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Investigation and Optimization of Biosorbent Capacities of Some Plants Used in Daily Life

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Abstract: In this study, sage, chamomile, and tarragon leaves, which are used as spices and consumed as beverages in daily life, were considered as different biosorbents that can be used in water purification by biosorption. At the same time, the effects of the parameters of initial dye concentration (10-200 mg/L), temperature (20-50 ºC) and contact time (0-120 min) on biosorption capacity were investigated. The biosorption processes were found to follow Freundlich isotherm and pseudo-second order (PSO) reaction kinetics. In the study, the process was also modeled using multi-tree evolutionary computation based automatic programming (AP) methods. The methods used initial dye concentration, temperature, and contact time as variables. According to the simulation results, these methods obtained nonlinear mathematical models of the processes with R^2 values as high as 0.99 for each biosorbent. By providing the most accurate models to accurately predict biosorption capacity, this study will make a significant contribution to the field of water treatment using experimental and AP methods.

Keywords: Biosorbent, plant, dye, automatic programming methods, genetic programming.

Günlük Hayatta Kullanılan Bazı Bitkilerin Biyosorbent Kapasitelerinin İncelenmesi ve Optimizasyonu

Öz: Bu çalışmada, biyosorpsiyon ile suyun arıtılmasında kullanılmak üzere günlük hayatta baharat olarak kullanılan ve içecek olarak tüketilen adaçayı, papatya ve tarhun yaprakları farklı biyosorbentler olarak ele alınmıştır. Aynı zamanda, başlangıç boya konsantrasyonu (10-200 mg/L), sıcaklık (20-50 ºC) ve temas süresi (0-120 dk) parametrelerinin biyosorpsiyon kapasitesi üzerindeki etkileri araştırılmıştır. Biyosorpsiyon süreçlerinde Freundlich izotermi ve yalancı ikinci mertebe (Pseudo Second Order, PSO) reaksiyon kinetiğinin takip edildiği belirlenmiştir. Çalışmada ayrıca süreç, çok ağaçlı evrimsel hesaplama tabanlı otomatik programlama (Automatic Programming, AP) yöntemleri kullanılarak modellenmiştir. Yöntemler, başlangıç boya konsantrasyonu, sıcaklık ve temas süresini değişken olarak kullandılar. Simülasyon sonuçlarına göre bu yöntemler süreçlerin doğrusal olmayan matematiksel modellerini her bir biyosorbent için 0.99'a varan R^2 değerleri ile elde etmişlerdir. Biyosorpsiyon kapasitesini doğru bir şekilde tahmin etmek için en doğru modelleri sağlayan bu çalışma, deneysel ve AP yöntemleri ile su arıtımı alanına önemli bir katkı sağlayacaktır.

Anahtar kelimeler: Biyosorbent, bitki, boya, otomatik programlama yöntemleri, genetik programlama.

1. Introduction

Water is the essential ingredient for the continuation of life. Unfortunately, with the development of industry and modern life, water pollution is increasing [1]. Synthetic dyes used in many industries are released into nature due to their presence in water flow systems. Due to their resistance to biological water treatment processes, they remain as colored and toxic waste in the environment [2]. Dyes that are stable against oxidizing agents increase the oxygen requirement of aquatic plants by affecting photosynthesis [3]. They can also cause skin irritation on humans can also be carcinogenic [4].

Various techniques are available to remove pollutions from water, such as ultrafiltration, electrodialysis or reverse osmosis [4]. Adsorption technique is a simple, cost-effective and effective method for removing dyes from wastewater [5]. The biosorption method using materials of biological origin is a physicochemical process. Various agricultural wastes used as biosorbent have various functional groups such as carbonyl and carboxyl that can form bonds with cationic and anionic dyes [6]. Methyl orange is a toxic and mutagenic dye known as anionic and azo dye. MO, which has high water solubility and low biodispersibility, is used in many sectors and laboratories. It is harmful to human health and the environment [7].

