International Journal of Chemical and Biochemical Sciences
(ISSN 2226-9614)

Journal Home page: www.iscientific.org/Journal.html

The Use of Artificial Intelligence Models for Predicting the Bioavailability and Toxicity of Chemical Combinations

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Abstract

There is a growing need for effective forecasting methodologies due to the increasing difficulty of determining the bioavailability and toxicity of chemical combinations in various settings and businesses. Conventional experimental techniques are frequently constrained by their high expense, time-consuming and limited range of applications. Using the Crow Search Algorithm (CSA) to adjust hyper parameters in Light Gradient Boosting Machine (LGBM) models is a novel strategy that this work investigates an effort to improve prediction performance and accuracy regard to the toxicity and bioavailability of combination chemicals. Using a vast database that includes different chemical combinations and the toxicity data that goes along with them, this study aims to maximize the performance of the LGBM model by means of CSA-driven hyper parameter adjustment. When evaluating the bioavailability and toxicity of chemical combinations, the resulting Crow Search tuned Light Gradient Boosting Machine (CST-LGBM) models show higher predictive capabilities. The suggested strategy has been identified in outperforming existing approaches after a comparative procedure incorporating many metrics; including accuracy (85%), specificity (84%), recall (88%) and F1 score (88%). The incorporation of CSA into LGBM models presents an effective strategy to improving the predictive accuracy of chemical combination toxicity and bioavailability by overcoming the limitations of traditional techniques. The outcomes of the research open up new possibilities for a dependable and effective method of assessing chemical combinations affect industry and the environment.

Keywords: Bioavailability, Toxicity, Chemical Combinations and Crow Search tuned Light Gradient Boosting Machine

Full length article *Corresponding Author, e-mail: ccnitj@gmail.com

1. Introduction

The evaluation of the bioavailability and toxicity of chemical combinations presents a significant problem in the changing field of chemical exposure and its possible effects on human health and the environment [1]. Tangled chemical interactions can have antagonistic or synergistic effects, weaving a tangled web that defies conventional risk assessment techniques. Protecting public health and the environment requires an understanding of the combined effects of novel compounds that industries continue to incorporate into a variety of products and processes [2].

Bioavailability, a crucial parameter relates to the degree and speed, a material which is taken by an organism, dispersed, digested and eliminated. Evaluating a drug's bioavailability is challenging enough, when many chemicals collaborate; the process becomes much more complicated [3]. Furthermore, the toxicity of chemical mixtures adds another level of complication because the effects of individual chemicals can either increase or decrease depending on their interaction with other compounds. Understanding the cumulative effects of these chemicals becomes essential for protecting human health and environmental sustainability as new compounds are introduced into a wider range of products and processes [4]. The number of chemical mixes found in consumer goods, manufacturing operations and

