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Treatment prediction of sugar industry wastewater in moving-bed biofilm reactor using multi expression programming

M. Talebidalouei[a], Seyed Ahmad Mirbagheri[a,*], Pouria Nakhaei[b]

[a]*Faculty of Civil Engineering, K.N. Toosi University of Technology, Tehran, Iran, emails: mirbagheri@kntu.ac.ir (S.A. Mirbagheri), talebi_mary92@yahoo.com (M. Talebidalouei)*
[b]*Faculty of Civil Engineering, Amirkabir University of Technology, Tehran, Iran, email: p.nakhaee@aut.ac.ir (P. Nakhaei)*

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ABSTRACT

Minimizing water consumption and optimizing wastewater treatment of the sugar industry is one of the most water consuming industries that have significant importance. In this research, the advanced treatment of sugar factory wastewater in a three-step process was carried out using a combined process integrating a moving-bed biofilm reactor (MBBR) and membrane separation processes. The integrated system yields a high-quality effluent by resulting 99.25%, 98%, and 99.2% removal for chemical oxygen demand (COD), nitrate, and total suspended solids, respectively. Determining the level of wastewater treatment requires laboratory equipment with sophisticated measuring devices which is time-consuming and costly. Hence, equations for predicting the removal rate of COD and nitrate are derived from the data obtained from the treatment of sugar wastewater with the integrated system. The equations provide a quick and easy initial estimation for researchers. In this regard, wastewater with COD of 2,000 mg/L and nitrate of 55 mg/L were synthesized. The treatment is performed for five filling ratios (FR) of 40%, 45%, 50%, 55%, and 60% of MBBR with the Kaldnes k2, and four hydraulic retention times (HRT) of 6, 8, 10, and 12 h. Artificial intelligence called multi expression programming (MEP) was used to develop models for predicting the COD and nitrate. The input variables are FR and HRT, and the output variable is the final removal level of organic matters. Excellent correlation between the MEP-based models and the experimental results was achieved which indicates that COD and nitrate models are capable of effectively estimating the amount of COD and nitrate removal. Parametric sensitivity analysis was used to determine the impact of input parameter changes on the output parameter.

Keywords: Wastewater; Sugar; Moving-bed biofilm reactor; Membrane separation; Multi expression programming

1. Introduction

Due to the discharge of various wastewater into the environment, today, many regulations have been legislated for environmental protection and health reasons. Thus, the municipal and industrial wastewaters have to be purified to reach the standard limit of toxic composition levels. In order to reach the standard limit, the combination of biological processes and small footprint separation technologies have received much attention in the last decade from wastewater treatment professionals [1].

The sugar industry is known as one of the most water-consuming industries producing a high organic load. The effluent production of this industry has a high cost of treatment and can cause serious environmental problems, which requires new methods and technologies to treat sugar wastewater [2,3]. So far, researchers have used a variety of methods for the treatment of sugar factory wastewater [3–7].

* Corresponding author.

For example, for the treatment of the sugar factory wastewater Ragen et al. [8] and West Stewart used up-flow anaerobic sludge blanket reactor, Farhadian et al. [6] and Borghei et al. [2] used up-flow anaerobic fixed bed and up-flow aerobic immobilized biomass reactor, respectively [9]. Chemical oxygen demand (COD) and turbidity reduction in sugar wastewater were investigated by Sahu and Chaudhari [3] utilizing catalytic thermal treatment (thermolysis) and Güven et al. using the electrochemical treatment.

In recent years, considerable innovations have been observed in the biological wastewater treatment sector. The biological process is one of the best and most applicable methods in the treatment of high concentration wastewater and the reduction of COD and organic materials [1,10–15]. Essentially, the new development goal is to obtain higher treatment performance to meet stringent effluent discharge limits and easier biosolids–liquid separation [16].