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In this study, some plants that can be drunk as tea in daily life or used in meals are considered as biosorbent. For this purpose, the biosorption reaction of sage, tarragon and chamomile leaves against methyl orange (MO) dye was investigated by isotherm and kinetics studies. Initial dye concentration, contact time and temperature parameters were optimized for the process using automatic programming (AP) methods. Multi Gene Genetic Programming (MGGP) and Multi Hive Artificial Bee Colony Programming (MHABCP) were used for the study. MGGP was developed based on the Genetic Algorithm (GA). MABCP is inspired by the Artificial Bee Colony (ABC). Unlike the metaheuristics GA and ABC, the methods represent solutions with parse trees. For this reason, the equations used in metaheuristics to improve solutions are not used in the methods. AP methods use operators such as pruning and grafting that can improve trees. While MGGP tries to improve them with genetic operators such as crossover and mutation, MHABCP tries to improve them with another operator called information sharing mechanism. Both methods are more powerful than solutions that aim to grow horizontally by making the tree depth shallower and their standard versions. The main reason why these methods are preferred in the study is that they can create nonlinear models of systems through automatic regression. Moreover, these methods are used in various fields to successfully solve engineering problems, such as predicting the performance of tunnel boring machines [8], inferring error severity from symbolic regressed inferential sensors [9], the artificial ant problem [10], automatic feature selection [11].

The contributions and motivations of the study can be listed as follows:

- To the best of our knowledge, these experiments were the first to use multi-tree structured methods, whose success has been proven in many problems, and whose successes were compared.
- The models generated by the methods were ranked according to their error values, and the models with the lowest error were determined for the experiments.
- The ability of the best models to represent the system is presented to the readers with various visual graphics.

The remainder of this paper as follows. Section 2 provides explanations of material and method. Section 3 presents data analysis, parameters, and evaluation criteria. Section 4 describes results and discussion. Finally, the paper concludes in Section 5 with summarizing the observations and remarking the future work.

2. Material and Method

In the study, MO was obtained from Surechem Product company. All the plants were obtained from local markets.

For MO biosorption, a solution volume of 100 mL was used in glass flasks with a volume of 250 mL. 0.2 grams of dried leaves of sage, tarragon and chamomile tea were added to the dye solution and the process was continued for 120 min. Samples were taken at certain intervals, filtered and the absorbance of the samples was measured at 464 nm in UV vis spectroscopy. Dataset for optimization was obtained using absorbance data of samples taken at certain intervals. The dye concentration was examined in the range of 10-200 mg/L, temperature 20-50 ºC and contact time 0-120 min.

Biosorption efficiency and biosorption capacity values (q) were calculated according to Equations 1 and 2. qe is the biosorption capacity at equilibrium and qt is the biosorption capacity at time t.

$$qe = \frac{(Co - Ce).V}{m} \quad (1)$$

$$qt = \frac{(Co - Ct).V}{m} \quad (2)$$

2.1. Multi-Tree based automatic programming methods

The multi-tree AP methods extend the models horizontally by expressing them as combinations of multiple trees, unlike the standard versions. The depth of each tree is chosen to be rather shallow so that the crossover and mutation operators can work more effectively [12]. In addition, these shallow trees also allow for displacement with the high-level crossover/hive exchange mechanism.

A representative model example of the methods is given in Figure 1, and an example of a high-level crossover/hive exchange mechanism is shown in Figure 2. As can be seen in Figure 1, the methods generate trees of mathematical functions and terminals (such as x, y). Each tree is multiplied by various automatically generated coefficients and summed. Model generation is completed by adding bias to the collection, similar to neural networks. Model trees can be exchanged, as shown in the example of the high-level crossover/hive exchange

mechanism. The displacement points are determined randomly. Here, the suitability of the new model resulting from the displacement of the trees is evaluated by the parameter $Gmax/Hmax$. This parameter defines the maximum number of trees that the model can have.

