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**A new hybrid firefly algorithm and black hole algorithm for
QSAR/QSPR modeling**

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Abstract: Chemometrics' quantitative structure-activity relationship (QSAR/QSPR) modelling is crucial for making predictions. Chemical data has the unique feature of having a large number of descriptors and a small number of chemical substances. For the QSAR/QSPR prediction to perform better, descriptor selection must be used. It is thought that choosing a descriptor is an NP-hard optimization problem. In the literature, many metaheuristic algorithms have been developed to address this issue. One of the most intriguing new advances in application to enhance the exploration and exploitation capabilities of the basic metaheuristics algorithms is the use of hybrid metaheuristics algorithms. In order to maximize descriptor selection, this work suggests a new hybrid firefly algorithm (FFA) and black hole algorithm (BHA) that combines the FFA and BHA's strengths. In order to increase the exploration and exploitation capabilities of the FFA method in QSAR/QSPR modelling with high prediction performance and quick computing time, we hybridize in an effort to minimize trapping at local optima. The experimental results, which were based on eight benchmark chemical datasets, show that the proposed hybrid method may achieve good prediction performance while decreasing the number of selected descriptors and speeding up computation.

خوارزمية الفراشات المضيئة الهجينة وخوارزمية الثقب الاسود لنمذجة QSAR/QSPR

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المستخلص

أحد أكثر التطورات الجديدة إثارة للاهتمام في التطبيق لتعزيز قدرات الاستكشاف والاستغلال لخوارزميات metaheuristics الأساسية هو استخدام خوارزميات metaheuristics الهجينة. من أجل تعظيم اختيار الوصف، يقترح هذا العمل خوارزمية هجينة جديدة للفراشات المضيئة (FFA) وخوارزمية الثقب الأسود (BHA) تجمع بين نقاط قوة FFA و BHA. من أجل زيادة قدرات الاستكشاف والاستغلال لطريقة FFA في نمذجة QSAR/QSPR مع أداء تنبؤي عالي ووقت حوسبة سريع، نقوم بالتهجين في محاولة لتقليل الملاءمة عند المستوى الأمثل المحلي. تعد نمذجة العلاقة الكمية بين البنية والنشاط (QSAR/QSPR) الخاصة بالقياسات الكيميائية أمراً بالغ الأهمية للتنبؤات. تتميز البيانات الكيميائية بميزة فريدة تتمثل في وجود عدد كبير من الوصفات وعدد صغير من المواد الكيميائية. لكي يؤدي تنبؤ QSAR/QSPR أداءً أفضل، يجب استخدام اختيار الوصف. يُعتقد أن اختيار واصف يمثل مشكلة تحسين NP-hard. في الأدبيات، تم تطوير العديد من خوارزميات metaheuristic لمعالجة هذه المشكلة. تظهر النتائج التجريبية، التي استندت إلى ثماني مجموعات بيانات كيميائية مرجعية، أن الطريقة الهجينة المقترحة قد تحققت أداءً جيداً للتنبؤ مع تقليل عدد الوصفات المختارة وتسريع الحساب. **الكلمات المفتاحية:** خوارزمية الفراشات، خوارزمية الثقب الأسود، الهجين، QSAR، اختيار الوصف.

1. Introduction

Quantitative structure-activity (property) relationship (QSAR/QSPR) modeling is one of the important topics in chemometrics. "These models use both the activity of chemical compounds and output variables (descriptors) to provide a model that characterizes the relationships between them.

With the development of technologies in the chemometrics, there are a limited number of chemical compounds related to very large number of descriptors. Number of compounds is usually in the range of hundreds and number of descriptors in thousands. This is presenting a challenge for chemometricians to conduct the statistical methods [1-3]. QSAR/QSPR datasets often contain a large number of irrelevant or redundant descriptors that may significantly degrade the prediction accuracy and increase the time of the computations [4].

