Research Article

Intelligent CO_2 Monitoring for Diagnosis of Sleep Apnea Using Neural Cryptography Techniques

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In biomass wastage, carbon is one of the adsorbent materials. Biomass wastage contains complex materials, and pressure, various temperatures, and presence of various chemical components which are subjected to the adsorption of carbon are a tedious task, and it is used in the sustainable waste management system. While screening the biomass wastage management system, prediction of activated carbon's quality and understanding of the mechanism of adsorption of CO_2 are a complicated task. Many research works have been developed; the main issues are inaccurate and inefficient prediction of carbon available in the various feedstock of biomass wastage. To overcome these issues, this paper proposed gene expression programming (GEP) with K-nearest neighbour (GEP-KNN). The key advantage of the proposed work shows excellent performance in the prediction of adsorbing carbon and accuracy. The accuracy of the GEP-KNN algorithm with different K values produced the highest accuracy at $K = 9$ and $k = 10$ of 95.12% and 95.67%; the lowest accuracy is $K = 1$ of 65.34%.

1. Introduction

In the ecosystem of the globe, one of the main sources is storage of carbon in the terrestrial ecosystem which creates terrestrial biomass [1]. The huge amount of carbon availability in the ecosystem plays a vital role in reducing global warming [2, 3]. Adsorption of carbon in biomass wastage has been taken as a vital role for reducing CO_2 emission [4–7]. Activated carbon is an adsorbent component of biomass wastage with large adsorption capacity, superior surface reactivity, and high porosity. It can be used in the field

of water treatment, agricultural wastage water treatment, industrial application, and pharmaceutical [8–10]. The toxic pollutants available in the terrestrial, industrial wastage water, and drinking water are important environmental issues. Adsorption has become one of the best techniques in removing pollutants. Activated carbon acts as an adsorbent material for purifying the water and reduces the pollutant content.

For implementing the concept of adsorption of carbon in the biomass wastage system, so much research works have been done. The major drawbacks are poor quality, ineffectiveness, high time consumption, and inaccuracy. To

overcome these drawbacks, the proposed work GEP-KNN predicts the adsorption of CO_2 in the biomass wastage system. This proposed work provides the best technique in the aspects of providing highly accurate detection of CO_2 in an effective way. Time consumption is also low and minimizes the error rate. This proposed work fills gaps of existing research work by impacting the interaction of biomass wastage system and implementing the properties of activated carbon using GEP-KNN.

Machine learning approaches include support vector regression, linear regression, and random forest regression for the prediction of iodine component in the activated carbon product. This technique includes various types of straw like carbonization and activation methods [11]. Implementing geometric expression programming includes Symbiotic Gene Expression Programming (SGEP) which is based on the concept of symbiotic algorithm which improves the process, and it has low-efficiency issues when it handles a complex problem [12]. This paper [13] computationally proposed GEP in terms of the expression tree. Therefore, it can reduce the chromosomes. The main contribution of this work includes

(1) improving efficiency; we proposed GEP with KNN. This classifier provides high-quality prediction of CO_2 in the biomass wastage system

(2) implementing texture properties in biomass wastage and performing the evaluation in the metric measures of the correlation coefficient, RMSE, and bias

The paper has been organized as follows: Section 2 describes the review of the literature, Section 3 introduces prediction of CO_2 in the biomass wastage system using GEP with KNN, Section 4 discusses the experimented results, and Section 5 concludes the paper with future directions.

2. Review of Literature

Due to the development of industrialization and increase in population, the environment got polluted and there is increased global warming. To reduce global warming in the polluted environment, adsorption of carbon from biomass wastage is needed to protect our globe from global warming. The form of activated carbon is in a microporous form of carbon with the structure of volume, surface area, and capacity of high adsorption [14]. For reducing the emission of CO_2, adsorption is needed in the aspects of cryogenic, adsorption, membrane, and microalgal biofixation. It separates CO_2 and reduces the regeneration energy requirements [15]. Adsorption of isotherms of CO_2 is available and also at various pressures and temperatures by using the volumetric process [16]. This paper [17] proposed that activated carbon is taken as a precursor and provided into disposal of sustainable wastage. And it associates developing the environment which increases concerns; there is an increased research interest to find low-cost biomass waste materials as well as low-cost processes for production.