medications highlights the need for trustworthy predictive models to be developed as soon as possible [5]. Traditional toxicological approaches concentrate on the investigation of individual compounds in isolation; frequently neglect the dynamic nature of real-world exposures. Computational modeling advances combined with multidisciplinary research present a viable path toward improving our capacity to forecast the toxicity and bioavailability of chemical mixtures [6]. Interpreting molecular interactions in complicated mixtures is a major difficulty. Researcher behavior predictions at molecular scale are made possible by computational technologies such as "Molecular Docking" computations and "Quantitative Structure-Activity Relationship (QSAR)" method. The comprehensive understanding of the potential effects of chemical combinations on biological pathways and cellular activities is made possible by combining these instruments with systems biology methodologies [7]. The goal of this work is to improve the predicted accuracy and efficiency of the toxicity and bioavailability of chemical combinations by integrating the Crow Search Algorithm (CSA) into Light Gradient Boosting Machine (LGBM) models for hyper parameter optimizing. The study [8] assessed to determine Machine Learning models "Random Forest (RF)", "Artificial Neural Network (NN)"worked at predicting changes in the bioavailability of complicated chemicals in polluted soils that had been treated with compost or charcoal. The obtained results showed that NN and RF could simulate the bioavailability of various pollutants, and that RF could identify, which input measures were actually important for predicting toxicity. Additionally, ML models offered excellent applicant tools, while NN models provided an appropriate and consistent output. The study [9] examined the prospect of incorporating metallic bioavailability models into environmental quality standards, looked at evidence supporting the mechanistic theory behind metal bioavailability models and discovered basic recommendations for developing or applying bioavailability-based contaminants prototypes. Achieving equilibrium between mechanistically valid models and streamlined methods were difficult. The study [10] examined the possibility of forecasting oral or Intravenous (IV) medication exposure and oral bioavailability in rats. The outcomes of silico models, which were built on the identical endpoints for intake, distribution, metabolism and excretion as well as the chemical composition, were used as the input variables. They attained accuracy and precision near 70% in the forecasting challenge for an unambiguous signal for limited oral bioavailability based on its chemical makeup. The study [11] evaluated the bioavailability of Micro Plastic (MP) absorbed polycyclic aromatic hydrocarbons (PAHs), to marine copepods as well as the absorption rates of two model PAHs, phenanthrene and fluoranthene, to MP fragments in ocean water. Findings demonstrated the significance of temperature, particle size, and the kind of polymer in impacting the pace and mechanism by organic pollutants that were hydrophobic sorb from ocean water to MP. The study [12] evaluated the effects of the quantity of biological components in the Rybnik reservoir deposits on the motion and environmental toxicity of substances. The following were the order in which the organic material fractions composed Non-hydrolyzing carbon (Cnh) over fulvic acid (Cfa) over humic acid (Cha) over dissolved organic carbon (DOC). These findings suggested that trace elements become less harmful to Vibrio fischeri when they compound with organic materials. The study [13] acquired the "Essential Oils" (EOs) of plants by three hours of distillation under steam from I. asarifolia and I. setifera. Utilizing the Machine Learning (ML) methods, they determined the toxic effects of the main chemicals of Ipomoea setifera and Ipomoeaasarifolia EOs. Their findings represented a significant advancement in our knowledge of the molecular mechanism of action, pharmaceutical kinetics and toxicity of the chemical components. The study [14] evaluated for one week, the combined effects on Daphnia magna of two distinct types of (polyethylene (PE) microbeads and polyethylene terephthalate/polyamide (PET/PA) fibers) micro-plastics and three distinct chemical compounds (Roundup Gran, glyphosate acid, and glyphosate-monoisopropylamine salt). According to their findings, plastic particles could change their toxic effects of pollutants like herbicides in addition to their possible detrimental direct impacts. The study [15] intended to evaluate the toxic effects of Sm3+, La3+, Nd3+ and their mixtures (ternary 1:1:1) to creatures that belong to different trophic levels of main consumers (Daphnia similis and micro crustaceans), main producers (Raphidocelissubcapitata and Chlorella vulgaris), and decomposing organisms (Penicilliumsimplicissimum and Aspergillus japonicus). According to their study, Nd3+ was deemed extremely harmful to Daphnia similsince, it was an element that has most poisonous to five out of the six studied species. The remaining research is structured in Section 2 explains the Methodology. Section 3 evaluates the experimental result and Section 4 presents the study's conclusion

2. Materials and Methods

2.1. Dataset

In this study, we utilized the Leadscope Toxicity Database's severe chemical toxicity data for this investigation. The "Registry for the Evaluation of Toxic Effects on Chemical Substances" (RTECS) was the source of these data. We first employed data sets of different measurements of the rat oral, rabbit epidermis, mouse subcutaneous and its oral toxicity data with 15,752, 52,228, 34,233, and 2,296 entries, accordingly to assess the effect of training set length on efficiency [16].

2.2. Crow Search tuned Light Gradient Boosting Machine (CST-LGBM)

In CST-LGBM, the combined use of Light Gradient Boosting Machine and Crowd Search Optimization enhances the precision of bioavailability and toxicity forecasts for comprehensive risk assessment.

