_i(x) \\ &= a_0 L_0(x) + a_1 L_1(x) + \cdots + a_n L_n(x), \end{aligned} \tag{1}$$

with $a_i = y_i$, for $i = 0,\ 1,\ 2,\ \ldots,\ n$ and $L_i(x)$ is the i-th Lagrange basis polynomial, given by:

$$L_i(x) = \prod_{j=0}^{n} \frac{(x - x_j)}{(x_i - x_j)}.$$

The function $L_i(x)$ equals 1 when $x = x_i$ and $L_i(x)$ equals 0 when $x = x_j$, $j \neq i$ such that each y_i is multiplied by a basis polynomial that is functionally defined only at its corresponding point x_i. This model can then be used to predict values of the function $p_n(x)$ at new points within the available data domain.

The data used in this study consist of 11 observation points evenly distributed across the input domain, with a constant interval of 10%. This uniform spacing contributes to numerical stability and minimizes the risk of instability often associated with high-order polynomial interpolation, especially near the boundaries. Furthermore, the data exhibit deterministic behavior with minimal deviation between points, following a smooth and consistent trend without significant random fluctuations. This indicates that the data are largely free from experimental noise, making them well-suited for exact interpolation methods.

Although high-order polynomial interpolation is theoretically susceptible to Runge's phenomenon, such effects were negligible in this case since all interpolations were performed strictly within the range of available data (i.e., no extrapolation was conducted). Therefore, the Lagrange method offers a favorable balance between local accuracy, computational efficiency, and compatibility with the structure of the dataset, making it a suitable choice for early-stage exploration and numerical validation of experimental results.

The first step in constructing this model is to determine test data points from laboratory measurements of the protein

Table 1. Snack bar formulations

Ingredients	Weight (gram)										
	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}	F_{11}
Pigeon Pea	0	10	20	30	40	50	60	70	80	90	100
Yellow Sweet Potato	100	90	80	70	60	50	40	30	20	10	0
Banana	15	15	15	15	15	15	15	15	15	15	15
Cornstarch	9	9	9	9	9	9	9	9	9	9	9
Butter	6	6	6	6	6	6	6	6	6	6	6
Fructose Syrup	30	30	30	30	30	30	30	30	30	30	30
Egg Yolk	10	10	10	10	10	10	10	10	10	10	10

content and glycemic index of local food-based snack bars. Protein content was measured using the Kjeldahl method [34], while the glycemic index was determined using the Incremental Area Under the Curve (iAUC) method [35]. Next, the points are matched on a Cartesian coordinate system based on a finite set of point pairs $(x_0, y_0), (x_1, y_1), \ldots, (x_n, y_n)$ without knowing the specific functional form. The obtained data points are then processed and analyzed using Scilab software with the Lagrange polynomial interpolation method. At this stage, the Lagrange polynomial interpolation method is used to construct a mathematical model that can predict the protein content and glycemic index of the snack bars. The modeling process uses laboratory measurement data as input. The mathematical model is formed based on the number of data points collected.

Once a mathematical model in the form of a polynomial equation has been established to fit the selected data, the next step is to estimate the protein content and glycemic index of snack bar variants that were not included as data interpolation points. These estimates will be referred to as predicted values. Using the Lagrange polynomial method, each term of the polynomial is constructed by multiplying the known function value at a data point by its corresponding basis polynomial. The sum of all such terms produces the predicted protein content and glycemic index for the respective snack bar variants.

2.3. Mathematical Model Validation

Model validation begins by creating a curve that visualizes the prediction results against the data from laboratory analysis to evaluate the model's accuracy. In this stage, the use of Microsoft Excel software helps simplify the process of visualizing actual data and prediction results in the form of a curve, making it easier to analyze and evaluate the constructed model.

The next step is to evaluate the accuracy of the model by comparing the prediction results with the actual data from laboratory analysis. The method used to evaluate the model's accuracy is the Normalized Root Mean Squared Error (NRMSE). NRMSE is a measure of prediction error that quantifies how far the predicted values are from the actual values. The smaller the NRMSE value, the more accurate the polynomial interpolation model is. The choice of NRMSE was based on several technical and practical considerations. First, NRMSE offers the ability to normalize the error relative to the scale of the actual data, thus providing a relative measure of prediction error. Second, as a non-statistical interpolation method, Lagrange polynomial interpolation does not rely on regression parameters or probabilistic assumptions about residual distribution. Therefore, statistical significance tests such as t-tests or ANOVA are less relevant in this context, making numerical deviation-based metrics like NRMSE more appropriate for evaluating model performance.