The development of civilization and agriculture and at the same time wastage from industry and agriculture are considered precursors of activated carbon production [18]. Similarly, open burning of wastage emits obnoxious gases and particulate matter which pollute the environment, and also, during the rainy season, deposition of wastage will block drainage channels. These deposited wastages are considered biomass wastage and exhibit activated carbon for adsorption [19, 20]. Tables 1 and 2 shows survey on adsorption of CO_2 in biomass.

3. Proposed Methodology

CO_2 adsorption in the biomass waste management system is at various temperatures and pressure with various thermodynamic properties like isosteric heat of adsorption, entropy, and Gibbs free energy. In this proposed work, we implement the fusion of GEP with KNN algorithm to improve the efficiency and accurate prediction of CO_2. The architecture of the proposed work (GEP with KNN) is given in Figure 1.

Figure 1 describes three phases, namely, data collection, preprocessing, and analysis of GEP-KNN.

3.1. Preprocessing

3.1.1. Normalization. To enhance the quality of the GEP-KNN algorithm's output, it undergoes data normalization by using the function of linear normalization as given below:

$$\text{Norm}_{i,j} = \frac{\text{data}_{i,j} - \text{Min}_j}{\text{Max}_j - \text{Min}_j}, \tag{1}$$

where $\text{Norm}_{i,j}$ is the value normalized for the data sample point $\text{data}_{i,j}$ and Max_j, Min_j are parameter values of minimum and maximum.

3.2. Applying Proposed Method of GEP-KNN

3.2.1. Overview of GEP. Gene expression programming (GEP) is an evolutionary-based computation algorithm. This algorithm is based on the inheritance concept of genotype from the genetic algorithm (GA) and phenotype from genetic programming (GP). The prediction of CO_2 in biomass GEP plays a vital role in the aspect of handling multiple components available in biomass wastage, and also, it is faster than genetic programming (GP). Genotype acts like GA, and phenotype is like a tree structure format with variable size and length. Based on the threshold values of phenotype and replicator, it produced the output. It implements the relationship between various components available in biomass wastage by applying the Boolean logical operators like AND, OR, and NOT with the algebraic operators of $+, -, \times, \div$.

3.2.2. GEP in Biomass Wastage. Finding the relationship of components in biomass wastage with respect to the variables used in the GEP algorithm is creating a population of linear chromosomes. For each component in the biomass waste, the position of CO_2 genes of these chromosomes and its variable is placed. Once CO_2 is identified and its position is filled, evaluate the fitness of each CO_2 component (chromosome) in biomass wastage. In the GEP algorithm, all

TABLE 1: Adsorption of CO_2 in biomass.

Author	Aim	Adsorbent	Pollutant
Delgado-Moreno et al. [21]	New insights into the efficient removal of emerging contaminants by biochars and hydrochars derived from olive oil wastes	Biomass	Biochars and hydrochars
Egirani et al. [22]	Powdered and granular activated carbon from Palmae biomass for mercury removal	Biomass	Mercury removal
Govindan et al. [23]	Activated carbon derived from Phoenix dactylifera (palm tree) and decorated with MnO_2 nanoparticles for enhanced hybrid capacitive deionization electrodes	Biomass	Dactylifera with MnO_2 nanoparticles
Khorasgani et al. [24]	Briquetting grass and tree leaf biomass for sustainable production of future fuels	Biomass	Briquetting grass and tree leaf
Anastopolous et al. [25]	Agricultural biomasses for the removal of toxic metal(oid)s from contaminated aqueous solutions	Biomass	Toxic metal(oid)s
Wei et al. [26]	Petrochemical wastewater and produced water from oil and gas production are reviewed	Chitosan-activated montmorillonite, nutshell filters, etc.	Petrochemical wastewater and produced water from oil and gas
Doshi et al. [27]	Recovery of spilled oils using biomass and polymers, as sorbents or separators	Biomass	Diesel, crude oil, gasoline, waste lubricating oil, etc.
Wong et al. [28]	The use of ACs prepared from magnetic materials and nanoparticles in wastewater purification compared to biochars derived from biowaste	Biomass	Dyes, heavy metals

TABLE 2: The parameters which are used in GEP model.

