RESEARCH ARTICLE

# Extraction and antioxidant activity analysis of polysaccharides and flavonoids in corn silk

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**Corn silk's polysaccharide and flavonoid antioxidant properties have great promise for health advantages and natural product utilization. Effective extraction and evaluation of these substances are critical for their optimal medicinal and nutritional use. Conventional approaches for determining antioxidant activity in corn silk are often labor-intensive and time-consuming with existing predictive models often lacking accuracy and generalizability. This study was to obtain polysaccharides and flavonoids from maize silk, analyze their antioxidant activities, and create a predictive model to appropriately assess these activities. To tackle the shortcomings of previous methods, this work proposed the Tri-model antioxidant stacking approach (TMASA), a cutting-edge machine learning technique, to improve the accuracy of antioxidant activity forecasts. TMASA employed three base classifiers including k-nearest neighbors (k-NN), naive bayes (NB), decision tree (DT) and a meta-classifier, multilayer perceptron (MLP), to predict three key antioxidant activities of 2,2-diphenyl-1-picrylhydrazyl (DPPH) (%), 2,2'-azino-bis (3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) (%), and ferric reducing antioxidant power (FRAP) ($\mu$mol FeSO$_4$/g). The TMASA was trained and validated utilizing the maize silk extract antioxidant activity dataset (MSEAA), a comprehensive dataset derived from controlled laboratory experiments that included extraction process attributes as well as antioxidant measurements. The model was evaluated using performance metrics including accuracy, precision, recall, F1-score, and Matthew's correlation coefficient (MCC). The results showed that the proposed TMASA presented the best accuracy, precision, recall, F1-score, and MCC, showing its efficiency at accurately assessing the antioxidant properties of corn silk extracts. This study not only increased the comprehension of antioxidant activity in corn silk but also set a novel benchmark for predictive modeling in natural product research.**

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## Introduction

Corn silk, the long, thread-like strands found at the tip of a corn ear, has long been considered an agricultural waste of limited utility [1]. However new research has revealed its tremendous possibility due to the existence of bioactive substances, specifically polysaccharides and flavonoids [2]. These chemicals have powerful antioxidant qualities, providing corn silk a significant resource for health advantages and use in natural products [3]. Effective extraction and evaluation of polysaccharides and flavonoids are critical for their optimum medicinal and

nutritional use [4]. Polysaccharides and flavonoids are renowned for their capacity to scavenge free radicals, reducing oxidative stress, and related health hazards. The antioxidant activity of these substances can be tested using many assays such as 2,2-diphenyl-1-picrylhydrazyl (DPPH) antioxidant activity, 2,2'-azino-bis (3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) antioxidant activity, and ferric reducing antioxidant power (FRAP) [5].

Antioxidants are essential for human health because they combat oxidative stress and neutralize free radicals that can lead to chronic diseases including cancer and cardiovascular ailments [6]. Natural antioxidants obtained from fruits, vegetables, and other plant sources are progressively studied because of their possible health advantages and less adverse compared to synthetic alternatives [7]. Jideani *et al*. investigated the role of antioxidants in different vegetables and fruits, highlighting their potential to reduce chronic disease risk in both dietary and supplement forms. The results emphasized the many methods of antioxidant action and the significance of including antioxidant-rich foods in the diet for disease prevention [6]. The efficiency of plant-derived antioxidants was corroborated by Rahaman *et al*. who reviewed the pharmacological importance of antioxidants in natural products [7]. The study examined the health effects of antioxidants found in fruits, seeds, and other natural sources, emphasizing their role in reducing oxidative stress and associated illnesses. This thorough examination suggested the importance of functional foods with strong antioxidant capacity in treating free radical illnesses. Akbari *et al*. discussed how natural antioxidants could assist minimize oxidative stress and regulate diseases caused by free radical damage. Their study focused on the therapeutic possibility of plant-derived antioxidants in fighting ailments like cancer, cardiovascular diseases, and neurological disorders [8]. Hoang *et al*. explored the use of natural antioxidants in skincare products and found that, while natural antioxidants were safe and potentially beneficial, their efficiency *in vivo*

needed strong evidence due to varying biological functions [9]. Lu *et al*. evaluated the antioxidant properties of natural pigments found in fruits like carotenoids and flavonoids and investigated the antioxidant activity of these pigments, highlighting their health advantages and prospective applications in the food and cosmetic industries. The results confirmed the important function of fruit pigments in antioxidant defense and their promising uses [10].