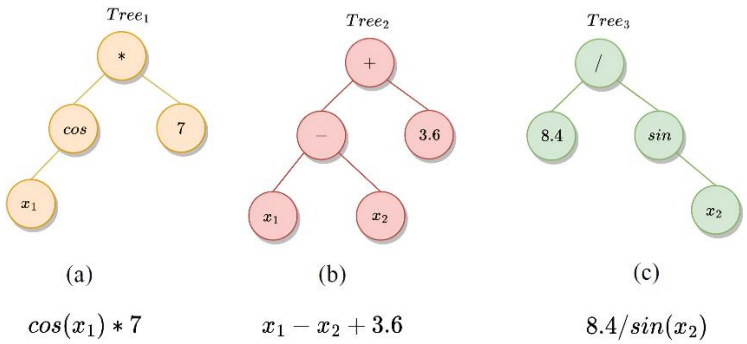

Figure 1. Multi-tree AP methods

Two different well-known AP methods were used in this study. One method is Multi Gene GP (MGGP) and the other is MHABCP. Both methods were developed according to metaheuristics. MGGP, Genetic Algorithm; MHABCP adopts the principles of ABC. After generating models with multitree structures, the methods try to evolve them with their own improvement operators until the stopping criterion(s) are satisfied. MGGP improves the models using crossover, mutation, and high-level crossover. The improvement operators of MHABCP are the information sharing mechanism and the hive exchange mechanism. Details of the algorithms can be found in [13].

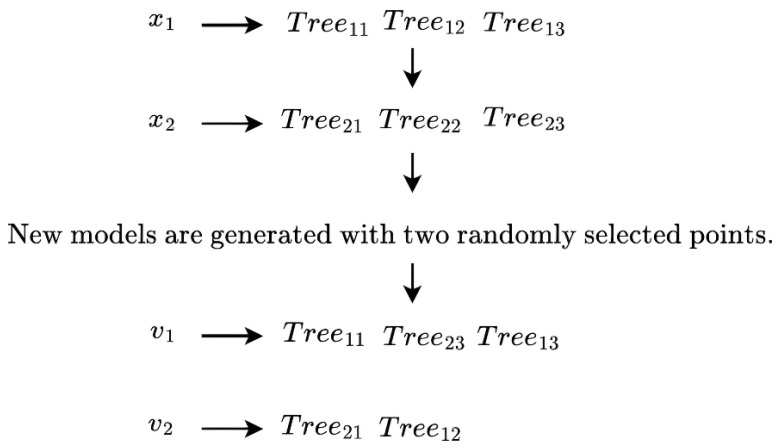

Figure 2. High level crossover/Hive exchange mechanism

3. Experimental Design

In this section, we presented the data set and details of the evaluation criteria and parameters.

3.1. Data and analysis

Sage, chamomile, and tarragon leaves were considered as different biosorbents, and three separate datasets were used for each in the conducted experiments. These datasets were generated under laboratory conditions. The total number of samples in each dataset is 34, with 27 randomly assigned to the training set (approximately 70%) and the remaining 7 to the test set (approximately 30%) [14]. They used in the experiments consist of 4 features, including 3 features and 1 target variable (biosorption capacity). These features are, respectively, (x_1) initial dye concentration (10-200 mg/L), (x_2) temperature (20-50 ºC), and (x_3) contact time (0-120 min). Models were created using these features through the AP methods. Predictions were made on the target variable with a biosorption mechanism.

3.2. Parameters

The parameters of AP methods were selected to be the same for a fair comparison. While high-level crossover, crossover, mutation, and direct reproduction operators are used in MGGP to improve solutions, information sharing mechanism and hive exchange mechanism operators are used in MHABCP. These parameters are presented in Table 1.

Table 1. Parameters of AP methods

Parameters	**MGGP**	**MHABCP**
Population size	300	-
Colony size	-	300
Generation	500	500
Maximum tree depth	5	5
Crossover rate	0.84	-
Mutation rate	0.14	-
Direct reproduction rate	0.02	-
Tournament size	15	-
Limit	-	50
Maximum number of gen/hive	2	2
Information sharing mechanism rate	-	0.8
Hive exchange mechanism rate	-	0.2
High level crossover	0.2	-
Functions	$+, -, *, /, square, cube$	

3.3. Evaluation criteria

Root mean squared error ($RMSE$) and coefficient of determination (R^2) were used to evaluate the performance of AP methods. These criteria are presented in Equations 3 and 4.

$$RMSE = \sqrt{\sum_{i=1}^{n} \frac{(\hat{y}_i - y_i)^2}{n}} \tag{3}$$

$$R^2 = 1 - \frac{\sum_i (y_i - \hat{y}_i)^2}{\sum_i (y_i - \bar{y})^2} \tag{4}$$

where $\hat{y}_i$ is the predicted values of y, $\bar{y}$ is the mean value of y, and y_i is the observed values of y.