Parameter	Parametric function name	Parametric value
P_1	Function set	$+, -, \times, /, \sqrt{}, e^x, \ln(x)$, etc.
P_2	Chromosome's value	20-50
P_3	Size of head	5, 7, 9
P_4	Number of genes	4
P_5	Function for linking	Addition, multiplication
P_6	Function for fitness in error type	MAE, customized fitness for error function
P_7	Rate of mutation	0.055
P_8	Rate of inversion	0.1
P_9	Recombination rate of one point	0.4
P_{10}	Recombination rate of two points	0.4
P_{11}	Recombination rate of gene	0.2
P_{12}	Transposition rate of gene	0.2

identification of CO_2 component (chromosome) is represented by expression tree (ET) format. That is similar to gene's phenotype [29]. Then, select the next component as the next generation; construct the linear genotype state of the chromosome as applied.

The most important parameters used in the GEP algorithm is creating expression trees (ET) and chromosomes. The process of transforming information (chromosomes) to ET is based on a set of rules, and it is known as translation. Evaluate the genetic code by one-to-one relationship between chromosome symbols with terminal values or functions. The GEP algorithmic steps are given in Algorithm 1.

Algorithm 1 seems to evaluate the fitness function and choose the functions and terminals. Construct the structure of chromosomes based on the gene number and length and number of generations. Apply linking function and train the model of GEP until current generation is evaluated and repeat the process for executing the next generation.

3.2.3. KNN. The K-nearest neighbour algorithm is one of the most popular classification algorithms. The KNN algorithm is selecting the new component of the unknown category for the classification. The KNN classification algorithm can be
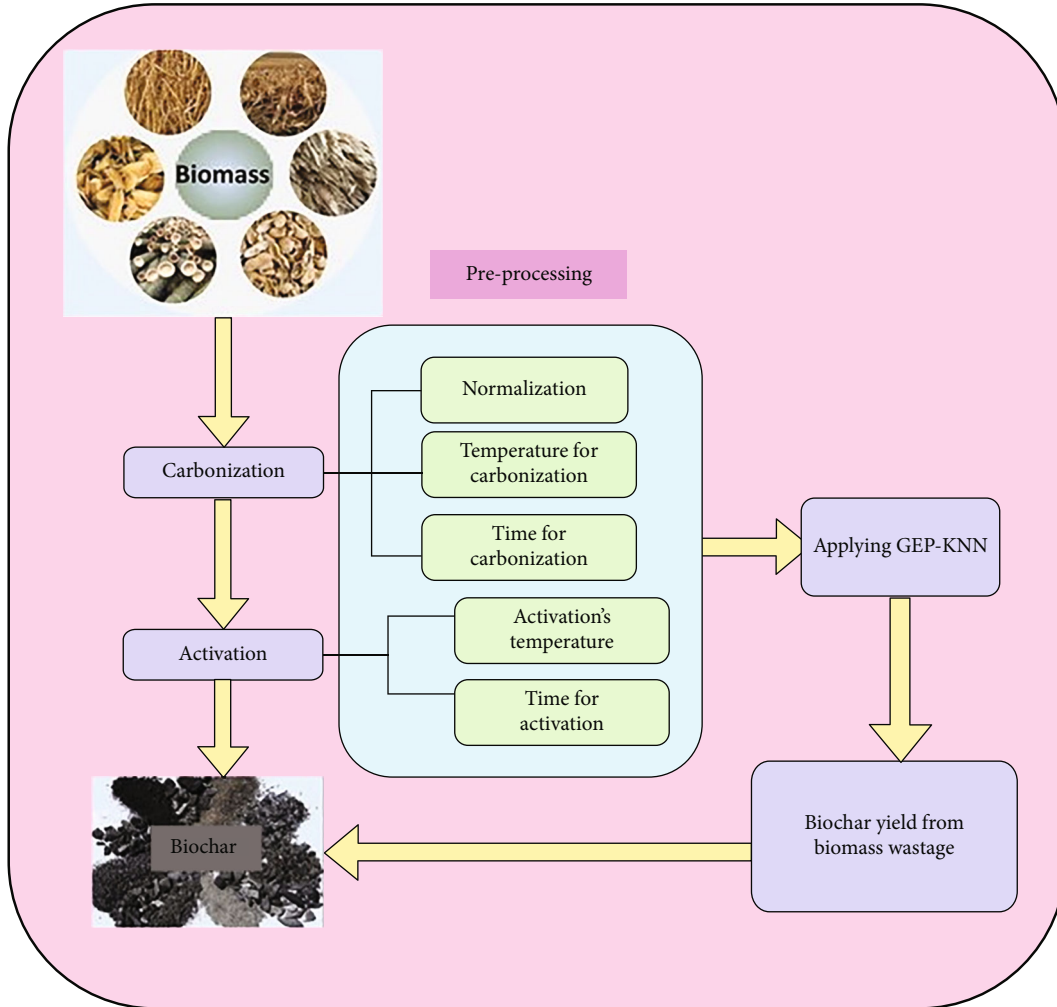
FIGURE 1: Architecture of proposed work.