2.2.1. Crow Search optimization

This computational approach that makes use of Crow Search Optimization forecasts the bioavailability and toxicity of chemical combination, improving risk assessment in pharmaceutical and ecological uses. To optimize forecasting models, the algorithm imitates the foraging

behavior of crows, providing a reliable method for evaluating the beneficial effects of chemical combinations on biological structures.

Step 1: Crows memory and activation

Crow positions (c) start out at random in the searching area dimension (M).

$$position\ of\ crows\ (c) = \begin{bmatrix} c_{1,2} & c_{1,2} & \cdots & c_{1,y} \\ c_{2,1} & c_{2,2} & \cdots & c_{M,y} \\ c_{M,1} & c_{M,2} & \cdots & c \end{bmatrix} \quad (1)$$

Equation (2) is used for establishing the crow's memory. The food that will be used for recognizing crows has been arranged at random

.

$$memory\ of\ crows\ (r) = \begin{bmatrix} r_{1,2} & r_{1,2} & \cdots & r_{1,y} \\ r_{2,1} & r_{2,2} & \cdots & r_{M,y} \\ r_{M,1} & r_{M,2} & \cdots & r_{M,y} \end{bmatrix} \quad (2)$$

Step 2: Finding and creating a new position

Consider that there are two crows, crow$w$ and crow y, and that crow w is unaware of the exact position and whereabouts of crow y. Finding the food in the concealed areas will reveal the crow's optimal perch.

$$w^{jq+1} = w^{jq} + \beta + fly^{jq} * (max^{jq} - w^{jq}) \quad (3)$$

The revised location of the crow is represented byw^{jq+1}in the equation previously, where β − denotes the random function and its value falls in the interval of (0, 1). The symbol fly^{jq} − indicates the crow's length for a fly. The maximum number of crow iterations for fly is represented by max^{jq}. The original and new positions are contrasted to determine which is best and the superior position is taken into consideration.

Step 3: Determining the ideal position

The following equation can be used to determine the direction of another crow and the ideal crow position to seek for food that is concealed.

$$w^{jq+1} = \begin{cases} w^{jq} + \beta + fly^{jq} * (max^{jq} - w^{jq}) + \beta \geq oq^{jq} \\ random\ position\ , Otherwise \end{cases} \quad (4)$$

The aforementioned formula is used to determine the crow's revised location. The random number generated value for each iteration is more than or close to the crow probability (oq^{jq}).

Step 4: Assessment of the fitness function

Crow's fitness function is computed by taking into the updated location and memory consumption.

$$n^{jq+1} = \begin{cases} w^{jq}, e(w^{jq+1}) is\ better\ than\ e(n^{jq+1}) \\ n^{jq+1}\ , Otherwise \end{cases} \quad (5)$$

If the crow's new site appears to be more favorable than its previous one. The fitness function is revised according to the memory and the updated location.

Step 5: Looking for the end condition

This process is iterated till the ideal location and memory are reached. After determining the aforementioned circumstance. The crow's food is located in the concealed location.

2.2.2. Light Gradient Boosting Machine

The application of Light Gradient Boosting Machine, a potent machine learning method makes easier to forecast chemical combinations bioavailability and toxicity with accuracy. It captures intricate relationships by utilizing ensemble learning and tree-based models, offering a reliable technique for assessing how different chemical mixtures affect the environment and public health. Based on the decision tree method, “Light Gradient Boosting Machine (LGBM)” is a dispersed, outstanding quality gradient boosting framework that is used for a various machine learning applications such as categorization and ranking. LGBM is essentially an ensemble technique that adds the forecasts from several decision trees to provide a final prediction that is well-generalized. LGBM is noteworthy for its additive training approach, which involves teaching every new tree model to forecast the remainders, or errors of the previous models. Assuming we aspire to build a LGBM model with T trees, the additive training procedure for a dataset containing n samples may be explained as follows:

$$\hat{z}_j^{(0)} = 0$$

$$\hat{z}_j^{(1)} = e_1(w_j) = e_1(w_j) + \hat{z}_j^{(0)}$$

$$z_j^{(2)} = e_2(w_j) + z_j^{(1)} = e_1(w_j) + e_2(w_j)$$

$$\hat{z}_j^{(s)} = \sum_{l=1}^{s} e_l(w_j) = e_s(w_j) + \hat{z}_j^{(s-1)} \quad (6)$$