From the practical point of view, chemometricians need to identify only a small number of the most significant descriptors. Descriptor selection is the method of selecting an optimum subset of relevant descriptors that can improve the computational efficiency of the statistical method with small prediction error [5, 6]. Consequently, several descriptor selection methods have been proposed and studied in the literature. These methods can be divided into three broad categories: the filter, wrapper, and embedded methods [5].

In many real-world optimization problems, finding optima requires expensive evaluations in terms of computation. In recent years, metaheuristic algorithms, such as and firefly algorithm and black hole algorithm, are a computational technique inspired by observation in nature that are used to overcome the time consuming of computations [7]. Searching for the best d descriptors out of the D available for modeling is known to be an NP-hard problem. These metaheuristic algorithms have been successfully used to implement and optimize the descriptor selection.

Generally, metaheuristic algorithms employ different strategies to keep the balance between exploration and exploitation for searching the solution. The exploration provides to discover distinct areas in the search space. On the other hand, the exploitation allows scanning the local search space for better solutions. However, the exploration process of some of the metaheuristic algorithms can perform a very good, while in some others the exploitation process performs better [8].

The hybrid algorithms can be used to increase the performance of the search algorithm. In the hybridization, good properties of two algorithms are combined to enhance the performance of each algorithm [9-11].

In this paper, a new hybrid firefly algorithm and black hole algorithm is proposed to perform descriptor selection. Our proposed algorithm can efficiently exploit the strong points of both firefly and black hole algorithms in finding the most significant descriptors in constructing QSAR/QSPR models with high prediction performance. The experimental results show the favorable performance of the proposed method when the number of descriptors is high and the sample size is low.

2. Methodology

2.1.Descriptor selection

The descriptor selection method is a procedure that reduces or minimizes the number of descriptors and selects some subsets of original descriptors. Selecting the most relevant descriptors is one of the challenging tasks for large dataset. The descriptor selection has been proven to effectively remove irrelevant and redundant descriptors. In addition, it can improve the performance of classifiers and reduce the computational time. Descriptor selection using metaheuristic algorithms have been applied successfully in QSAR/QSPR classification [12-22].

Let S be a dataset of n observations with D descriptors and A be the set of all the D descriptors. Descriptor selection is to choose d descriptors from D , where $d \leq D$, so that the objective function, $f(\cdot)$, is maximized or minimized subject to the problem. In this way, descriptors selection becomes a combinatorial (discrete) optimization problem where the objective is to find the best descriptor subset $|B| = d$. By minimizing the prediction error, the optimization problem is defined as

$$\begin{aligned} \min f(X) \\ \text{s.t. } X = (x_1, x_2, \dots, x_d), x_j \in \{0, 1\}, j = 1, 2, \dots, d \end{aligned} \quad (1)$$

2.2.Firefly algorithm

Firefly algorithm (FFA) belongs to the family of metaheuristic algorithms proposed by Yang [23]. FFA has been proved to be a good performance and the effectiveness for solving various optimization problems [24]. The FFA has been inspired by the simulation of the social behavior of fireflies on the basis of the flashing lights or the flash attractiveness [25]. FFA has two significant aspects. The first aspect is the variation in light intensity while the second aspect is the formulation of attractiveness.

Each firefly has light intensity I and attraction β . Light intensity, is calculated by the objective function. Attraction is inversely proportional to the distance between the fireflies and determines the distance traveled by the fireflies. The fireflies will move to any others with a brighter flash, and the step size is determined by the attraction.

Mathematically, assume that there are n_f of fireflies in the swarm are randomly distributed in the D-dimensional search space. During the evolutionary process, each firefly has a position vector denoted as $\mathbf{x}_i = \{x_{i1}, x_{i2}, \dots, x_{id}\}$, where $i = 1, 2, \dots, n_f$ and $d \in D$ is the dimensionality of the solutions.