Corn silk, an underutilized byproduct of maize farming, has been recognized as an excellent source of antioxidants. Lapčík *et al*. studied maize silk extracts and found a high antioxidant activity that varied with the maturation stage. This study underlined the significance of extraction conditions and developmental stages in maximizing antioxidant capacity [11]. Ong *et al*. concentrated on antioxidant peptides produced from maize silk and employed both *in vitro* and *in silico* approaches for purification and characterization. The study underlined the potential of maize silk-derived peptides as natural antioxidants, indicating their use as functional food components [12]. Similarly, Zhang *et al*. improved the extraction of polysaccharides from maize silk and tested their antioxidant activity. The study discovered that maize silk polysaccharides had strong antioxidant activities both *in vitro* and *in vivo*, suggesting its usage as antioxidant agents in food and medicine [13]. Singh *et al*. evaluated the antioxidant possible of different corn silk cultivars at various developmental phases, as well as their effects on glycemic response. The studies discovered variations in antioxidant activity and techno-functional qualities, which had significance for the creation of value-added products and medicinal applications [1, 14].

Despite the crucial insights presented by these investigations, measuring corn silk's antioxidant activity remains a significant difficulty. Conventional methods for determining antioxidant characteristics are frequently labor-intensive and time-consuming, which necessitate significant chemical analysis and have the

potential to produce inconsistent results, limiting their practical use. Furthermore, previous predictive models for antioxidant activity usually show shortcomings in accuracy and generalizability, resulting in variable and inaccurate findings. There is a necessity for more effective, precise, and generic techniques for evaluating and predicting corn silk's antioxidant potential. This study aimed to solve these shortcomings by constructing a unique model that improved predicted accuracy and accelerated the evaluation process, thus enhancing the comprehension and utilization of cornsilk's antioxidant characteristics. The study proposed the Tri-model antioxidant stacking approach (TMASA), a cutting-edge machine learning technique aimed to improve the accuracy of antioxidant activity forecasts, using three base classifiers of k-nearest neighbors (k-NN), naive bayes (NB), and decision tree (DT), as well as a meta-classifier named multilayer perceptron (MLP) to predict three important antioxidant activities of DPPH, ABTS, and FRAP. This study provided significant advances in the realm of natural product research, nutraceuticals, functional foods, and machine learning. Researchers and industry experts could use the updated prediction model to maximize antioxidant extraction and usage from corn silk and other natural sources.

## Materials and methods

### Dataset preparation
Maize silk extract antioxidant activity dataset (MSEAA) acquired by a series of controlled laboratory experiments that used various extraction methods and settings was used in this study to create and evaluate the TMASA, which included several features that reflected the conditions and properties of the extraction procedures and the subsequent antioxidant activity. To separate the antioxidant components from maize silk, each sample went through a specialized extraction method. The collection procedure involved recording specific details on the extraction parameters like the method

employed, extraction time, temperature to ensure the uniformity and reproducibility of the outcomes. The dataset included numerous important features including a distinct sample ID assigned to each sample for separate monitoring and assessment and the information of extraction techniques including the name of method like solvent extraction, ultrasound-assisted extraction, and microwave-assisted extraction, the extraction time, the extraction temperature, solvent type and volume, and the pH of the extract. Compositional metrics included polysaccharide content and flavonoid content. The antioxidant activity was indicated by DPPH antioxidant activity, ABTS antioxidant activity, and FRAP antioxidant activity. The dataset also captured the extract's yield, which represented the proportion attained from the initial corn silk amount. This sample dataset emphasized the differences in extraction procedures, circumstances, and consequent antioxidant activity, laying the groundwork for the development of the TMASA model. Each feature provided critical data for comprehending the parameters impacting antioxidant activity in corn silk extracts.