Where $e_s$represents the learnt function for the decision tree and $\hat{z}_j^{(s)}$is the anticipated outcome of the j^{th} example at the s^{th} iteration. As shown by equation 6, we add a new function e (or the learned residuals) to the framework in each iteration while maintaining the existing model$\hat{z}_j$. The following goal can be minimized to obtain the $e_s$of all iterations.

$$\mathcal{L}^{(s)} = \sum_j^m k(z_j, z_j^{(s)}) + \sum_{s=1}^{S} \Omega(e_s) \quad (7)$$

The initial term is the loss function, which calculates the variance between the desired outcome $\hat{z}_j$ and the prediction$\hat{z}_j^{(s)}$. The subsequent term is the normalization term, which penalizes the level of complexity of the model.

More specifically, LGBM is a "Gradient Boosting Decision Tree (GBDT)" prototype. "Gradient-based One-side Sampling (GOSS)" and leaf-wise growth are the two unique methodologies LGBM uses for training each individual decision tree (e) and dividing the data. The goal of GOSS is to address the difficult issue with traditional GBDT executions, which must calculate the information gain for each potential split by going over each feature of each data point. The key finding of GOSS is data instances with higher gradients are more important for computing information gain. The Light Gradient Boosting Machine (LGBM) and the Crow Search Algorithm (CSA) are effective machine learning methods, with their own special advantages. Combining both approaches to forecast the toxicity and bioavailability of chemical mixtures is a viable strategy that makes use of LGBM's effectiveness and CSA's optimization skills. Crows clever hunting techniques served as the model for the metaheuristic algorithm known as CSA. Because it replicates the way crows naturally look for food, it performs well in global optimization issues. The model may search the large space of possible feature combinations by integrating CSA, increasing the probability of discovering the best answers. This is important when estimating toxicity and bioavailability because it's necessary to determine the complex interactions between different chemical characteristics. Contrarily, LGBM is a gradient boosting system that excels in managing massive data sets and feature spaces with many dimensions. It is a great option for forecasting applications because of its parallel processing capabilities, effective training procedure, and capacity to handle categorical information. The model is able to utilize LGBM's prediction accuracy and generalization abilities when used in conjunction with CSA, assuring reliable performance on a variety of chemical combinations. The CST-LGBM for predicting the bioavailability and toxicity of chemical combinations is demonstrated in Algorithm 1.

Algorithm 1: CST-LGBM

$$
\begin{aligned}
&import\ numpy\ as\ np\\
&from\ sklearn.mode\\
&-selectionimport\ Train\_Test\_split\\
&from\ sklearn.ensemble\\
&import\ GradientBoostingClassifier\\
&from\ CSO\ import\ CSO\\
&X, y\ =\ load\_data()\\
&X\_Train, X\_Test, y\_Train, y\_Test\\
&=\ Train\_Test\_split(X, y, Test\_size\\
&=0.2, random\_state=42)\\
&def\ objective\_function(params):\\
&learning\_rate\ =\ params[0]\\
&n\_estimators\ =\ params[1]\\
&max\_depth\ =\ params[2]\\
&lgbm\_classifier\\
&=\ GradientBoostingClassifier\ (learning\_rate\\
&=\ learning\_rate, n\_estimators\\
&=\ n\_estimators, max\_depth\ =\ max\_depth)\\
&lgbm\_classifier.fit(X\_train, y\_train)\\
&accuracy\ =\ lgbm\_classifier.score(X\_Test, y\_Test)\\
&return-accuracy\\
&cso\_optimizer\ =\ CSO(objective\_function, dimension\\
&=3, min\_bound\\
&=[0.01,50,1], max\_bound\\
&=[0.5, 200, 10], num\_particles\\
&=30, max\_iter=50)\\
&best\_params\ =\ cso\_optimizer.run()\\
&best\_learning\_rate, best\_n\_estimators, best\_max\_depth\\
&=\ best\_params\\
&final\_lgbm\_classifie\\
&=\ GradientBoostingClassifier(learning\_rate\\
&=best\_learning\_rate, n\_estimators\\
&=best\_n\_estimators, max\_depth=best\_max\_depth)\\
&final\_lgbm\_classifier.fit(X, y)
\end{aligned}
$$