4. Result and Discussion

4.1. Initial dye concentration

The particle size for sage, tarragon and chamomile is in the range of 0.5-2 mm each. Biosorbent particle size can affect biosorption. Different results have been obtained on this subject in the literature. In a study in which egg shell was used as a biosorbent, it was reported that biosorption efficiency and biosorption capacity increased as the particle size increased [15]**.** In another study, it was suggested that a small adsorbent size increased the surface/volume ratio and contact surface [16]. In this study, the size of the biosorbents are close to each other and the effect of particle size on biosorption was not examined.

The biosorption capacity of MO according to the initial dye concentration (range of 10-200 mg/L) was investigated for all 3 biosorbents. As the initial dye concentration increased (Figure 3), the biosorption capacity continued to increase with different increasing characteristics. The reason for this situation can be explained by the active sites on the surface of biosorbents [4]. In all biosorbents, q_e increased as the initial dye concentration increased, consistent with the literature [17]. It was observed that the qe values of sage tea and tarragon plant were very close to each other, and it was calculated that tarragon reached the highest qe as 49 mg/g. Chamomile has reached qe value of 30 mg/g.

Isotherms were used to investigate the usability of the biosorbent used and to understand the mechanism of the biosorption reaction. The formulation of the Freundlich isotherm is given in Equations 5. $Lnqe$ versus $LnCe$ plots plotted according to Equation 5 are in Figure 4 and the data obtained are in Table 2.

$$Lnqe = LnKf + \left(\frac{1}{n}\right) LnCe \quad (5)$$

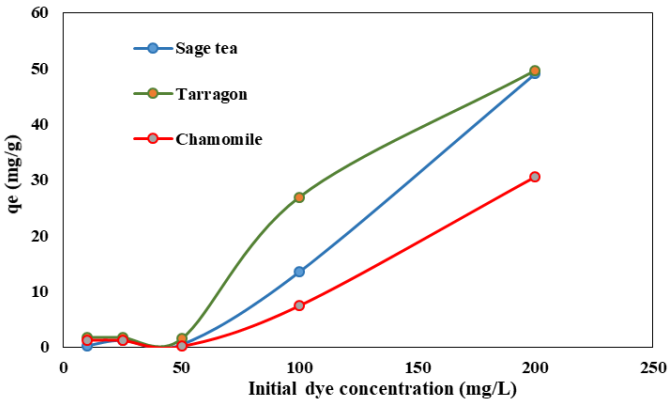

Figure 3. Effect of initial dye concentration on biosorption capacity

It is suitable for the Freundlich isotherm for MO biosorption of dry plant leaves. The Freundlich isotherm indicates heterogeneous biosorbent surface and multilayer adsorption. The value of n gives information about the process of the Freundlich isotherm. n value less than 1 indicates the presence of physical biosorption [1].