One of the growing technology which can handle high loads of particles is a moving-bed biofilm reactor (MBBR) [17]. It characterized by the growth of biomass on carriers that move freely in the water volume by aeration or a mechanical mixer and are kept within the reactor volume by a sieve arrangement at the reactor outlet [18]. After the removal of the soluble, biodegradable matter in the biological process, any biomass formed needs to be separated from the liquid stream to produce the required effluent quality [19]. High-quality effluent with no particles in suspension will be obtained by the combination of MBBR and membrane systems. Pinto et al. [20] and Vijayaraghavalu et al. [21] used MBBR with microfiltration/ultrafiltration and reverse osmosis (RO) (MF/UF/RO), as separation systems, for the treatment of industrial wastewater, but Pervissian et al. [22] only used MBBR and UF system. The purification of pesticide industry wastewater was carried out utilizing a membrane technology, MF and RO, in combination with MBBR by Cao et al. [1]. Wang et al. developed an innovative process integrating moving bed ceramic membrane bioreactor and RO to treat municipal wastewater [23]. The membrane technologies used in this research, such as slow sand filtration (SSF) and RO, are examples of compact separation systems which have a semipermeable membrane and allows the passage of liquid while the suspended solids are fully retained inside the bioreactor [24].

Laboratory experiments are challenging to carry out due to budget, time, or complexity. Therefore, numerous studies have presented methods to model, predict, or optimize the treatment processes to assist in better understanding of the bio-system and reducing costs and increasing the system performance [2,25–28]. In this paper, we present equations to assess the COD and nitrate for the integrated system so that they can be designed more economically and an estimation of the results of the waste treatment systems of sugar factory can be obtained. The data for the artificial intelligence (AI) method is obtained by performing several laboratory tests.

Genetic programming (GP) is a model of programming that uses the ideas of biological evolution to handle a complex problem [29,30]. Of several possible programs, the most effective programs survive and compete or cross-breed with other programs to continually approach closer to the needed solution. GP is an approach that seems most appropriate with problems in which there are a large number of fluctuating variables such as those related to AI. GP can be viewed as an extension of the genetic algorithm (GA), a model for testing and selecting the best choice among a set of results, each represented by a string. GP goes a step farther and makes the program or "function" the unit that is tested. So far, various studies have been conducted using various methods of AI and GP that have proven the superiority of GP methods. Recently, multi expression programming (MEP) as a variant of GP that uses a linear representation of chromosomes, has emerged. MEP differentiates from other GP techniques by encoding multiple solutions on the same chromosome [31]. The MEP approach is able to outperform similar methods of AI [32] significantly. There have been limited studies focused on applying MEP to civil engineering tasks [32–36].

The innovative aspects of this paper are (i) enhancing the biological treatment process of sugar industry wastewater using MBBR, (ii) using SSF system to remove biological particles grew in MBBR, (iii) removing nitrate, which was not significantly removed in the biological reactor, in denitrification process utilizing RO reactor, (iv) obtaining a new MEP-based model for determining the final concentration of COD and nitrate in the effluent. The proposed model used, filling ratio (FR) and hydraulic retention time (HRT) as the predicted variables.

2. Materials and methods

2.1. Specifications of the used sugar wastewater

The sugar wastewater used in this study is synthesized according to the range recommended by [25]. So that, to obtain 55 mg/L of nitrate (NO_3) and 2,000 mg/L of COD, 0.2 g of ammonium chloride (NH_4Cl) and 2 g of sugar were used per 20 L of water, respectively.

2.2. Input sludge to the reactor

In order to ensure the stability of the process and shortening the startup period, the selection of proper sludge in the installation stage is important. The biological sludge of the aerial pool of the wastewater treatment plant was used in the reactor. This sludge has characteristics of, pH = 7.92, temperature of 23 C, dissolved oxygen (DO) = 2.3 mg/L O_2, COD = 392 mg/L, total suspended solids (TSS) = 208 mg/L.

2.3. MBBR system operation

This system was presented for the first time by the Norwegian-university of science and technology and Kaldnes biotechnology. The MBBR process is used to remove organic matters. This process quickly decomposes organic soluble substances. However, insoluble organic substances that are suspended as fine particles are absorbed and consumed in biofilms, or discharge from the tank without being used [18]. Also, the advanced percentage of these particles hydrolyze. Hydrolysis in MBBR is a function of HRT. The number of hydrolysis increases by the increase in HRT.