The light intensity is defined as

$$I(r) = I_0 e^{-\gamma r^2}, \quad (2)$$

where γ is used to control the decrease of the light intensity or brightness and can be taken as a constant. The light intensity of a firefly depends on the intensity I_0 of light emitted by a firefly and the distance r_{ij} between two fireflies. The attractiveness is defined as

$$\beta(r) = \beta_0 e^{-\gamma r^2}, \quad (3)$$

where $\beta(r)$ represents attractiveness function of a firefly at a distance, r , and β_0 denotes the initial attractiveness of a firefly at distance $r = 0$ and it can be constant. For implementation usually β_0 set to be 1 for most problems.

The distance between any two fireflies i and j , at positions x_i and x_j in the search space, respectively, is the Cartesian distance which can be calculated using the following equation

$$r_{ij} = \|x_i - x_j\| = \sqrt{\sum_{d=1}^D (x_{id} - x_{jd})^2}. \quad (4)$$

The fireflies will try to move to the best position. This means that the lower light intensity one will be attracted by the brighter one. The location updates for each pair of fireflies i and j . For each firefly x_i , it is compared to other all fireflies x_j , $j = 1, 2, \dots, n_f$. If firefly j at position x_j is brighter than firefly i , then x_i will move towards x_j by the attraction. The movement is defined as:

$$x_{id}^{(t+1)} = x_{id}^{(t)} + \beta_0 e^{-\gamma r^2} (x_{jd}^{(t)} - x_{id}^{(t)}) + \alpha_t \varepsilon_{id}^{(t)}, \quad (5)$$

where α_t is the randomization parameter and $\varepsilon_{id}^{(t)} = (rand - 0.5)$, where $rand$ is a random number from uniform distribution with $[0, 1]$.

2.3.Black hole algorithm

The black hole algorithm (BHA) is one of the most recent evolutionary algorithms inspired from the black hole phenomenon in the space. This algorithm was introduced in 2013 by Hatamlou [26]. A black hole in space is what forms when a star of massive size collapses. The gravitational power of the black hole is too high that even the light cannot escape from it [27-29].

In BHA, the process begins by the initialization of the stars, which are acting as the population, in the search space. The initial population is randomly generated. The best objective function of an individual star is selected as the black hole and it starts absorbing populations (stars) surround it. Then, all the stars move towards the black hole. This movement can be formulated as follows

$$x_i^{t+1} = x_i^t + \theta \times (x_{BH} - x_i^t), \quad i = 1, 2, \dots, n_s, \quad (6)$$

where x_i^t and x_i^{t+1} are the locations of the i^{th} star at iterations t and $t+1$, respectively. x_{BH} is the location of the black hole in the search space, θ is a random number in the interval $[0,1]$, and n_s is the total number of stars (candidate solutions in the search space). It is important to mention that, the black hole does not move, because it has the best objective value and then attracts all other stars [26, 30-32].

After determining the movement of the stars using Eq. (7), if the objective function value of a star is better than the value of the black hole, the star is then selected as the black hole. During moving stars towards the black hole, there is the possibility of crossing the event horizon (border of the black hole).

The radius of the event horizon (Schwarzschild radius) in the black hole algorithm is calculated by

$$R = \frac{f_{BH}}{\sum_{i=1}^{n_s} f_i}, \quad (7)$$

where f_{BH} and f_i is the objective function value of the black hole and the i^{th} , respectively. When the distance between a candidate solution and the

black hole is less than Eq. (8), that candidate is collapsed and a new candidate is created and distributed randomly in the search space.

To perform the descriptor selection, a binary black hole algorithm (BBHA) was proposed [31, 33, 34]. Unlike the standard BHA, in which the solutions are updated in the search space towards continuous-valued positions, in the BBHA, the search space is modeled as an n-dimensional Boolean lattice and the solutions are updated across the corners of a hypercube. In addition, as the problem is to select or not a given descriptor, a solution binary vector is employed, where 1 corresponds whether a descriptor will be selected to compose the new dataset, and 0 otherwise.