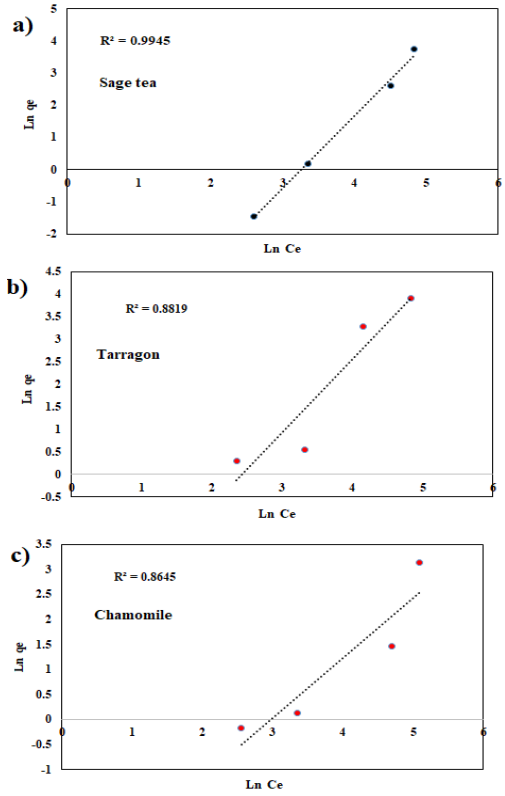

Figure 4. Freundlich isotherms of a) sage tea, b) tarragon and c) chamomile

Table 2. Isotherm data

Isotherms Freundlich	Sage tea	Tarragon	Chamomile
R^2	0.99	0.88	0.86
n	0.44	0.61	0.83
Kf	$6.28x10^{-4}$	0.019	0.029

4.2. Effect of contact time

MO biosorption mechanism kinetics for sage, tarragon and chamomile leaves were investigated with PSO reaction kinetics. The kinetics were analyzed according to the formula given in Equation 6. t/qt versus t plots drawn according to Equation 6 are given in Figure 5.

$$\frac{t}{q_t} = \frac{1}{k_2.q_e 2} + \frac{1}{q_e} t \tag{6}$$

It can be said that the biosorption reaction is compatible with PSO reaction kinetics. In this case, MO biosorption of all biosorbents may also indicate the presence of chemisorption [6]. With this result, it can be said that there is first a rapid biosorption in the reaction for sage, tarragon and chamomile and then a slower secondary step until equilibrium is reached [18].

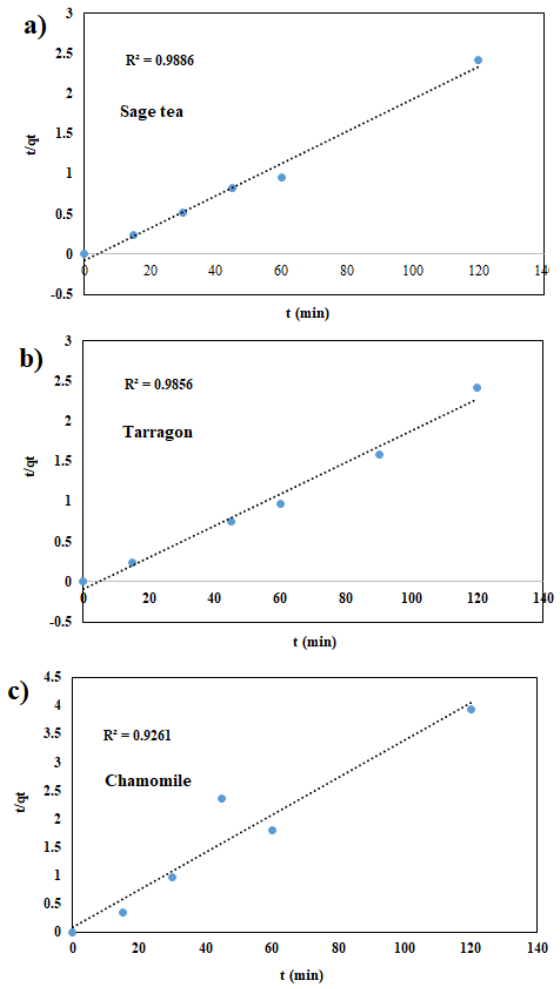

Figure 5. PSO kinetic graphs a) sage tea, b) tarragon, c) chamomile

4.3. Thermodynamic parameters

Temperature gives information about the feasibility of biosorption [18]. In this study the effect of temperature on the biosorption mechanism was investigated with thermodynamic parameters. Using Equations 6, 7 and 8, ΔH (enthalpy), ΔS (entropy) and ΔG (free energy) are obtained. Kc is the equilibrium constant due to biosorption and R is the ideal gas (8.314 J/mol.K) constant.

$$K_c = C_a/C_e \quad (6)$$

$$In\ K_c = \frac{\Delta S}{R} - \frac{\Delta H}{R}.\frac{1}{T} \quad (7)$$

$$\Delta G = \Delta H - T\Delta S \quad (8)$$

As seen in Table 3, negative ΔH values indicate an exothermic reaction, and negative ΔS values indicate reduced randomness [18]. Whether the adsorption reaction is exothermic involves physisorption or chemisorption or a mixture of both [19]. For biosorbents, the positive ΔG value increased as the temperature increased. This result indicates that biosorption may be preferred at lower temperature [20]. In addition, a positive ΔG value indicates that biosorption is not spontaneous [21].