In this study, a series of experiments in similar conditions are performed using Kaldnes k1 and k2 media. Comparing the formed biofilm on both Kaldnes at an equal time, it is concluded that more biofilm is formed on k2 than k1, illustrating k2 is a more appropriate medium for the experiment. The MBBR is filled with Kaldnes k2 media with volumes of 40%, 45%, 50%, 55%, and 60%. The Kaldnes are approximately 19 × 14 mm. They have been used to provide suitable conditions for the growth and reproduction of bacteria and better formation of the biological layer on them. In this research, in order to provide aeration condition and mixing Kaldnes with wastewater, an air compressor along with air stones were used in the tank floor. The remaining COD and nitrate concentration in the wastewater after exiting the MBBR pilot are illustrated in Fig. 1 for five FRs and four HRTs.

2.4. Slow sand filtration

Filters play a vital role in water treatment plants, and they are generally referred to as water filtration processes. Filtration is a physical method that includes the operation of removing suspended fine particles from water that is not separated from it in the previous stages of the treatment, through passing from different layers such as gravel, sand, anthracite, and diatomite [37]. In this study, the sand with a coefficient of uniformity (Cu) of 3.8 and coefficient of curvature (Cc) of 1.25 to a height of 40 cm in the upper layer, pea gravel to a height of 10 cm in the middle, and finally a layer of 10 cm of rubble on the bed, was used. As illustrated in Fig. 2, the amount of COD and nitrate concentration after passing through sand filters are decreased compared to the MBBR outputs.

2.5. Reverse osmosis

In this process, high-pressure water passes through a series of semi-permeable membranes. This external pressure is higher than the normal osmotic pressure, which results in smaller molecules passing through the membrane pores. In RO, microorganisms are also removed from the water. In general, this process is used for desalination of water, but in recent years it has been considered to remove specific pollutants such as nitrates. In this method, in addition to nitrate, total soluble solids (TDS) also decrease. Operation of the RO membrane and nano-filtration in high-pressure cause severe clogging of the orifices, hence the experiments were carried out at a constant pressure of 10 bar [38]. According to Fig. 3, the COD and nitrate concentration of wastewater are declined substantially after passing through the RO pilot under high pressure for all FRs and HRTs. The obtained values of concentration after this pilot are the output for the total integrated system.

2.6. Testing method

2.6.1. MBBR acclimation period

In the acclimation period, 10 L synthesized sugar wastewater is loaded to the MBBR pilot, which 50% of its volume is filled with Kaldnes k2 media. After one week, the wastewater is added to the reactor, on every other day period, so that the nutrient and organic load is provided for microorganisms' growth. In MBBR, the aerobic bacteria use oxygen to convert ammonium chloride of the wastewater to nitrite and nitrate using Nitrosomonas and Nitrobacter bacteria, respectively. Meantime, the controlling parameters, including temperature, pH, and DO, are continuously measured to maintain them in the standard controlling condition, that is, 23°C, 7–8, and 3–4 mg/L, respectively. This process continues until the initial formation of the biofilm layer on the Kaldnes and reaching the mixed liquor volatile suspended