2.4. The proposed hybridization

The hybridization refers to merge different metaheuristics algorithms into a single framework. Therefore, a hybrid algorithm could take advantage of the used algorithms, and then yields more favorable performance than using a single algorithm [11].

FFA is excellent for local searches however it might get forced into local optima and thereby cannot perform global searches well [7, 35]. In the literature, several authors have been proposed different hybridization of FFA, such as [7, 9, 11, 34-48]. On the other hand, BHA can overcome local optimal solution [26]. The BHA has some common features with other metaheuristics algorithms.

To maintain a good balance between exploration and exploitation, the premature convergence of each algorithm and avoid trapping at local optima, hybridization has been proposed in our paper. In this work, a new hybrid algorithm, as a wrapper approach, of FFA and BHA is presented to enhance the performance characteristics of our proposed algorithm and to achieve faster convergence with the aim of escaping from local optima. Specifically, BHA is embedded in FFA to make FFA more effective by enhancing the exploration and exploitation of FFA algorithm. This hybridization will efficiently help to find the most significant descriptors in that related to the QSAR/QSPR models with high prediction performance. The flowchart of our new hybridization is presented in Figure 1.

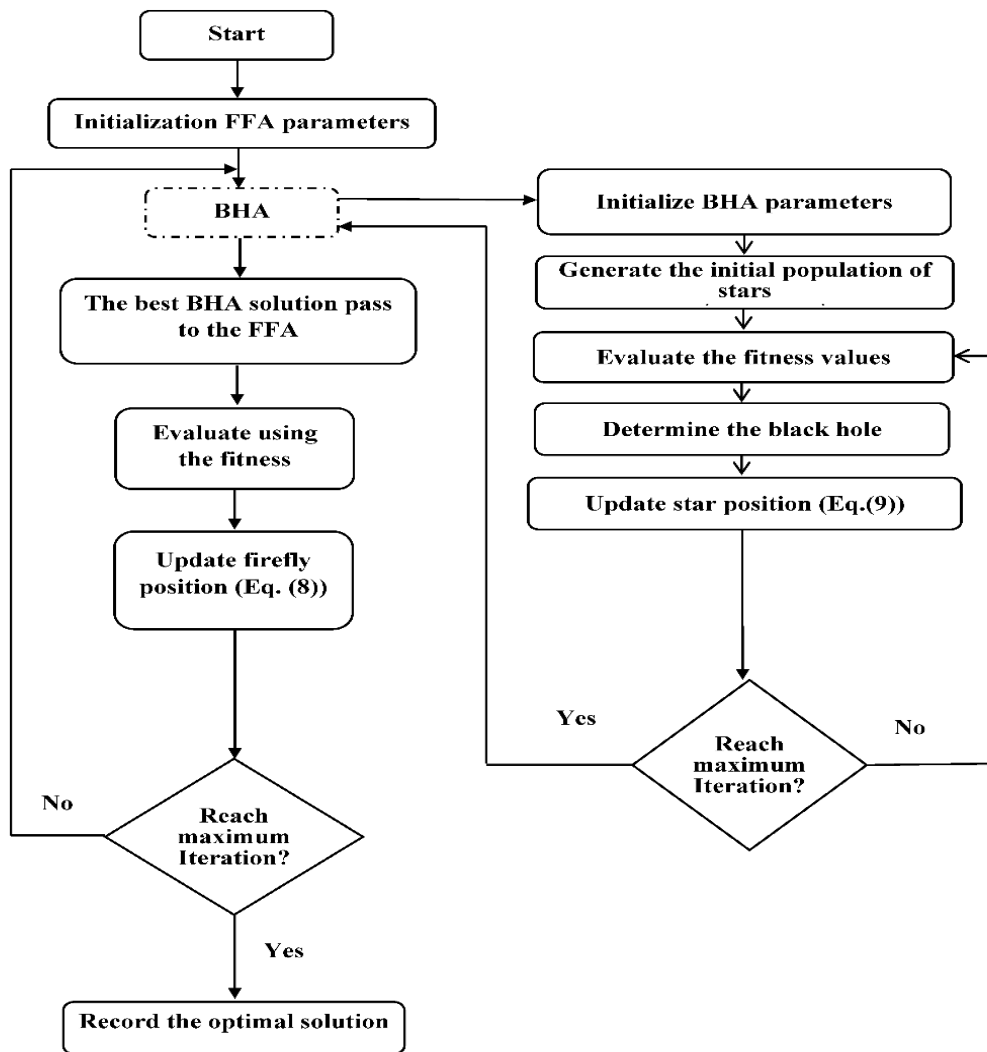


Figure (1): The flowchart of the new hybridization.

The parameter configurations for our proposed hybrid algorithm are presented as follows.

1. Initialization FFA parameters such that the population size $n_f = n_s = 40$, $\beta_0 = 1$, $\gamma = 0.25$, $\alpha = 0.2$, and the maximum number of iterations is $t_{\max} = 1000$.
2. The number of position for each firefly and star is represented by the total number of the descriptors in the QSAR/QSPR model.
3. The representation of the positions, in general, is depicted in Figure 2. The positions are randomly specified from the uniform distribution with 0 and 1.