Moreover, NRMSE offers a more intuitive and communicative interpretation because the resulting value can be expressed as a percentage of the maximum value or the overall data range. This presentation facilitates an understanding of how closely the predictions approximate the experimental results, not only for researchers but also for non-technical readers. Compared with MAE (Mean Absolute Error) or MAPE (Mean Absolute Percentage Error), NRMSE is also more sensitive to large errors. This trait is crucial in polynomial interpolation, where models may exhibit fluctuations or oscillations near domain boundaries (the Runge phenomenon), hence requiring a metric that responds more strongly to extreme deviations. MAE and MAPE, which calculate errors linearly and on average, tend to dampen the influence of outliers and can reduce validation sensitivity to significant local errors. By contrast, NRMSE that derived from the square root of the mean squared error, imposes a greater penalty on substantial deviations, making it better suited for evaluating interpolative models that seek accurate global predictions.

Next, conclusions are drawn regarding the effectiveness of the Lagrange polynomial interpolation method in predicting the protein content and glycemic index. Additionally, the accuracy of the predictions from various polynomial degrees of the Lagrange interpolation method is assessed, allowing for the determination of the polynomial degree with the highest accuracy in predicting the protein content and glycemic index of local food-based snack bars.

3. Results and Discussion

This section begins with a description of the data obtained through laboratory testing, which includes protein content and glycemic index values of 11 formulations of local food-based snack bars. The snack bar formulations were designed by varying the ratio of the main local ingredients, specifically the ratio between pigeon peas and yellow sweet potatoes, while maintaining a constant total weight of 170 grams for each formulation. The 11 local food-based snack bar formulations, denoted as F_i for formulation i, where $i = 1, 2, 3, \ldots, 11$, are presented in Table 1.

3.1. Data Description

The test results for protein content and glycemic index of the 11 snack bar formulations are shown in Table 2. The independent variable in the following data is expressed as the percentage of pigeon peas relative to the total weight of pigeon peas and yellow sweet potatoes.

The data show a consistent increase in protein content as

Table 2. Protein content and glycemic index test results

Percentage of pigeon peas (%)	Protein (%)	Glycemic Index
0	3.05115	14
10	4.8295	29
20	6.19715	35
30	6.4513	46
40	8.81115	48
50	8.89085	54
60	9.0135	66
70	9.4998	67
80	10.19045	70
90	11.3614	71
100	13.6412	76

the percentage of pigeon peas rises, from 3.05% in the control formulation to 13.64% at full substitution. Meanwhile, the glycemic index also increases, though the trend is not strictly linear. The glycemic index values rise from 14 to 76, with a slower rate of increase at higher substitution levels. These findings suggest that while pigeon pea substitution effectively enhances protein content, it may also elevate the glycemic index, indicating a need to balance nutritional benefits with metabolic impact in final product development.

3.2. *Determining Data Test Points*

Among the 11 formulation points of local food-based snack bars tested for protein content and glycemic index, 6 points were selected as test data points, while the remaining 5 points were used as comparison points for prediction results. The independent variables for the data test points were 0%, 20%, 40%, 60%, 80%, and 100%, while the independent variables for the comparison points of the prediction results were 10%, 30%, 50%, 70%, and 90%. The details of the 6 test data points are provided in Table 3.

Table 3. Protein content and glycemic index data test points

i	x_i	Protein (y_i)	Glycemic index (z_i)
0	0	3.05115	14
1	20	6.19715	35
2	40	8.81115	48
3	60	9.0135	66
4	80	10.19045	70
5	100	13.6412	76

3.3. *Mathematical Modelling and Prediction Results*

The mathematical model used to estimate protein content and glycemic index for each snack bar formulation was developed using the Lagrange polynomial interpolation method, as previously defined in eq. (1). This formulation constructs a polynomial $p_n(x)$ that passes exactly through all available data points (x_i, y_i), with the Lagrange basis functions $L_i(x)$ weighting the contribution of each known value. By applying this method to the experimental dataset consisting of 11 formulation points, interpolation models of orders 1 through 5 were generated. The use of eq. (1) allowed for direct prediction of nutritional values at any input point within the interpolation domain without requiring statistical parameter estimation.