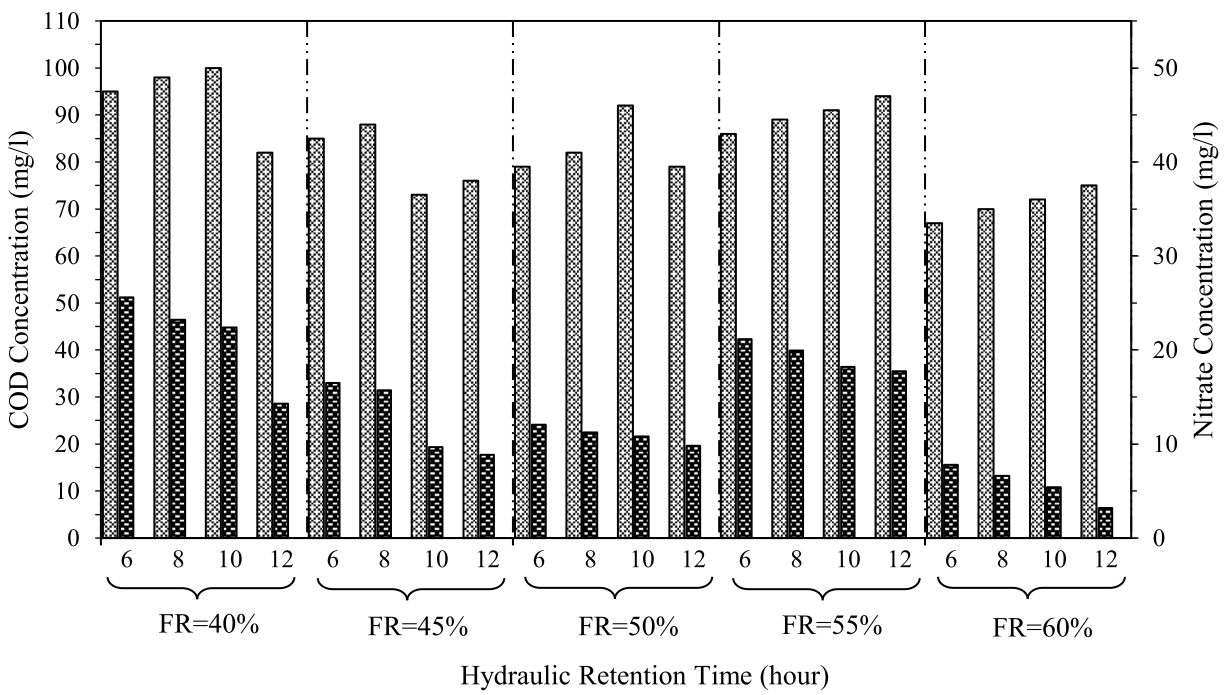

Fig. 1. Remaining COD and nitrate concentration in wastewater after the MBBR process.

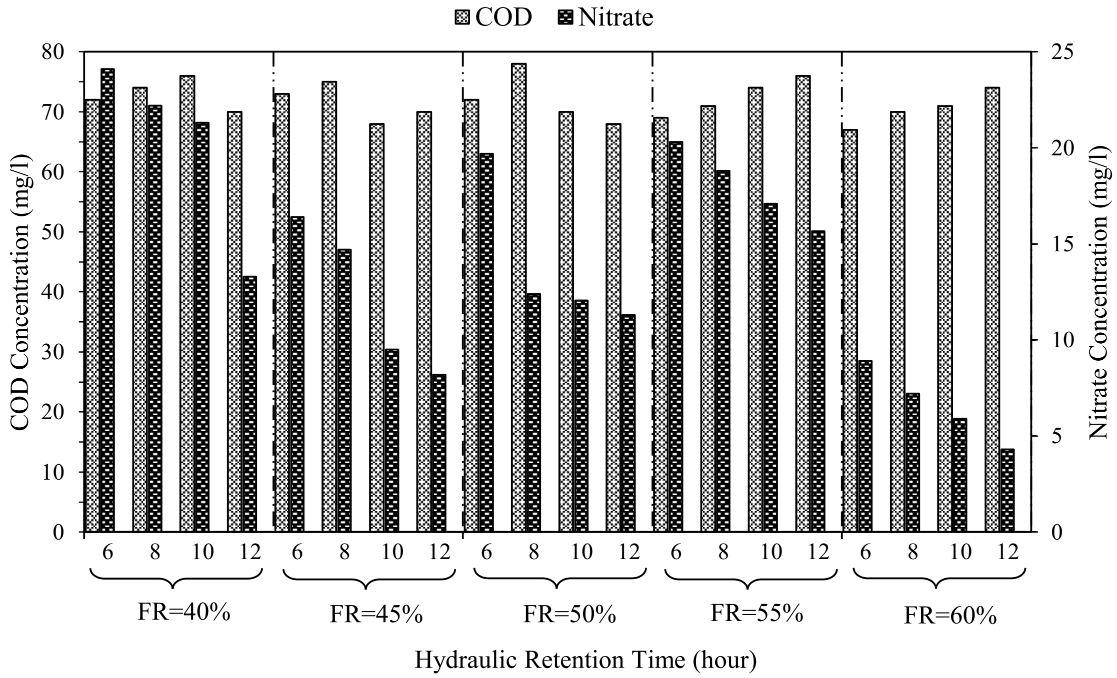

Fig. 2. Remaining COD and nitrate concentration in wastewater after the SSF pilot.