### Tri-model antioxidant stacking approach (TMASA)
The TMASA was employed in this study to improve the prediction accuracy of antioxidant activities of DPPH, ABTS, and FRAP in corn silk extracts by combining the abilities of three machine learning algorithms using a complex stacking ensemble method. The proposed model used k-NN, NB, and DT as the base classifiers and MLP as the meta-classifier and implemented them using the Weka software (https://ml.cms.waikato.ac.nz/weka). The flow diagram of the proposed TMASA model was shown in Figure 1. The data preprocessing stage guaranteed that the dataset was clean, consistent, and prepared for model training by preparing data with numerous critical processes. The initial task was to handle missing values. For numerical features, missing values were imputed with the mean of the available data, which preserved the dataset's central tendency while
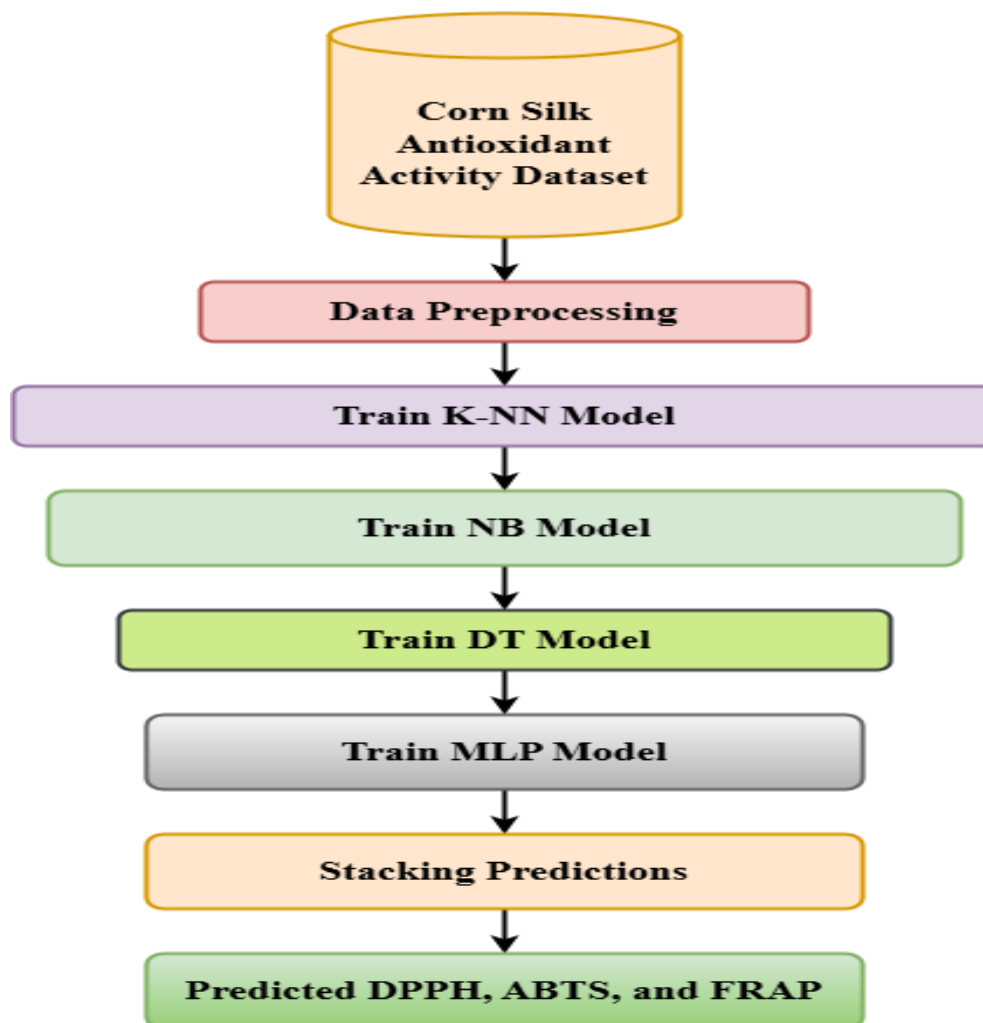
**Figure 1.** Flow diagram of TMASA algorithm.