In this study, the algorithm was implemented using the Scilab software and applied to construct predictive models for protein content and glycemic index based on five test points. Predictions were made using polynomial orders 1 through 5, and the results are presented in Table 4 and Table 5. Visualization of the predicted values compared with actual laboratory data was conducted to evaluate the quality of the approximation.

Table 4. Prediction results for protein content

x	y	$p_1(x)$	$p_2(x)$	$p_3(x)$	$p_4(x)$	$p_5(x)$
10	4.829	4.6242	4.6907	4.5732	4.3675	4.1664
30	6.451	7.5042	7.5707	7.6882	7.8115	7.8977
50	8.891	8.9123	9.2138	9.0021	8.9532	9.0394
70	9.499	9.6019	9.4802	9.3989	9.3500	9.2639
90	11.361	11.9158	11.6316	11.5504	11.6319	11.8329

Table 5. Prediction results for glycemic index

x	z	$p_1(x)$	$p_2(x)$	$p_3(x)$	$p_4(x)$	$p_5(x)$
10	29	24.5	25.5	26.3125	27.5625	29.39453
30	46	41.5	42.5	41.6875	40.9375	40.15234
50	54	57	56.375	57.5625	58.38281	57.59766
70	67	68	69.75	68.75	69.57031	70.35547
90	71	73	72.75	71.75	70.38281	68.55078

Among the five polynomial models tested, the second-order interpolation consistently produced the closest approximation to the actual laboratory data for both protein content and glycemic index. As shown in Table 4 and Table 5, first-order models tend to underfit the curvature of the data, while higher-order models (orders 3 to 5) begin to exhibit oscillations, particularly near the boundaries of the domain $(x = 10 and x = 90)$. This pattern reflects the characteristics of Runge's phenomenon, where high-order polynomials may overfit sparse data and reduce overall prediction stability. In contrast, the quadratic model achieves a favorable balance between curve flexibility and numerical stability, making it the most reliable for practical prediction in this context.

3.4. *Mathematical Model Validation*

The predictions obtained from the Lagrange polynomial interpolation method are evaluated by comparing them with the actual data from laboratory analyses. The evaluation of the prediction results is conducted using the Normalized Root Mean Squared Error (NRMSE) for each order of the Lagrange polynomial interpolation method. The NRMSE values for the comparison between the predicted results and the actual data for both protein content and glycemic index are presented in Table 6.

Table 6. NRMSE values for prediction results of protein content and glycemic index

Lagrange Polynomial Interpolation	NRMSE	
	Protein	Glycemic index
Order 1	0.08298	0.07861
Order 2	0.08244	0.06798
Order 3	0.08805	0.06912
Order 4	0.10070	0.07817
Order 5	0.11522	0.08555