3. Results and Discussion

The experimental setting entails optimizing the Light Gradient Boosting Machine (LGBM) parameters for chemical combination bioavailability and toxicity prediction through the application of CSA. LGBM and scikit-learn are two examples of libraries that are utilized with Python. For best results in the experiment, use LGBM version 3.3.1 and 16GB or more of RAM. The efficiency of the suggested and current methods was evaluated by means of accuracy, specificity, recall, and F1 score. "Support Vector Machine (SVM)", "Extreme Gradient Boosting (XGB)", "K Nearest Neighbors (KNN)" [17] were existing process compared to CST-LGBM. Accuracy is defined as the percentage of accurately anticipated results (bioavailability and toxicity combined) in relation to all forecasts in terms of predicting chemical combinations bioavailability and toxicity using the equation (8). In determining the impact of chemical combinations on bioavailability and toxicity, it is a gauge of the model's general accuracy and dependability. Greater precision signifies enhanced forecasting efficacy.

$$Accuracy\ =\ \frac{TN+TP}{(TN+TP+FN+FP)} \tag{8}$$

(Fig 1) and (Table 1) illustrates the accuracy. Compared to existing method SVM – 84%, XGB-82.6% our proposed method has higher accuracy of 85%. The recommended method, CST-LGBM, demonstrated notable improvements for Predicting the Bioavailability and Toxicity of Chemical Combinations when compared to the existing methods. Specificity is an efficiency parameter used in chemical combination prediction that assesses the capacity of a model to determine true negative cases in terms of bioavailability and toxicity as in the equation (9).

$$Specificity\ =\ \frac{TN}{(TN+FP)} \tag{9}$$

(Table 1) and (Fig 2) shows the specificity. Our proposed method has a higher specificity of 84% as compared to the existing methods, SVM-78% and XGB-83.2%.CST-LGBM, showed significant improvements for estimating the bioavailability and toxicity of chemical combinations. The recall for forecasting the toxicity and bioavailability of chemical combinations is explained as the proportion of all