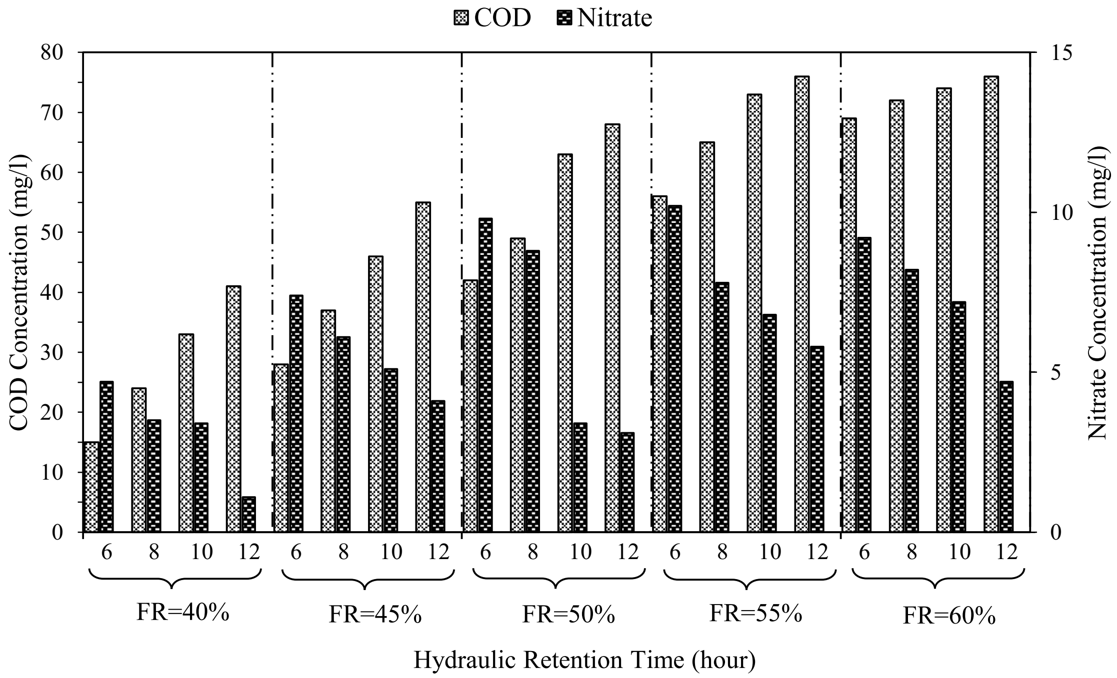

Fig. 3. Remaining COD and nitrate concentration in wastewater after RO pilot.

solids to steady-state, as illustrated in Fig. 4, which indicates the equilibrium of the system and the end of the adaptation period.

2.6.2. Integrated system operation

In the second stage of the experiment, five FRs of 40%, 45%, 50%, 55%, and 60% of Kaldnes, and four HRT of 6, 8, 10, and 12 h were used to examine the effects of them on the removal percentage. In the testing process, at first, the wastewater enters the MBBR with a specific percentage of filling with Kaldnes, and after the retention time, enters the sedimentation pond. After the sedimentation tank is filled, it enters the sand filter, and after passing through the RO membrane, the final outlet is taken. During the test, the parameters of COD, TSS, TDS, pH, NO_3, DO and turbidity

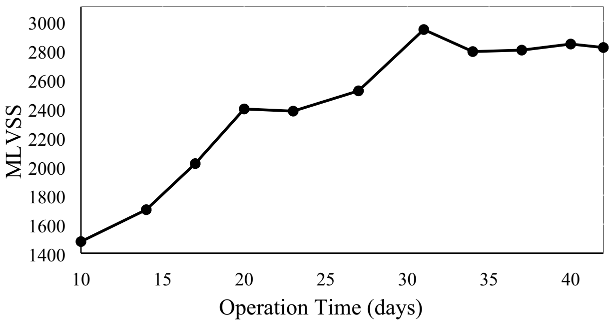

Fig. 4. Duration of reactor operation in the acclimation period.

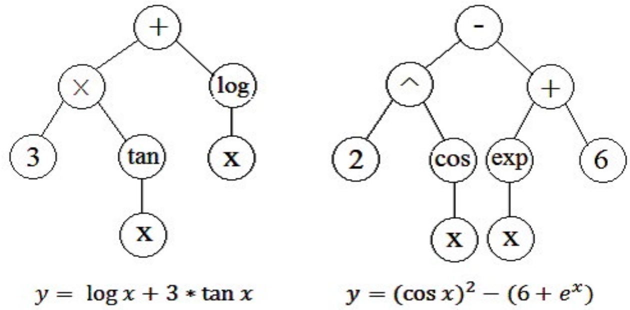

Fig. 5. A typical representation of the GP model.

are measured. Note that throughout this stage temperature, aeration, and pH levels should be constant.