Table 3. Thermodynamic data

Biosorbent	ΔH (J/mol)	ΔS (J/K.mol)	ΔG (293 K, kJ/mol)	ΔG (308 K, kJ/mol)	ΔG (323 K, kJ/mol)
Sage tea	-4.31	-9.25	2.7	2.84	2.98
Tarragon	-7.217	-17.4	5.09	5.31	5.6
Chamomile	-6.6	-19.22	5.6	5.91	6.2

Similar parameters have been discussed in the literature for MO removal with natural biosorbents or adsorbents. In the study of Zaghloul et al., MgAl layered double hydroxide was synthesized as an adsorbent in MO removal. It was determined that the adsorption reaction followed the PSO kinetic model and reached 197.62 mg/g q_e at an initial concentration of 100 mg/L [22]. In another study using graphene oxide, MO removal was examined for 100 minutes. The effect of the initial dye concentration was examined in the range of 0.2-0.8 mg/L and the highest q_e value was reached at 0.2 mg/L dye concentration. It has been reported that the reason for this situation is that GO has a negatively charged surface [23]. In a study in which *Momordica charantia L.* leaves were used as biosorbent, it was determined that MO biosorption followed the Freundlich isotherm and PSO [17]. Compared to the literature, it is thought that efficient results are obtained from the biosorbents we use in MO removal.

4.4. Simulation results and discussion

In this section, biosorption capacity prediction was performed for 3 different datasets (Chamomile, Sage tea, Tarragon) using AP methods. The simulation results of each dataset are presented in Tables 4, 5 and 6 respectively. The best values in the tables are bolded.

In the models generated by the AP methods for the chamomile dataset, MHABCP has shown better results in terms of mean $RMSE_{train}$ values. However, in their best performances, MGGP has produced a better model with a difference of approximately 0.7476. In contrast to $RMSE_{train}$, MGGP is more successful on mean in $RMSE_{test}$, and it is approximately 2.1 times better. The R^2 performance evaluation criterion approaching 1 indicates that the model's predictions are increasingly accurate and successful [24]. Therefore, in mean, MHABCP is better in ${R^2}_{train}$, and MGGP is better in ${R^2}_{test}$, with the largest difference being 0.1467 in ${R^2}_{test}$. At the same time, in the best values of these criteria, MGGP is superior. A small standard deviation indicates that there is little difference between the models generated by the method [25]. Overall, MGGP has produced models with lower standard deviations, resulting in models that are closer in performance [26].

Table 4. Chamomile results

Criteria		Chamomile	
		MHABCP	MHGP
$RMSE_{train}$	**Mean**	**3.0971**	3.7995
	Best	1.8332	**1.0856**
	Std	1.3690	1.4601
$RMSE_{test}$	**Mean**	6.5142	**3.0994**
	Best	2.5828	**0.6318**
	Std	1.8323	1.7224
${R^2}_{train}$	**Mean**	**0.9121**	0.8728
	Best	0.9741	**0.9909**
	Std	0.0883	0.0781
${R^2}_{test}$	**Mean**	0.7982	**0.9449**
	Best	0.9705	**0.9982**
	Std	0.0994	0.0508

Table 5. Sage tea results

Criteria		Sage tea	
		MHABCP	MHGP
$RMSE_{train}$	**Mean**	**2.3619**	2.6632
	Best	1.2262	**0.2922**
	Std	0.6329	1.1782
$RMSE_{test}$	**Mean**	6.8539	**4.2737**
	Best	2.6748	**0.8327**
	Std	1.1058	1.5764
${R^2}_{train}$	**Mean**	**0.9875**	0.9823
	Best	0.9969	**0.9998**
	Std	0.0068	0.0148
${R^2}_{test}$	**Mean**	0.8937	**0.9544**
	Best	0.9842	**0.9985**
	Std	0.0278	0.0293

In the models generated for sage tea, MHABCP performs better in terms of $RMSE_{train}$ on mean, while MGGP outperforms in $RMSE_{test}$. Similar to Daisy, MGGP has produced better results than MHABCP according to these evaluation criteria. Both methods have very close ${R^2}_{train}$ values, with differences of only 0.0052 and 0.0029 in means and best values, respectively. In ${R^2}_{test}$, however, MGGP has a more successful model with a score of 0.9985.