4. In BHA and FFA, the position of each firefly and star is needed to transfer into a probability vector because the position is binary. The hyperbolic tangent function was employed, which is defined as in Eq. (8) and Eq. (9), respectively,

$$S(x_i^{t+1}) = |\tanh(x_i^{t+1})| \quad (8)$$

$$x_i^{t+1} = \begin{cases} 1 & \text{if } \phi < S(x_i^{t+1}) \\ 0 & \text{otherwise} \end{cases}, \quad (9)$$

where ϕ is a uniform random number alternating between 0 and 1.

d_1	d_2		d_{d-1}	d_D
1	0		1	0

Figure (2): Representation of the positions.

5. The fitness function is defined as

$$f = \min \left[\frac{1}{n} \sum_{i=1}^n (y_{i, \text{test}} - \hat{y}_{i, \text{test}})^2 \right], \quad (10)$$

where $y_{i, \text{test}}$ and $\hat{y}_{i, \text{test}}$ are, respectively, is the true value and the predicted value of the response variable in the testing dataset.

2.5.Evaluation criteria

The prediction performance of the used methods was measured by the mean-squared error (MSE) and leave-one-out internal validation (Q^2_{int}), which are defined by

$$MSE_{\text{train}} = \frac{\sum_{i=1}^{n_{\text{train}}} (y_{i, \text{train}} - \hat{y}_{i, \text{train}})^2}{n_{\text{train}}}, \quad (11)$$

and

$$Q^2_{\text{int}} = 1 - \left[\frac{\sum_{i=1}^{n_{\text{train}}} (y_{i, \text{train}} - \hat{y}_{i, \text{train}})^2}{\sum_{i=1}^{n_{\text{train}}} (y_{i, \text{train}} - \bar{y})^2} \right], \quad (12)$$

respectively.

Furthermore, the test dataset was used to validate the model by computing the following criteria

$$MSE_{\text{test}} = \frac{\sum_{i=1}^{n_{\text{test}}} (y_{i, \text{test}} - \hat{y}_{i, \text{test}})^2}{n_{\text{test}}}, \quad (13)$$

and

$$Q_{ext}^2 = 1 - \frac{\sum_{i=1}^{n_{test}} (y_{i,test} - \hat{y}_{i,test})^2}{\sum_{i=1}^{n_{test}} (y_{i,test} - \bar{y}_{train})^2}, \quad (14)$$

respectively, where Q_{ext}^2 is the external validation, n_{train} and n_{test} represent the training and test sample sizes, the $y_{i,train}$, $y_{i,test}$, $\hat{y}_{i,train}$, and $\hat{y}_{i,test}$ stand for the experimental activity of the training dataset, test dataset, and their corresponding predicted values. While $\bar{y}$ and $\bar{y}_{train}$ represent the mean of all the activity values and the mean of the training activity values, respectively.