Step 1. Initialize the population.
Step 2. Execute chromosome expression as ET.
Step 3. Calculate fitness function by using
    $\text{fit}_i = \sum_{j=1}^{c_i} (M - |\text{Chr}_{(i,j)} - \text{Targ}_j|)$ where M is the selection range value and $\text{Chr}_{(i,j)}$ is the fitness value of individual chromosome and
Targ_j is the target value of fitness value for j. $|\text{Chr}_{(i,j)} - \text{Targ}_j|$ is the precision.
Step 4. If $|\text{Chr}_{(i,j)} - \text{Targ}_j| \leq 0.01$, then the precision value is 0.
Step 5. $\text{fit}_i = \text{fit}_{max} = \text{Chr}_i M$; here, consider $M = 100$, and now, $\text{fit}_{max} = 1000$.
Step 6. Create chromosomes by selecting the set of terminals and function by using parametric value P_1.
Step 7. Select the architecture of chromosomes in the aspects of head length and number of genes in the chromosome.
Step 8. Use the parametric value of P_5 linking all subexpression functions of tree value by using addition operation. There are three
types of transportation and three types of recombination.
Step 9. Use all operators of genetic, namely, mutation, three types of transportation, and three types of recombination as in the para-
metric table.
Step 10. To create a new chromosome, go to Step 2. Repeat it until all chromosomes get evaluated.

ALGORITHM 1: GEP for biomass wastage.

used to compute both regression and classification. Selecting the sample training $P = \{x_1, x_2, \cdots, x_n\}$, and sampling data is distributed in A and categorized into $D_1, D_2, \cdots, D_n$. From the training data set of values, evaluate the nearest sample value using discriminant function F_i. Identify K of the neighbour samples with $F_i(x) = K_i$, where $i = 1, 2, 3, \cdots, N$. Select the sample of data and evaluate $y_i(x) = \text{Max}(K_i)$. The algorithm for KNN is given in Algorithm 2.

Step 1. Split the data set into the training and testing data sets and consider training sample data set $P = \{x_1, x_2, \cdots, x_n\}$. And the category of sample $D = D_1, D_2, \cdots, D_n$. And testing sample data $S = \{S_1, S_2, \cdots, S_N\}$.
Step 2. Take the initial k value and choose the initial nearest neighbour to X.
Step 3. Evaluate the distance between the test data set and all other training data set values.
Step 4. Sort the output distance values in ascending order and select the appropriate k value.
Step 5. Choose the closest k known sample values.
Step 6. Count the sample of categories with the highest probability within the k known sample values.
Step 7. Implement the category of test sample data value as the category obtained by statistics using Step 6.

ALGORITHM 2: KNN algorithm.

Step 1. For each instance value in the training data set $\text{tins}_i \in T//T$ is the training data set.
Step 2. Encode component (chromosome) chr_j of biomass wastage in tins_i.
Step 3. For each instance value tins_i in T
Step 4. Read tins_i and chr_j into GEP
Step 5. Consider chr_j as y and tins_i as x.
Step 6. Initiate the basic component functions of GEP: function set, link function, mutation selection, crossover, and fitness using Equation (3).
Step 7. For each generation, GEP implement Algorithm 1 (Step 3 to Step 5)
Step 8. Until termination condition or fitness criteria satisfied.
Step 9. Output of GEP represents $\text{chr}_j = f(\text{tins}_i)$
Step 10. Initialize KNN(GEP)// using Algorithm 2
Step 11. Consider σ as threshold value
Step 10. For each chr_j in training data set do
Step 11. Evaluate $y_e = f(\text{tins}_{ei})$
Step 12. If $|y_e - \text{chr}_j| \leq \sigma$
Step 13. $\text{tins}_{ei} \in \text{chr}_j(2)$
Step 14. Else $\text{tins}_{ei} \longleftarrow \text{KNN.classify}(\text{chr}_j)$
Step 15. End if
Step 16. End for
Step 17. End for
Step 18. $\text{tins}_{ei} \longleftarrow$ evaluate the prediction list
Step 19. End

ALGORITHM 3: Adsorption of carbon GEP-KNN (proposed).