Table 6. Tarragon results

Criteria		Tarragon	
		MHABCP	MHGP
$RMSE_{train}$	**Mean**	3.2723	**2.4563**
	Best	1.7549	**1.2868**
	Std	0.4429	0.7456
$RMSE_{test}$	**Mean**	1.8342	**1.5646**
	Best	1.1370	**0.6129**
	Std	0.4267	0.4115
${R^2}_{train}$	**Mean**	0.9788	**0.9872**
	Best	0.9940	**0.9968**
	Std	0.0052	0.0071
${R^2}_{test}$	**Mean**	0.9905	**0.9930**
	Best	0.9965	**0.9990**
	Std	0.0043	0.0036

In the tarragon dataset, MGGP performs well in terms of mean evaluation criteria and achieves the best values. However, MHABCP produces values that are very close to those of MGGP. For example, in terms of mean ${R^2}_{train}$ and ${R^2}_{test}$, they differ by only 8.4% and 2.5%, respectively, which is a very small margin. The standard deviation values are also similar between the methods. This indicates that the methods generate close values for this dataset.

4.5. Analysis of the best models of AP methods

In this subsection, the best models generated by the AP methods are presented. Table 7 and 8 provide simplified mathematical equations for the models.The models in Tables 7 and 8 were generated by combining different functions provided in Table 1.

Table 7. The best models obtained by MGGP

Dataset	Simplified Model
Chamomile	$\frac{6.1\times10^{15}x_2^2}{2.3\times10^{18}x_2-4.6\times10^{18}x_3}+6.6\times10^{-4}x_1^2+2.5\times10^{-8}x_3(2.9x_2-1.0x_1x_2)(3.1x_2-1.0x_1x_3)$ $+\frac{5.4\times10^{15}(x_2-1.0x_3)^2(x_1^3+x_2x_1-1.0x_3)}{3.8\times10^{22}x_3-3.8\times10^{22}x_2+\frac{3.8\times10^{22}x_1}{x_2}}+\frac{6.1\times10^{15}x_2x_3}{9.2\times10^{18}x_1-9.2\times10^{18}x_3}$ $+3.5\times10^{-6}\frac{(x_1+2.7)^3\left(x_2-1.0x_3+x_1(x_2-0.48)\right)}{x_3^3}$ $-\frac{4.7\times10^{-4}x_1^2x_3^2}{(x_2-0.85)^2(x_2-1.0x_3)^2}+\frac{4.1\times10^{15}x_2^2(x_1+x_1x_3)(3.1x_2-1.0x_1x_3)}{1.2\times10^{24}x_2-2.4\times10^{24}x_3}+3.9\times10^{-8}$
Sage tea	$-\frac{8.0\times10^{15}x_1^4}{x_3}+\frac{8.0\times10^{15}x_1^3x_2^2}{\frac{1.5\times10^{23}x_3}{x_2}+\frac{1.5\times10^{23}x_1x_2}{x_3}}-\frac{1.0(7.5\times10^{15}x_2x_3x_1^3-2.0\times10^{19})}{1.9\times10^{22}x_2x_3-\frac{1.9\times10^{22}(x_1-1.5)}{x_3}}$ $-\frac{1.0(-7.6\times10^{15}x_2x_1^4+7.6\times10^{15}x_3x_1^2)}{2.6\times10^{21}x_3+9.4\times10^{21}x_2x_3}-5.8\times10^{-8}x_3^2(x_2-7.2)^2-1.1\times10^{-7}x_1^2x_2x_3$ $+1.1\times10^{-7}x_1^2x_2(x_2-1.0x_3)+\frac{7.3\times10^{-12}x_1^2((x_1-1.0x_2)^2-1.0x_1^3)(x_2-1.0x_3)^2}{x_3^2}-6.0\times10^{-4}$