3. Data sets:

Eight benchmark data set, which they used in [49, 50], have been used for QSAR modeling. The eight benchmark data sets are: (1) a set of 114 angiotensin converting enzyme (ACE) inhibitors with their pIC_{50} values ranging from 2.1 to 9.9. (2) A set of 111 acetyl-cholinesterase (AChE) inhibitors with pIC_{50} values ranging from 4.3 to 9.5. (3) A set of 163 ligands for the benzodiazepine receptor (BZR) with pIC_{50} values ranging from 5.5 to 8.9. (4) A set of 322 cyclooxygenase-2 (COX2) inhibitors which they have pIC_{50} values that range from 4.0 to 9.0. (5) A set of 397 dihydrofolate reductase inhibitors (DHFR) with pIC_{50} values for rat liver enzyme ranging from 3.3 to 9.8. (6) A set of 66 inhibitors of glycogen phosphorylase b (GPB) have pK_i values ranging from 1.3 to 6.8. (7) A set of 76 thermolysin inhibitors (THER) have pK_i values ranging from 0.5 to 10.2.9 (8) And finally, a set of 88 thrombin inhibitors (THR) have pK_i values ranging from 4.4 to 8.5. The characteristics of the eight used datasets are listed in Table 1. In order to build a persuasive QSAR model, each dataset was randomly separated into a training data set and a test data set according to the proportion of 80%:20%.

Dragon software (version 6.0) was used to generate 4885 molecular descriptors including all 29 blocks based on the optimized molecular structures. Preprocessing steps were carried out to include consistent and useful descriptors. The first step is to discard the descriptors that had zero values. Then, remove the descriptors that had constant value for all compounds. After that, the descriptors in which 90% of their values were zeros were removed. Finally, descriptors with a relative standard deviation of less than 0.001 were deleted.

Table (1): The characteristics of the four used datasets

Datasets	# compounds (n)	# Descriptors (d)
ACE	114	2341
AchE	111	1764
BZR	163	3068
COX2	322	4191
DHFR	397	2553
GPB	66	1740
THER	76	2937
THR	88	1885

3. Results

The proposed method, FFA-BHA, is evaluated and validated to test the predictive ability of the constructed QSAR models of used datasets depending on the linear regression model. Further, to prove the predictive performance of the FFA-BHA, the obtained results of the original FFA and BHA are compared with the FFA-BHA. Table 2 summarizes the number of molecular descriptors selected by each of the used methods and the prediction assessment criteria.

In terms of the selected descriptors, it is clearly seen that FFA-BHA selected the lowest molecular descriptors comparing with FFA and BHA for the used datasets. For example, among the 4191 molecular descriptors for the COX2 dataset, 17 descriptors were selected by FFA-BHA compared to 23 selected descriptors by FFA and 22 selected descriptors by BHA. As a result, the FFA-BHA provides an easy interpretable QSAR models.

Regarding the predictive performance, as can be seen from Table 2, the FFA-BHA achieved the lowest MSE_{train} in the used datasets among the other used algorithms. For instance, in the GPB dataset, the MSE_{train} of the FFA-BHA was about 30.95% and 22.94% lower than that of the FFA and BHA, respectively. Depending on the testing dataset, it is noteworthy that FFA-BHA reduced the MSE_{test} significantly in comparison with FFA and the BHA. In the THR dataset, for example, the reduction of MSE_{test} using FFA-BHA was 36.97% and 26.81% compared with FFA and BHA, respectively.