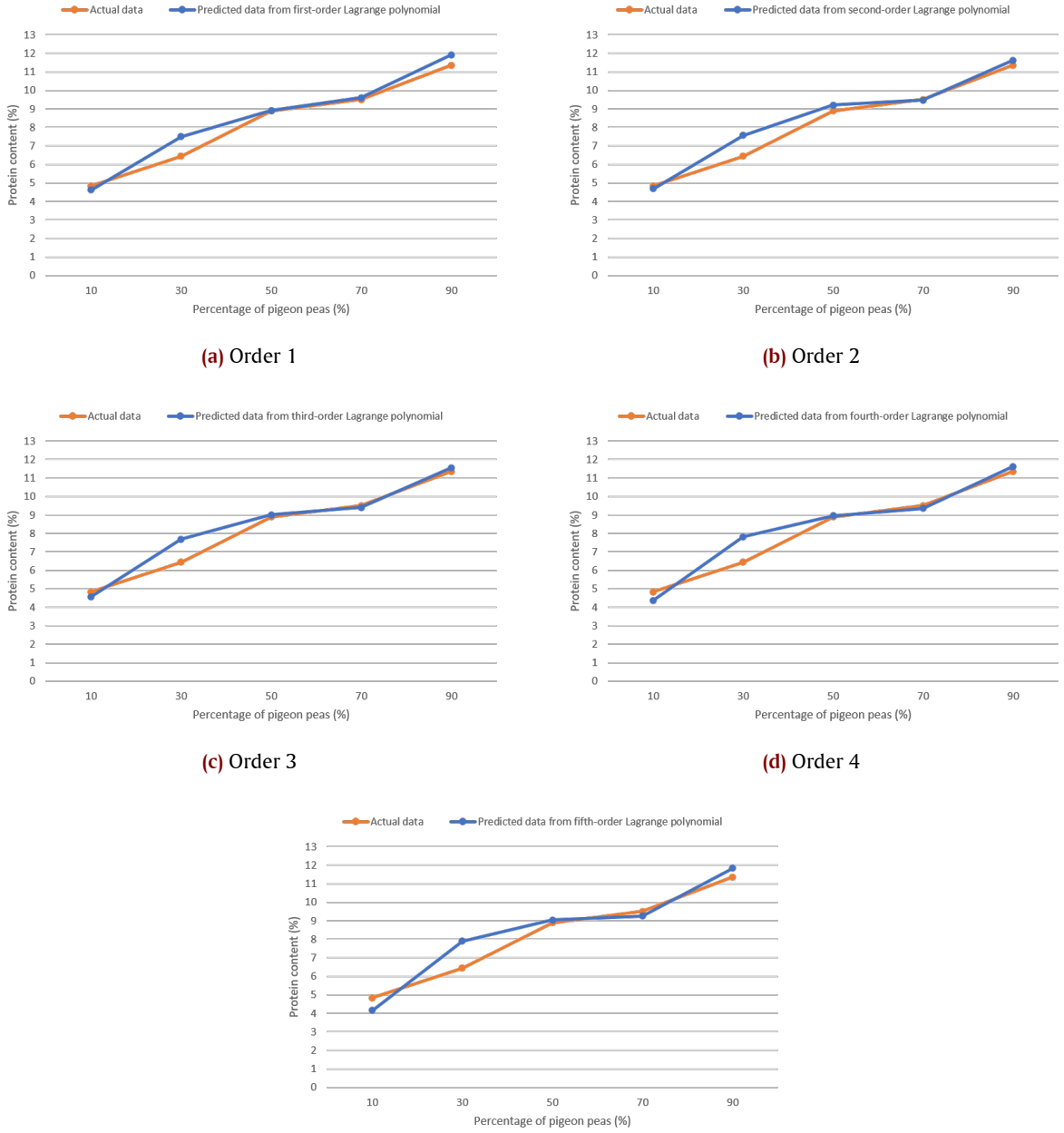


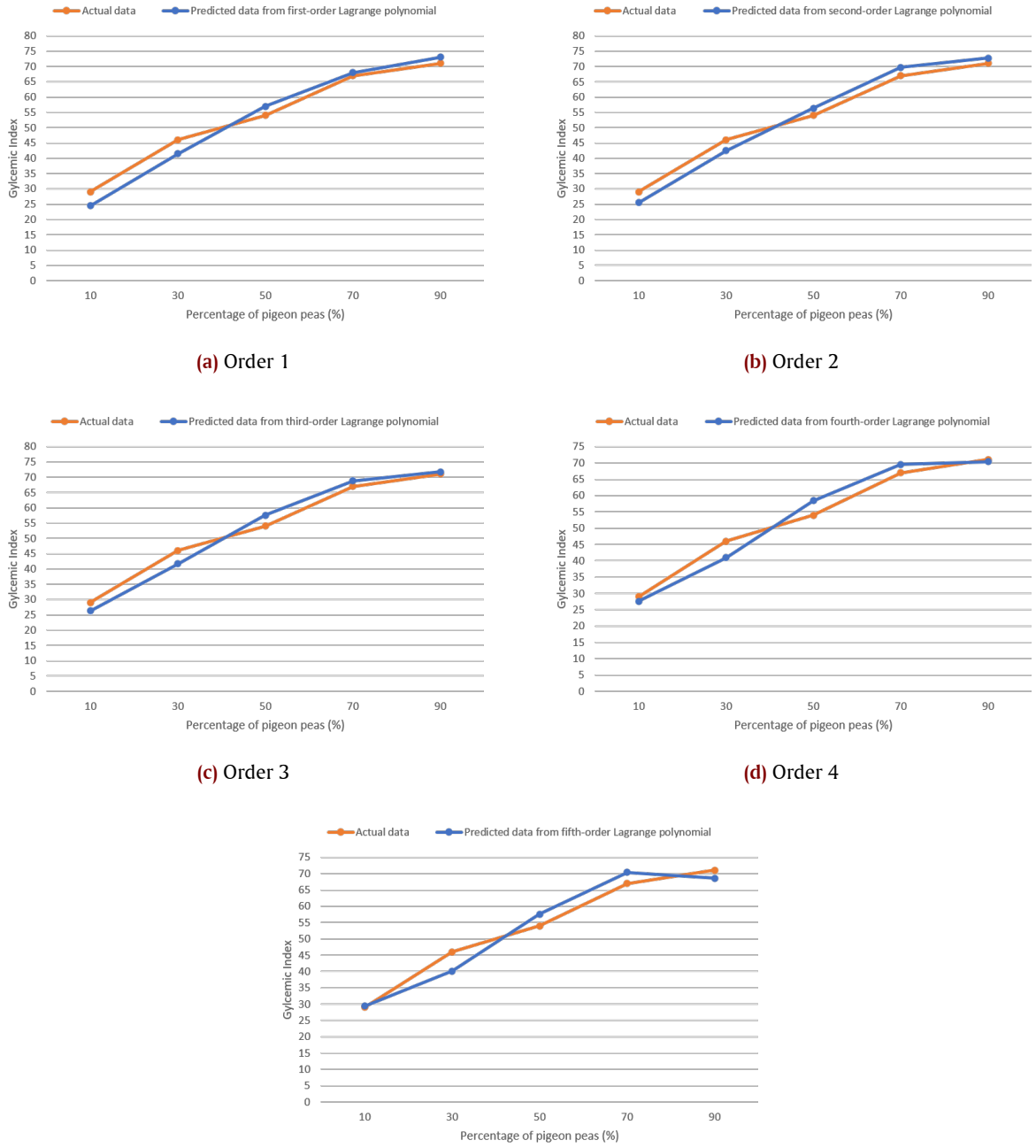
Figure 1. Comparison curves of actual protein content (laboratory results) and predicted protein content using Lagrange polynomial interpolation with varying polynomial orders: (a) order 1; (b) order 2; (c) order 3; (d) order 4; (e) order 5

Based on Table 6, the NRMSE values for the predicted protein content and glycemic index for orders 1, 2, 3, 4, and 5 show the good results, with NRMSE values approaching 0. This indicates that the Lagrange polynomial interpolation method for orders 1, 2, 3, 4, and 5 is effective in predicting the protein content and glycemic index of local food-based snack bars.

Furthermore, the smallest NRMSE value for the predicted protein content and glycemic index was obtained using the Lagrange polynomial interpolation method of order 2. This means that, among orders 1, 2, 3, 4, and 5, the highest accuracy in predicting the protein content and glycemic index of local food-based snack bars was achieved with the Lagrange polynomial interpolation method of order 2.

Next, the comparison curves between the protein content obtained from laboratory analysis and the predicted protein content, as well as between the glycemic index from laboratory analysis and its predicted values, are presented in Figure 1 and Figure 2, respectively. These curves were generated using Microsoft Excel.

In Figure 1, which represents the protein content data, all interpolation models follow the increasing trend in protein concentration as the percentage of pigeon peas increases. However, the degree of closeness between the predicted and actual values varies. First-order interpolation (Figure 1a) shows a linear



(a) Order 1

(b) Order 2

(c) Order 3

(d) Order 4

(e) Order 5

Figure 2. Comparison curves of actual glycemic index values (laboratory results) and predicted glycemic index values using Lagrange polynomial interpolation with varying polynomial orders: (a) order 1; (b) order 2; (c) order 3; (d) order 4; (e) order 5

approximation that fails to capture the natural curvature of the data. In contrast, second-order interpolation (Figure 1b) demonstrates a close approximation to the actual values, following a curve that tends to be quadratic. For orders 3 to 5 (Figure 1c–Figure 1e), although the predicted values remain relatively close to the actual data, fluctuations or sharp bends appear that deviate from the experimental pattern, an indication of Runge's oscillation phenomenon.