Tarragon	$1.5\times10^{-4}\left(x_2+\frac{x_2}{x_1}-10.0\right)^2-1.5\times10^{-3}x_1+1.5\times10^{-4}x_1x_2$ $-\frac{0.53\left(x_3+\frac{x_2}{x_3}-8.7\right)^2}{(2.0x_3-1.0x_1+5.2)^2}-6.0\times10^{-4}x_2^2+\frac{6.3\times10^{14}x_1(2.0x_1-1.0x_3)}{3.6\times10^{16}x_3+\frac{3.6\times10^{16}x_3}{x_2(x_2-1.0x_3)}}$ $+\frac{5.6\times10^{15}x_2(x_1-1.0x_3+3.0)}{\frac{2.9\times10^{17}(x_1+x_3)}{x_3-2.1}-2.9\times10^{17}x_3+\frac{2.9\times10^{17}x_2}{x_1}+6.2\times10^{17}}$ $+\frac{2.3\times10^{15}x_1(x_2-5.5)}{3.6\times10^{16}x_3+\frac{1.5\times10^{16}x_1}{x_2}}-\frac{2.6\times10^{-6}x_1^2(x_3^2-1.0x_3+x_2)}{x_3^2\left(\frac{x_3}{x_1}-\frac{1.0x_3}{x_2}\right)}+0.38$

Additionally, despite the low number of samples in the datasets, the equations are quite complex. Information regarding these equations is presented in Table 9.

Table 8. The best models obtained by MHABCP

Dataset	Simplified Model
Chamomile	$\frac{5.7\times10^{-3}(x_1-5.0)^3(0.12x_2+1.0)}{(x_2+1.0)\left(x_1-\frac{1.0x_3}{x_2}\right)}-\frac{4.7\times10^{15}x_3^4(x_2+x_3)^2}{3.9\times10^{24}x_3-1.6\times10^{26}}+1.4\times10^{-6}$
Sage tea	$3.8\times10^{-8}x_1^3x_2-\frac{1.0(2.9\times10^{15}x_1^2+2.9\times10^{15}x_3x_1)}{7.6\times10^{22}x_3^3+1.5\times10^{23}x_2}$ $-3.8\times10^{-8}x_2^3+3.8\times10^{-8}x_3^3+\frac{0.25(x_1^2+x_3x_1)^3}{x_3^3+2.0x_2^3}+9.7\times10^{-4}$
Tarragon	$\frac{4.9\times10^{14}x_2(x_1-6.2)(0.16x_1-0.32x_3)}{3.6\times10^{16}x_2+4.9\times10^{16}}-\frac{3.6x_1(x_2+1.3)}{x_3(x_3-8.4)(x_3-13.0)\left(\frac{x_1}{x_3}-6.5\right)}+0.7$

As can be seen from Table 9, the tree structures of the models produced by MGGP have more complexity and number of nodes. Tree depths were taken the same when generating the models.

Table 9. Tree structures of the best models

Dataset	Tree Structure	MGGP	MHABCP
Chamomile	Node	81	37
	Depth	5	5
	Complexity	446	140
Sage tea	Node	114	40
	Depth	5	5
	Complexity	431	159
Tarragon	Node	111	40
	Depth	5	5
	Complexity	429	152

5. Conclusion

In this study, dry leaves of sage tea, tarragon, and chamomile were used to remove MO from an aqueous solution. It was observed that the biosorption capacity increased as the initial dye concentration increased. For the same process parameters, the highest biosorption capacity (49 mg/g) was obtained with tarragon leaves. After the experiments, the biosorption capacity for the biosorbents was modeled using the most commonly used evolutionary computation AP methods. The simulation results show that the error values of the models produced with AP methods are quite low. At the same time, the R^2 values of these models are high, although the number of samples is small. Both methods used in the study gave very similar results; MGGP gave slightly better results than MHABCP. Therefore, this study shows that biosorption processes can be modeled using AP methods. In future studies, it is planned to use different AP methods to model different separation processes.

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