avoiding biases that could be induced by utilizing arbitrary imputation values. Missing values in categorical features were replaced with the mode, the most common value, which preserved the most prevalent category and lessened the impact of missing data. The transform category featured utilizing label encoding, which assigned a distinct number to each category and converted it to a numerical representation appropriate for machine learning techniques. After encoding, numerical features were normalized using the min-max method, which scaled the numerical attributes to a range of 0 to 1, guaranteeing that all features participated equally in the model and preventing a single attribute from dominating due to its size. The

base classifiers were trained after data preprocessing. To predict antioxidant activity, k-NN, NB, and DT models were trained using the preprocessed dataset. Each model was trained independently to learn various elements and patterns from the dataset. The diversity in these models assisted in capturing the many underlying relationships between the attributes and the target variable. The stacking ensemble technique was applied after training the basis classifiers. Predictions for each sample in the dataset were derived using the k-NN, NB, and DT models and were concatenated to create a new feature vector that incorporated the base classifier outputs and was used as the meta-classifier's input. The MLP model was then trained on the

additional feature vectors to forecast antioxidant activity. This stacking procedure enabled the meta-classifier to learn from the combined benefits and shortcomings of the basic classifiers, thus boosting overall prediction accuracy. To predict a new sample, the predictions from the k-NN, NB, and DT models for that sample were received and combined to generate a new feature vector for the sample. The MLP model then used this new feature vector to forecast DPPH, ABTS, and FRAP antioxidant activity. This multi-step strategy ensured that the final predictions gained from the different insights gathered by each base classifier were refined and aggregated by the meta-classifier.

## Antioxidant activity prediction

The prediction of DPPH, ABTS, and FRAP antioxidant activities entailed multiple procedures. The k-NN, NB, and DT models were first trained using preprocessed dataset to predict DPPH, ABTS, and FRAP antioxidant activities. These fundamental classifiers identified various patterns and relationships in the dataset, resulting in a wide range of predictions. During the stacking phase, these three models' predictions were concatenated to create new feature vectors to be utilized for training the MLP meta-classifier. For each new sample, the procedure was repeated as the basic classifiers presented predictions, which were merged and utilized by the meta-classifier to forecast DPPH, ABTS, and FRAP antioxidant activities. This method ensured the final forecast advantages from the benefits of numerous models, thus enhancing accuracy and robustness.

## Comparison of TMASA with other algorithms

The prediction results of TMASA algorithm were compared with the independent results obtained through four distinct machine learning models, respectively, including k-NN, NB, DT, and MLP using Java and the Weka tools. The comparison was based on numerous evaluation metrics including accuracy, precision, recall, F1-score, and Matthews correlation coefficient (MCC).