3. Genetic programming

GP is a relatively new evolutionary method [39] that creates computer programs to solve a problem using the principle of Darwinian natural selection [40]. It was introduced by Koza, which is an applied method due to its precision [40]. GP is an extension of the GA [41]. In GA, decision variables are entered into the search process in the form of genes.

Nevertheless, in optimization problems, it is possible that in addition to numbers, mathematical or logical operators also participate as decision variables in the optimization process. Typically, when the mathematical relations are unknown, a set of numbers and operators enter the search process. Generally, GP is used to determine the structure of natural or artificial phenomena in order to explain the mathematical model of problems.

Unlike GA, GP operates on the tree structure of the equations rather than a series of binary numbers. Tree structures are created from a set of functions (mathematical operators used in equations), and terminals (problem variables and constant numbers) [40]. Fig. 5 shows a typical representation of two chromosomes in GP.

GP defines an objective function in the form of qualitative criteria and then solves it for measuring and comparing different methods. Next, corrects the data structure in a step-by-step process and finally, provides the right solving method. GP has successfully been applied to some of the civil engineering problems [42–46].

4. Multi expression programming

Many advances have been made in GP in recent years. A new variant of GP is MEP that was developed by Oltean and Dumitrescu [31]. MEP is a method for automatic generation of computer programs. Mainly it can be used for generating mathematical expressions for data analysis (regression and classification). MEP differentiates from other GP techniques by encoding multiple solutions on the same chromosome. In the simplest variant, MEP chromosomes are linear strings of instructions. The three-address code inspired this representation. MEP strength consists in the ability to encode multiple solutions, of a problem, in the same chromosome. In this way, one can explore larger zones of the search space. For most of the problems, this advantage comes with no running-time penalty compared with GP variants encoding a single solution in a chromosome.

An example of an MEP chromosome will show how MEP individuals are translated into computer programs. The first symbol in a chromosome must be a terminal symbol, as stated by the proposed representation scheme. It should be noted that numbers to the left stand for gene labels that do not belong to the chromosome. Using the set of arithmetic operators as $F = \{+, -, \times\}$ and the set of terminals as $T = \{x_1, x_2, x_3\}$, the example is given as follows:

0: x_1
1: x_2
2: – 0, 1
3: x_3
4: × 2, 3
5: – 3, 4

The translation of the MEP chromosomes into computer programs can be obtained by parsing the top-down chromosome starring with the first position. A terminal symbol specifies a simple expression. A function symbol specifies a complex expression obtained by connecting the operands specified by the argument positions with the current function symbol [47]. In the present example, genes 0, 1, and 3 in the previous example encode simple expressions formed by a single terminal symbol. These expressions are:

$E_0 = x_1,$
$E_1 = x_2,$
$E_3 = x_3,$

Gene 2 indicates the operation – on the operands located at positions 0 and 1 of the chromosome. Therefore, gene 2 encodes the expression:

$$E_2 = x_1 - x_2 \quad (1)$$

Gene 4 indicates the operation × on the operands located at positions 2 and 3. Therefore gene 4 encodes the expression:

$$E_4 = (x_1 - x_2) \times x_3 \quad (2)$$

Gene 5 indicates the operation – on the operands located at positions 3 and 4. Therefore gene 5 encodes the expression:

$$E_5 = x_3\,(x_1 - x_2) \times x_3 \tag{3}$$

Fig. 7 shows the forest of the tree of the MEP chromosome which is because of its multi expression representation. Each of these expressions (E_0~E_5) can be considered as a possible solution to the problem. The fitness of each expression encoded in an MEP chromosome is defined as the fitness of the best expression encoded by that chromosome. The fitness of an MEP chromosome (f) may be computed using the following equation symbol [47]:

$$f = \min_{i=1,m}\left\{\sum_{j=1}^{n}\left|F_j - O_j^i\right|\right\} \tag{4}$$

where n is the number of fitness cases, F_j is the expected value for the fitness case j, O_j^i is the value returned for the j^{th} fitness case by the i^{th} expression encoded in the current chromosome, and m is the number of chromosome genes.