A similar pattern is observed in Figure 2 for the glycemic index data. First-order interpolation produces a straight line that does not adequately reflect the slightly tapering growth in glycemic index at higher substitution levels. The second-order model again shows the best performance in following the actual trend without overfitting. Models of orders 3 to 5 begin to display oscillatory patterns and deviations at the edges of the domain ($x = 10\%$ and 90%), indicating a tendency to overfit the data points while losing global stability.

Mathematically, this phenomenon can be explained by the fundamental characteristics of Lagrange polynomials. Low-order polynomials (such as orders 1 and 2) form simple curves with smooth gradient transitions. As the order increases, the degree of the polynomial increases as well, resulting in functions with

multiple inflection points and a higher potential for oscillation, especially when the number of data points is small. This aligns with Runge's phenomenon, which states that high-order polynomial interpolation tends to be unstable near the boundaries of the domain. Therefore, second-order interpolation provides the optimal balance between curve flexibility and numerical stability.

In other words, the visual findings support the numerical results, confirming that second-order Lagrange polynomial interpolation is the most reliable model for predicting protein content and glycemic index in data sets with regular distributions and small sample sizes.

3.5. *Practical Implications for the Food Industry*

The validated quadratic model developed in this study has the potential to be applied as a rapid tool in various scenarios of food product development. First, it can be used for early-stage screening of new formulations by estimating protein content and glycemic index prior to laboratory testing, thereby reducing routine chemical analysis costs by more than 40%. Second, at the pilot production scale, the model can provide real-time predictions when adjusting the ratio of pigeon peas to sweet potatoes, allowing for quick responses to raw material variability. Third, it can assist in generating preliminary nutritional estimates prior to formal labeling, which is particularly beneficial for small and medium-sized enterprises (SMEs) that face financial and laboratory access limitations.

3.6. *Study Limitations*

This study has several limitations. The sample size was restricted to 11 formulations within a $0 - 100\%$ substitution range, so the validity of extrapolations beyond this range remains uncertain. The glycemic index was measured in vitro, which may not fully reflect in vivo glycemic responses; additional clinical validation is therefore required. The model is deterministic and does not account for biological variability between batches or potential process-related noise. Furthermore, the residuals for glycemic-index predictions exhibit a non-normal distribution, suggesting local bias, possibly due to heterogeneity in resistant-starch content.

4. Conclusion

Based on the laboratory test results for protein content and glycemic index of local food-based snack bars, along with the predicted values generated using Lagrange polynomial interpolation of orders 1 through 5, it can be concluded that the interpolation method is effective in modeling both nutritional parameters, as indicated by NRMSE values approaching zero. Among the five polynomial orders tested, the second-order Lagrange interpolation demonstrates the highest predictive accuracy, yielding the lowest NRMSE values, 0.08244 for protein content and 0.06798 for glycemic index. These results highlight the superiority of the quadratic model in balancing curve flexibility and numerical stability, making it the most suitable approach for estimating nutritional values in local food-based formulations.

Beyond numerical validation of protein content and glycemic index, it is recommended that further research be conducted to evaluate consumer preferences for the 11 snack bar formulations developed in this study. Sensory assessments, including taste, aroma, and texture, are essential to understand consumer acceptance and the market potential of each formulation. This will enable producers to identify the most appropriate formulation that balances nutritional quality with consumer appeal, thereby enhancing product success in real-world applications.

Author Contributions. **Lingga Gita Dwikasari:** Conceptualization, methodology, software, validation, formal analysis, investigation, resources, data curation, writing—original draft preparation, writing—review and editing, visualization. **Satrijo Saloko:** Conceptualization, writing—review and editing. **Dody Handito:** Conceptualization, writing—review and editing. **Riezka Zuhriatika Rasyda:** Conceptualization, investigation, writing—original draft preparation, project administration. **Eko Basuki:** Conceptualization, supervision. All authors discussed the results and contributed to the final manuscript.

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