## Results and discussion

The effectiveness comparison study of TMASA algorithm with the other models across key metrics showed that TMASA algorithm consistently outperformed existing models across all assessment metrics with the best accuracy, precision, recall, F1-score, and MCC values (Table 1). TMASA outperformed the other models with an accuracy of 93.5%, demonstrating its capacity to accurately classify data in a broad range of cases. The nearest competitors were NB (89.7%) and DT (88.3%) trailed by multiple percentage points, while K-NN (86.5%) and MLP (83.9%) lagged even further behind. TMASA's greater accuracy indicated its consistency in making the most accurate predictions. TMASA dominated the precision by 92.9%, which reduced false positives more effectively than the other models. DT and NB demonstrated 89.6% and 88.8% precisions, respectively. Although they both provided high precision, they were still behind that of TMASA. K-NN and MLP generated more false positives with 85.8% and 82.8% precisions, which reduced their ability to make accurate predictions. TMASA's high precision suggested that it was extremely efficient at accurately detecting pertinent instances, resulting in fewer classification errors. The recall of TMASA was 92.3% compared to DT (89.0%), NB (88.3%), K-NN (84.8%), and MLP (82.6%), while DT and NB both missed more pertinent instances than TMASA, and K-NN and MLP continue to miss even more positive cases. The results showed that TMASA outperformed the other models and was the best at detecting true positive cases. It also confirmed TMASA's unparalleled capacity to capture pertinent information, surpassing the others in detecting true positives. The F1-score, that balanced precision and recall, showed TMASA's supremacy at 92.6%. Although DT (89.3%) and NB (88.6%) provided an excellent balance, neither of them could match TMASA's efficacy, while K-NN (85.4%) and MLP (82.8%) fell far short of achieving this equilibrium. TMASA's high F1 score demonstrated its outstanding abilities in both

**Table 1.** Comparative evaluation of TMASA algorithm and other models' effectiveness.

| Model | Accuracy (%) | Precision (%) | Recall (%) | F1-score (%) | MCC (%) |
|---|---|---|---|---|---|
| K-NN | 86.5 | 85.8 | 84.8 | 85.4 | 82.3 |
| NB | 89.7 | 88.8 | 88.3 | 88.6 | 85.6 |
| DT | 88.3 | 89.6 | 89.0 | 89.3 | 86.2 |
| MLP | 83.9 | 82.8 | 82.6 | 82.8 | 79.4 |
| TMASA | 93.5 | 92.9 | 92.3 | 92.6 | 90.0 |

precision and recall, rendering it the most well-rounded model. TMASA demonstrated an excellent MCC score of 90.0%, indicating its total consistency and dependability, followed by DT (86.2%) and NB (85.6%). However, the leading score of TMASA indicated its capacity to make balanced predictions across classes. K-NN (82.3%) and MLP (79.4%) trailed substantially with less consistency in their predictions. The highest MCC score obtained by TMASA suggested its strength and reliability in a variety of situations, surpassing all competitors in this critical metric. Such improved performance could be attributed to TMASA's innovative unique stacking ensemble technology, which efficiently combined the capabilities of numerous base classifiers and refined their predictions using a meta-classifier. By merging the predictive capabilities of K-NN, NB, and DT and refining the aggregated predictions using a MLP meta-classifier, TMASA successfully mitigated the restrictions of individual models.

This approach took advantages of the diversity of the base classifiers to capture numerous patterns and relationships within the data, while the meta-classifier improved the overall prediction by learning from the combined benefits and shortcomings of the base models. The results of this study clearly showed that TMASA algorithm outperformed the other previous models for predicting antioxidant activity. The thorough assessment across several parameters demonstrated TMASA's robustness and dependability, providing it an important tool for reliably measuring antioxidant activity in corn silk extracts. The originality of TMASA resided in its excellent incorporation of numerous machine learning approaches, which provided an important improvement in predictive effectiveness compared to conventional approaches.

**Conclusion**

This study developed the TMASA model to improve the prediction accuracy of antioxidant activity in corn silk extracts. The proposed TMASA model implemented using Java and the Weka tool outperformed standard models including K-NN, NB, DT, and MLP in terms of accuracy, precision, recall, F1-score, and MCC across all assessments. TMASA's success could be ascribed to its efficient integration of numerous base classifiers and prediction refinement *via* a meta-classifier, which demonstrated its durability and dependability in capturing complicated data patterns. Future research will investigate the use of TMASA in other crops or domains, thereby expanding its utility to different fields like medicinal plant analysis, food quality evaluation, or environmental monitoring, thus enlarging the scope and influence of this sophisticated prediction model.

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