Moreover, the prediction performance in the training dataset using Q^2_{int} of the FFA-BHA was 0.929, 0.903, 0.949, 0.951, 0.933, 0.936, 0.892 and 0.916 (>0.5) for all datasets, which was much better than those obtained

by the FFA and BHA, which indicated the better predictive ability of the FFA-BHA than FFA and the BHA. Furthermore, it is apparent that the Q^2_{ext} value for FFA-BHA was higher than FFA and the BHA, which indicated that FFA-BHA has greater predictive ability. The obtained results were compared to those of [49], which they used genetic algorithm with multiple linear regression (GA-MLR). The prediction performance of the FFA-BHA shows better enhancement compared with GA-MLR. In THER data set, for instance, the value of $Q^2_{int} = 0.892$ and $Q^2_{ext} = 0.881$ were better than those obtained by GA-MLR at $Q^2_{int} = 0.753$ and $Q^2_{ext} = 0.724$.

Table (2): Prediction evaluation criteria values for the training and testing datasets

Datasets	Methods	Training dataset			Testing set	
		# selected descriptor	MSE_{train}	Q^2_{int}	MSE_{test}	Q^2_{ext}
ACE	FFA-BHA	11	0.284	0.929	0.334	0.921
	FFA	17	0.480	0.846	0.571	0.835
	BHA	15	0.385	0.873	0.452	0.869
AchE	FFA-BHA	9	0.507	0.903	0.531	0.899
	FFA	14	0.795	0.799	0.823	0.802
	BHA	12	0.764	0.849	0.812	0.824
BZR	FFA-BHA	16	0.368	0.949	0.424	0.933
	FFA	22	0.475	0.899	0.537	0.894
	BHA	20	0.452	0.903	0.481	0.899
COX2	FFA-BHA	17	0.314	0.951	0.410	0.941
	FFA	23	0.436	0.897	0.637	0.884
	BHA	22	0.424	0.903	0.588	0.887
DHFR	FFA-BHA	20	0.438	0.933	0.494	0.921
	FFA	27	0.554	0.871	0.612	0.853
	BHA	25	0.522	0.903	0.581	0.899
GPB	FFA-BHA	12	0.638	0.936	0.726	0.922
	FFA	17	0.924	0.781	1.157	0.764
	BHA	15	0.828	0.896	0.936	0.858
THER	FFA-BHA	13	0.424	0.892	0.474	0.881
	FFA	19	0.621	0.806	0.711	0.795

Datasets	Methods	Training dataset			Testing set	
	BHA	17	0.574	0.833	0.592	0.829
THR	FFA-BHA	11	0.354	0.916	0.404	0.901
	FFA	16	0.551	0.826	0.641	0.815
	BHA	15	0.535	0.853	0.552	0.849

To further highlight the efficiency of the FFA-BHA, Figure 3 displays the execution time in seconds. The computational efficiency of FFA-BHA is comparable to FFA and BHA. It is noteworthy that FFA-BHA has the fastest convergence speed beating the FFA and BHA, where it requires the least amount of time to complete the optimized target.