TABLE 3: Evaluation of metric measures.

	Train			Test		
	GA [32]	GEP	GEP-KNN	GA	GEP	GEP-KNN
Correlation coefficient	0.8911	0.9443	0.9751	0.8911	0.9643	0.9951
Root mean square	7.4562	6.4185	5.3452	12.4551	16.6792	11.3452
Mean relative error	6.4597	4.6575	3.893	13.4563	6.5789	4.3678
Bias	-0.4522	-1.5482	-1.3793	-4.5824	3.4566	2.4367

The KNN algorithm describes the classification of the unknown component from extracting the features of it and compared it with the sample category of data. Choose the K-nearest neighbour and count the data which belongs to the same category of data.

3.2.4. Fusion of GEP-KNN Proposed Technology. In order to get high quality in an effective way of absorption of carbon in the biomass wastage system, this proposed work is implemented. The procedure for GEP-KNN is given in Algorithm 3.

Algorithm 3 describes fusion of GEP with the KNN algorithm. In the execution of GEP, it predicts the CO_2 component from biomass wastage. The training data set for each component undergoes Algorithm 1 and produces the output as adsorption of carbon and then applied to the KNN algorithm for getting more accurate and effective classification. Because the KNN algorithm is a supervised classification algorithm, it checks each component in the output set and chooses its neighbour value to evaluate the exact component.
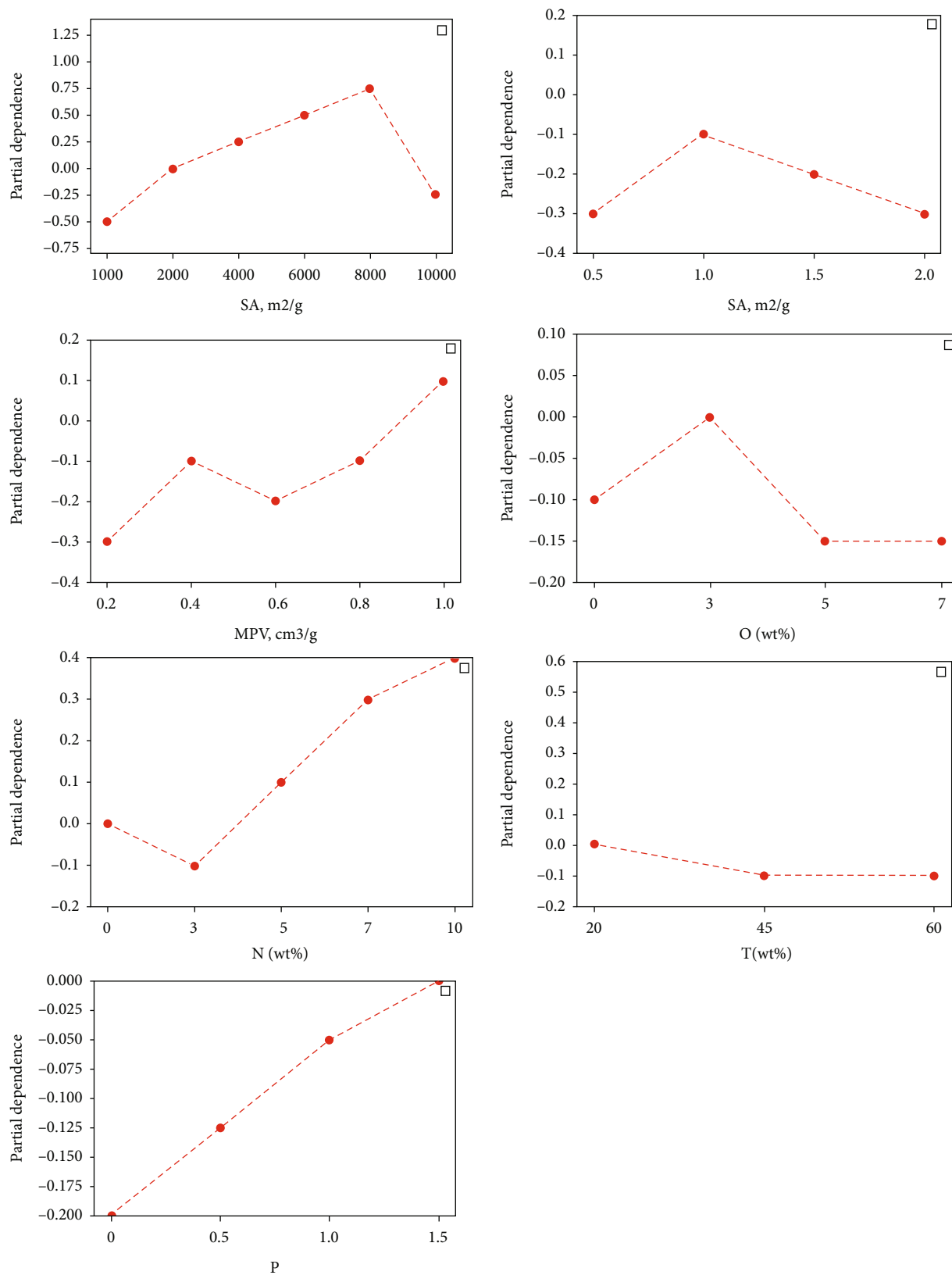
FIGURE 2: Input features of adsorption of CO_2 in biomass wastage.