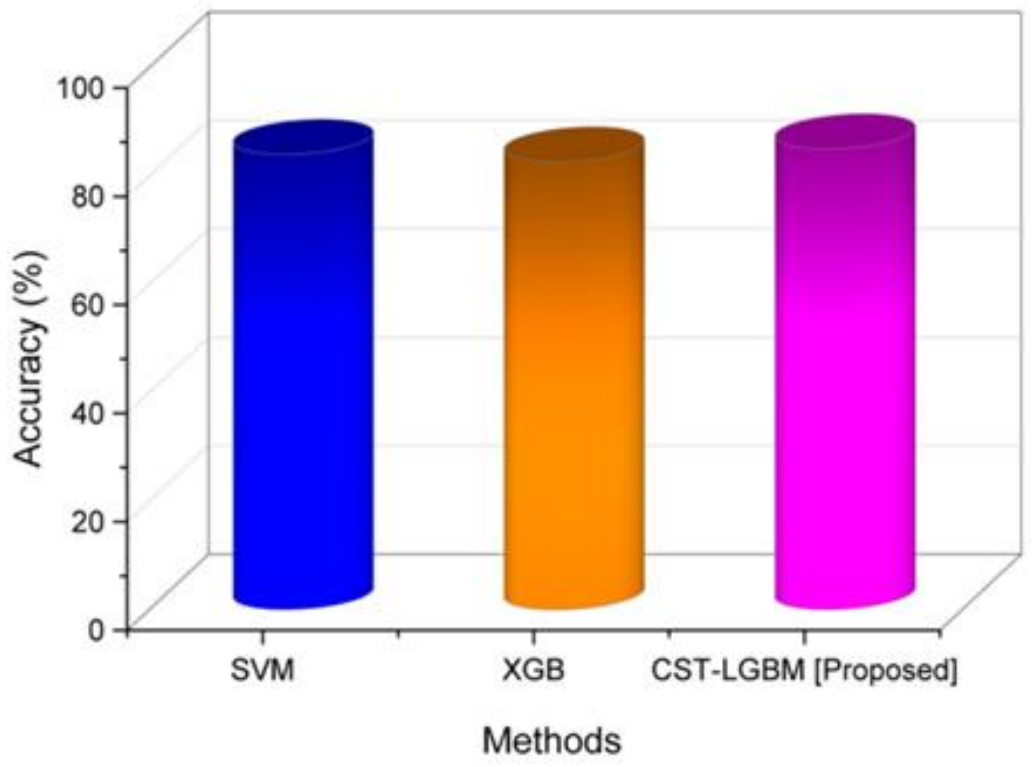

Figure 1. Outcome of Accuracy

Table 1. Demonstrates the Accuracy and Specificity

Methods	Accuracy (%)	Specificity (%)
SVM	84%	78%
XGB	82.6%	83.2%
CST-LGBM	85%	84%