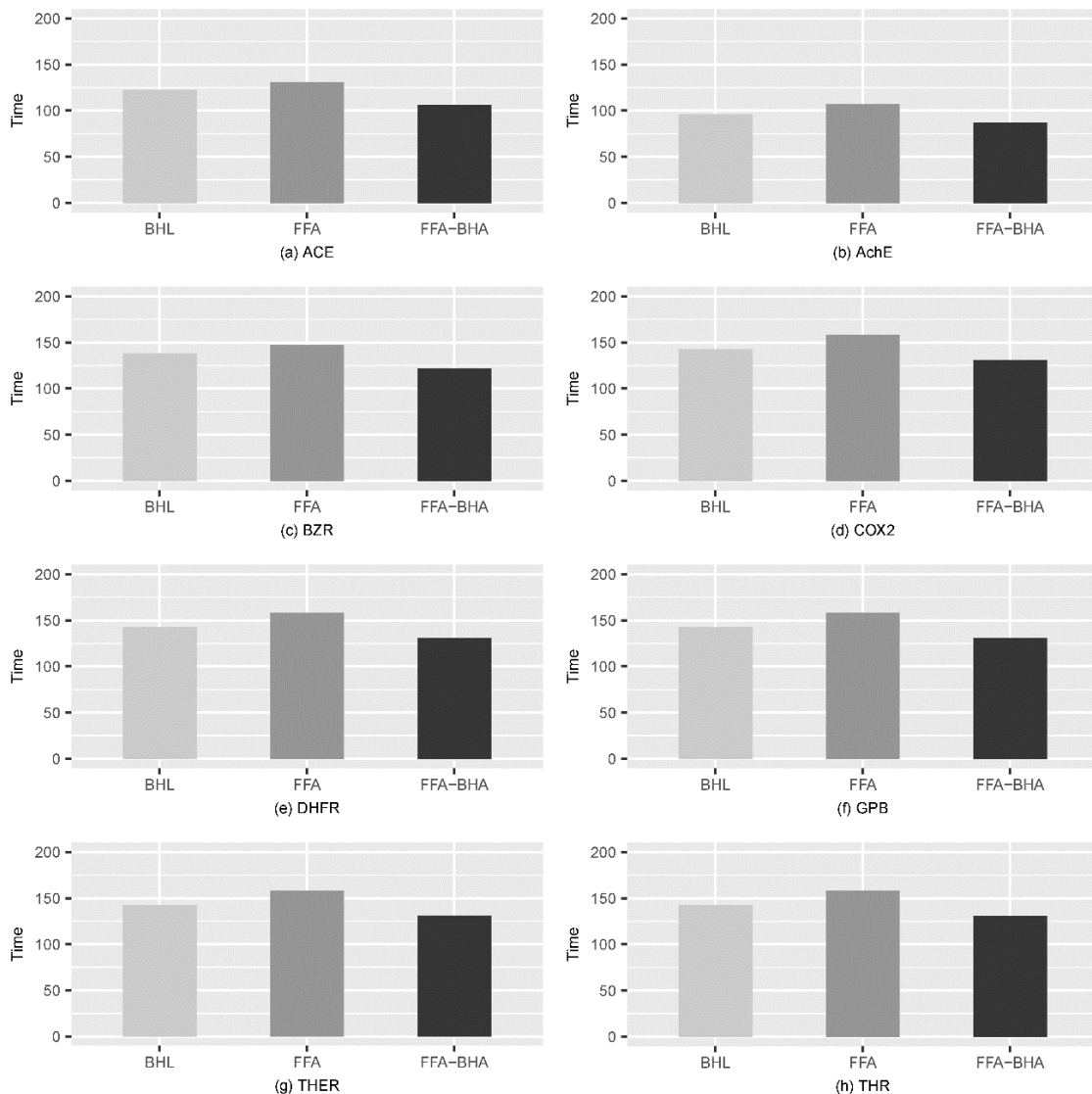


Figure (3): Computational time, in seconds, of the used algorithms.

To summary, the results in Table 2 and Figure 3 not only show that required computation times of FFA-BHA is less compared to the FFA and BHA, but also FFA-BHA is the better algorithm in terms of the best predictive performance". In addition, a comparison based on the prediction performance and computational times reveals that the hybridization has better performance for descriptor selection compared to the original FFA.

4. Conclusion

In this paper, a novel hybrid algorithm that combines the FFA and BHA algorithms was described. The benefits and characteristics of BHA and FFA are combined to offer a balance between the processes of exploration and exploitation. For eight benchmark datasets, an effective QSAR/QSPR model was created using the suggested hybrid technique. The suggested hybrid algorithm's prediction accuracy results for the training and testing datasets greatly outperformed FFA and BHA. Also, the computation-time results showed that the suggested hybrid approach can build a trustworthy and robust QSAR model in the shortest amount of time.

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