4. Result and Analysis

4.1. Data Collection. Data is collected from peer-viewed journals using different keywords like biomass, biochar, and CO_2 adsorption, and 632 data points were collected and used in this work [30]. Most of the data were collected from the researcher's report by using WebPlotDigitizer software [31]. The GEP model was implemented by using GeneXproTools 5.0. From the total data points, we randomly selected 80% of data points and labelled them as the training data set and the remaining 20% of data points are selected and labelled as the testing data set. The features of collected input data are divided into three categories, namely, properties of texture data, elementary composition of biomass wastage, and CO_2 adsorption parameters such as temperature and pressure. The texture properties of biomass wastage are total pore volume (TPV, cm^3/g), surface area (SA, m^2/g), and micropore volume (MPV, cm^3/g). The basic elemental compositions are carbon, oxygen, hydrogen, and nitrogen contents (wt%). These machine learning algorithms implemented as used here were performed in Python using the open-source scikit-learn library.

4.2. Performance of Metric Measures. The performance is evaluated in terms of correlation coefficient (R^2) and root mean square error (RMSE) as defined below:

$$R^2 = 1 - \frac{\sum_{n=1}^{N}(y \wedge - y)^2}{\sum_{n=1}^{N}(y \wedge - \bar{y})^2},$$

$$RMSE = \sqrt{\frac{\sum_{n=1}^{N}(y \wedge - y)^2}{N}},$$

$$MRE = \frac{(\widehat{y}_l - y_i)}{y_i} \times 100,$$

$$Bias\,(\%) = 100 \times \frac{1}{n} \times \sum_{i=1}^{n}\left[\frac{(\widehat{y}_l - y_i)}{y_i}\right],$$

(2)

where $\widehat{y}$, y, and $\bar{y}$ are predicted, actual, and mean values of the targeted component, and n is the number of data points for any instance, and N is the total number of data points. In this work GEP-KNN, the metric measures of its performance based on accuracy, specificity, sensitivity, precision, and *F*-score evaluation matrices were employed:

$$accuracy = \frac{TP + TN}{TP + TN + FP + FN},$$

$$precision = \frac{TP}{TP + FP},$$

$$recall = \frac{TP}{TP + FN},$$

$$F1\text{-}Score = \frac{2 * precision * recall}{precision + recall}.$$

(3)

Table 3 shows evaluation of metric measures.

Table 4: Metric measure report.

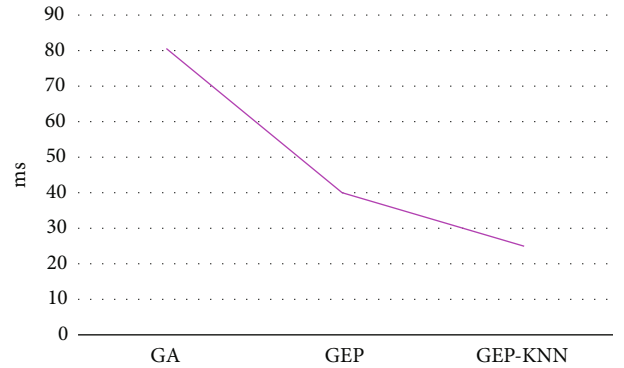| Parameter	GA	GEP	GEP-KNN
TP	142	160	130
TN	113	128	50
FP	75	45	25
FN	80	50	20
Accuracy	0.79	0.90	0.98
Precision	0.72	0.91	0.95
Recall	0.71	0.94	0.97

Figure 3: Computation time.