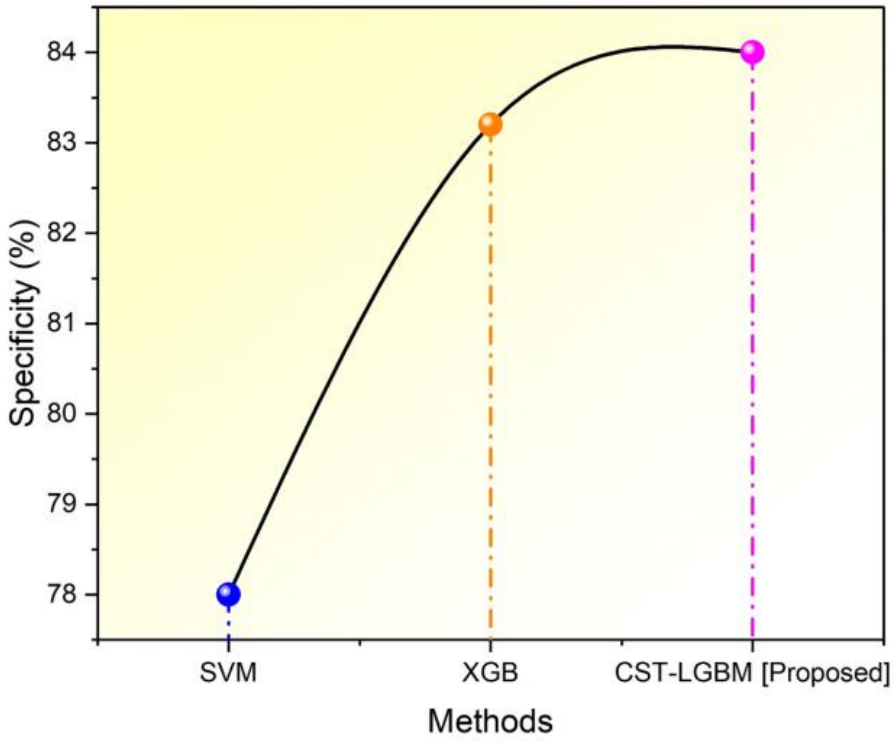

Figure 2. Outcome of Specificity

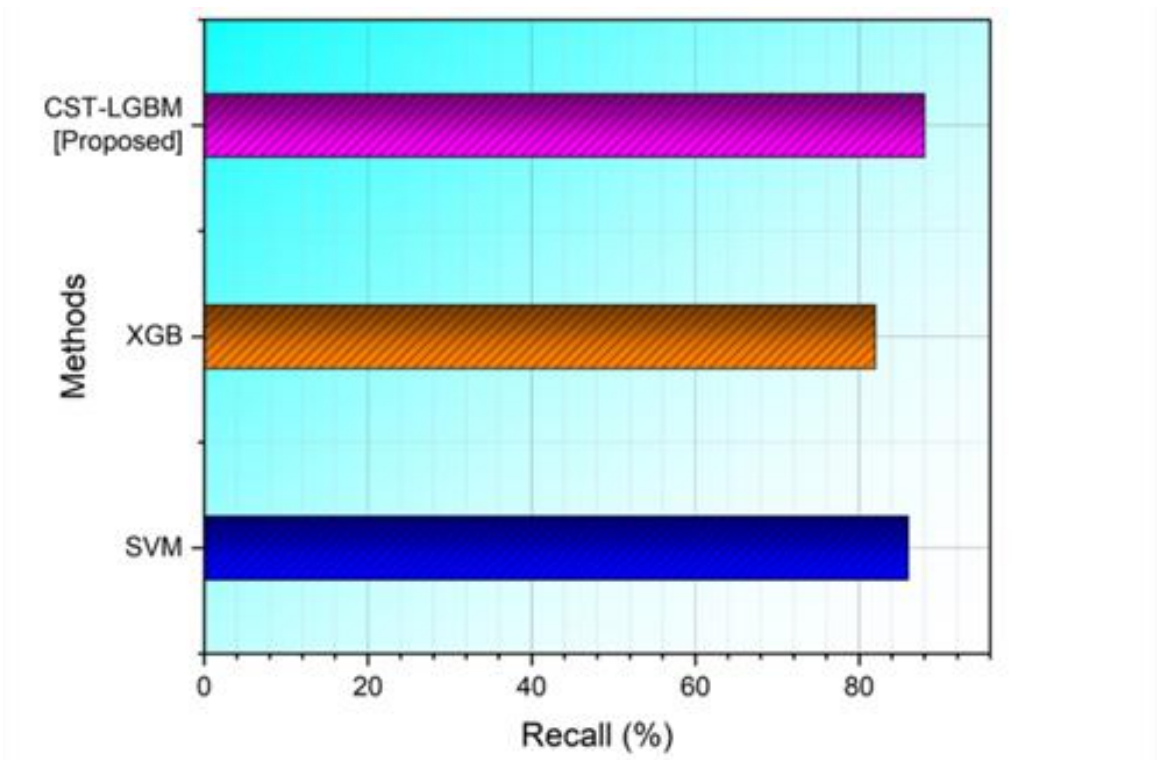

Figure 3. Outcome of Recall

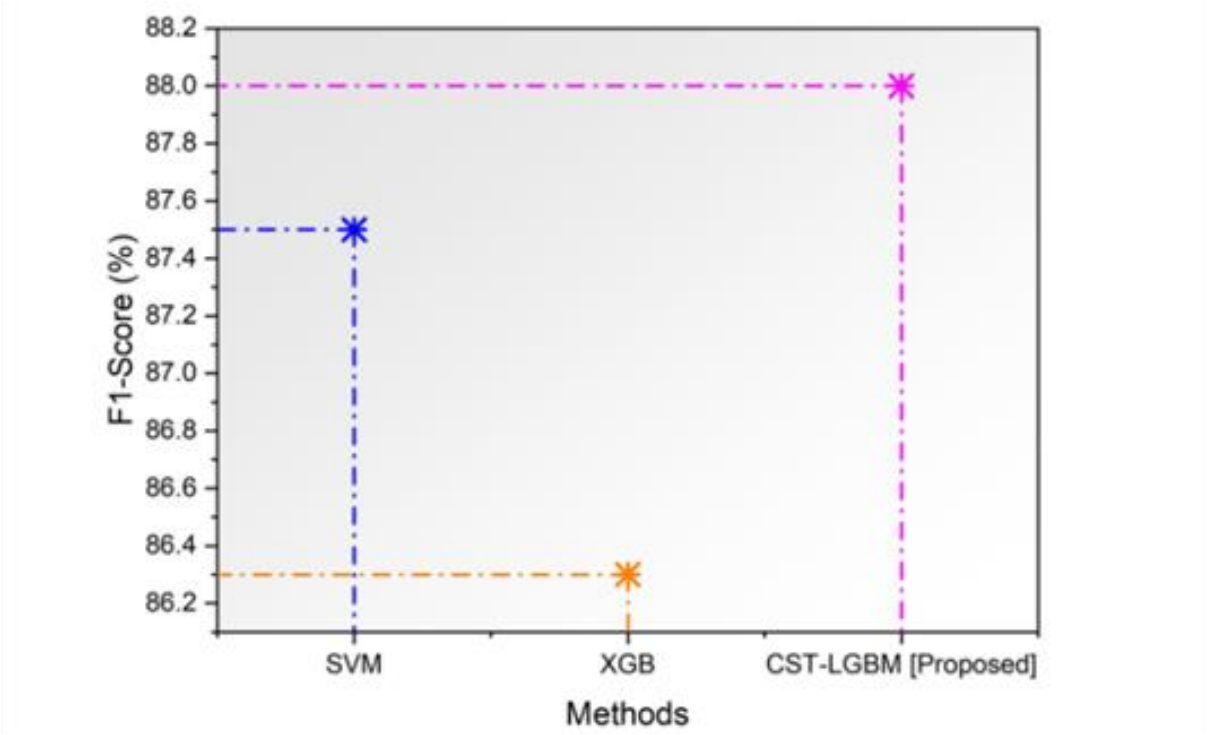

Figure 4. Outcome of F1-score

Table 2. Demonstrates Recall and F1-score

Methods	Recall (%)	F1-score (%)
SVM	86%	87.5%
XGB	82%	86.3%
CST-LGBM	88%	88%

actual positive occurrences to the true positive events, or instances of bioavailability or toxicity that are detected in equation (10). It assesses the model's susceptibility to identifying bioavailability or toxicity in chemical combinations by measuring its capacity to detect and accurately identify all beneficial results.

$$Recall = \frac{TP}{(TP+FN)} \quad (10)$$

(Table 2) and (Fig 3) indicates the recall. The technique we propose, that has a greater recall of 88% compared to existing methods, SVM (86%), XGB (82%). The proposed approach, CST-LGBM, showed significant improvements for predicting the bioavailability and toxicity of chemical combinations. The harmonic average of recall and precision is the F1-score for estimating the toxicity and bioavailability of chemical mixtures. Its total effectiveness for chemical combination effects can be assessed with a single score that includes recall and accuracy, providing a balanced assessment of the model performs that accounts for both erroneous and false positive results as given in the equation (11).

$$F1 - score = \frac{2}{(1/recall + 1/precision)} \quad (11)$$

The F1-score is shown in (Fig 4) and (Table 2). Proposed approach has an enhanced F1-score of 88% compared to both existing methods, SVM (87.5%) and XGB (86.3%). Predicting the bioavailability and toxicity of chemical combinations was significantly improved by CST-LGBM.

4. Conclusions

Chemical mixtures are becoming more complex, which makes necessary to develop efficient methods for predicting their bioavailability and toxicity in various ecological and industrial scenarios. The scope, expense and duration of conventional experimental approaches are constrained. Through the improvement of model parameters and the negotiation of complex data relationships, this approach guaranteed a deeper understanding of chemical interaction. For chemical combinations, the Crow Search tuned Light Gradient Boosting Machine (CST-LGBM) models outperformed other models in terms of bioavailability and toxicity prediction. Numerous parameters, including accuracy (85%), specificity (84%), recall (88%), and F1 score (88%) are assessed during the comparison process against other existing methods. Crowd Search Tuned Light Gradient Boosting has limitations in terms of interpretability, data reliance and potential overfitting when used to predict the bioavailability and toxicity of chemical combinations. Enhancing explain ability for reliable predictions in chemical combination bioavailability and toxicity, incorporating multi-omics data, and improving models are some potential future directions.

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