Table 3 shows that the performance of evaluation based on correlation coefficient, RMSE, MRE, and bias implemented in genetic algorithm (GA), GEP, our proposed work (GEP-KNN) algorithms in both training and testing data sets. The correlation coefficient shows strongly correlated 0.94 in the training phase and 0.96 in the testing phase. RMSE shows below 8% in the training phase and in the testing phase below 17%. For the bias value, it is underestimated in the training phase whereas in the testing phase, GEP and GEP-KNN algorithms are overestimated compared with GA. For the mean relative error, in the training phase, there is a little bit of increase when compared with the testing phase for each algorithm. That is, GA error is increased in the testing phase and so on. Figure 2 shows adsorption of CO_2 in biomass wastage input features like SA, MPV, TPV, oxygen (O), temperature (T), and pressure (P).

Figure 2 shows the impact of input features of CO_2 adsorption in biomass wastage. The input features like surface area (SA, m^2/g) reach 8000 m^2/g. Total pore volume (TPV, cm^3/g) got the maximum reach at -0.1 cm^3/g. Micropore volume (MPV, cm^3/g) reaches 1 cm^3/g. Table 4 shows the report of performance metric measures.

From Table 4, the accuracy of GEP-KNN (proposed work) is higher as compared to other classifier algorithms of GA and GEP. In Table 4, the next higher accuracy is GEP which is also closer to GEP-KNN. Figure 3 shows the computation time for CO_2 adsorption in various algorithms like GA GEP and GEP-KNN.

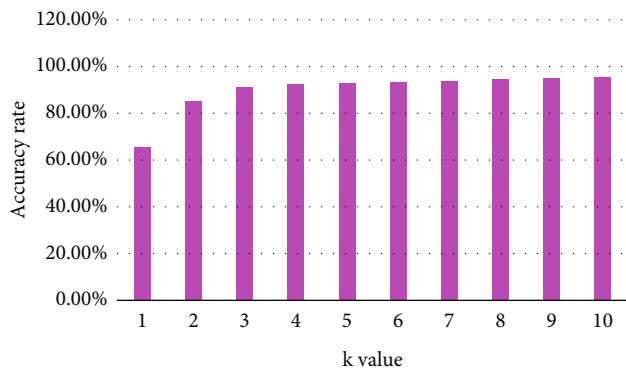Figure 3 shows that the proposed work needs less computation time for the prediction of CO_2 adsorption in

FIGURE 4: Accuracy rate for various K-values.

TABLE 5: Effectiveness.

Algorithms	TN	TP
GA	65	55
GEP	45	34
GEP-KNN	92	82

biomass wastage. Figure 4 shows the accuracy rate for implementation GEP-KNN with various K values.

Figure 4 shows that the value of K having the highest accuracy is $K = 9$ and $k = 10$ with the rate of accuracy as 95.12% and 95.67%; the lowest accuracy is $K = 1$ of 65.34%. Table 5 shows the effectiveness of various machine learning algorithms in terms of various influent indicators by using

$$\text{Effectiveness} = \frac{N - L}{N} \times 100, \qquad (4)$$

where N is the total number of testing data and L is the total number of losing test data.

Table 5 shows that the effectiveness of our proposed work produces better results compared with other existing algorithms.

5. Conclusion

The adsorption of CO_2 in biomass wastage uses evolutionary algorithms of gene expression programming (GEP) with K-nearest neighbour (KNN). This algorithm is implemented in the aspect of texture properties of biomass wastage like total pore volume (TPV, cm^3/g), surface area (SA, m^2/g), and micropore volume (MPV, cm^3/g). Based on these texture properties, our proposed work (GEP-KNN) effectively predicts the adsorption of CO_2 in biomass wastage at a minimum error rate value and low computation time. The accuracy of the GEP-KNN algorithm with different K values produced the highest accuracy at $K = 9$ and $k = 10$ of 95.12% and 95.67%; the lowest accuracy is $K = 1$ of 65.34%. Our proposed work GEP-KNN outperforms the best result compared with existing classifiers. In future work, this will be

extended by using various ML algorithms, and also, we will upgrade our work in various texture properties for predicting various components in biomass wastage.

Data Availability

All the required data is available in the manuscript itself.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Acknowledgments

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