5. Result and discussion

5.1. Experimental results

Fig. 6 shows the COD, nitrate, and TSS for the different FR and HRT.

The first and the most convenient feed for decomposition by bacteria is sugar content. Therefore, in the least retention time, a large proportion of the COD of the wastewater is reduced. Also, increasing the FR causes the Kaldnes to encounter more and prevent the formation of biofilms on their surface. In this paper, as can be seen, by Fig. 6, the removal efficiency is decreased with increasing the retention time and FR, that in the least retention time (6 h) and the lowest FR (40%) the most removal occurs, that is, 99.25% COD removal.

The anoxic condition which needs at least 0.5 mg/L of DO is needed to remove nitrate in the biological treatment. Since the bioreactor of this research is aerobic and its DO is about 3–4 mg/L, 60%–70% of the nitrate removal is due to biological treatment in the MBBR, and the rest of the removal process is with physical treatment (RO membrane). In biological treatment, the ammonium converts to nitrite and then to nitrate, by two nitrification and denitrification reactions, respectively. These reactions require more retention time than the COD removal process. As a result, most removal occurs in the most retention time (12 h), that is, 98% nitrate removal. The FR discussion for the COD removal stands for nitrate removal as well.

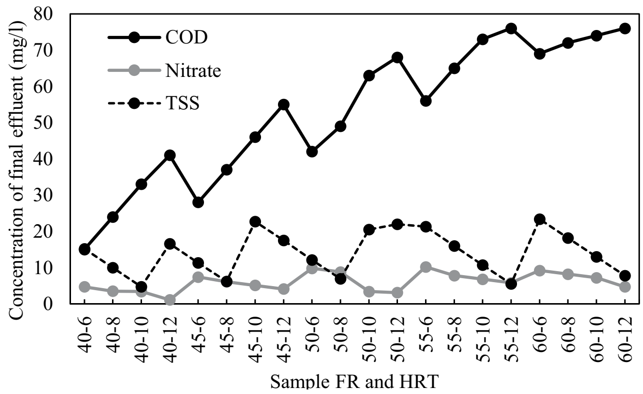

Fig. 6. COD, nitrate, and TSS values of the combined system.

5.2. Development of the MEP model

In this section, the modeling of COD and nitrate with the MEP approach will be explained. Out of the 20 sample data, 15 data (75%) were taken randomly for the training process and the remaining 5 data were used for evaluation of model performance [48,49]. The application of the MEP approach includes the following steps. In the first step, the training and test dataset are introduced into the program. This dataset consists of the set of terminal T which contains independent variables: T = {FR, and HRT}. Secondly, the selection of the appropriate set of function F. The function selection is not obvious and depends on the user experience, the user understanding of the problem domain and nature, or other researches in the field. Given the fact that in the field of this study so far no similar study has been done, the necessary functions can be selected as a good guess for modeling and a good knowledge of laboratory tests process. In this study, for building the MEP model, several kinds of function sets including addition, subtraction, division, multiplication, sine, cosine, logarithmic, and exponential functions, were examined. The best function set was found as addition, subtraction, division, and multiplication.

In the third step, as the model generalization capability of MEP will be affected by parameter selection [33], the MEP parameter setting (i.e., population size and chromosome length) and the MEP operators (i.e., mutation and crossover

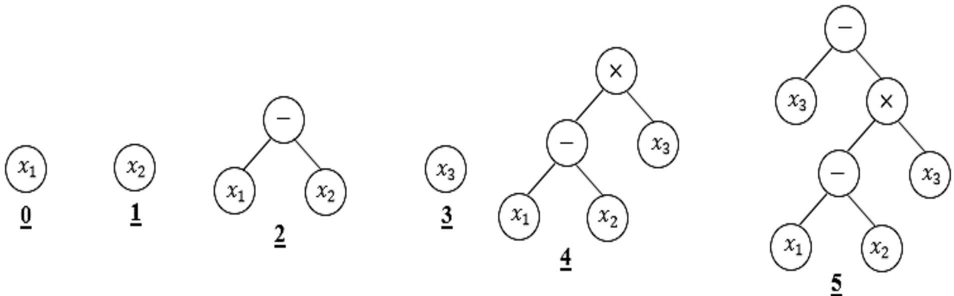

Fig. 7. Expressions encoded by an MEP chromosome.

probabilities) during evolution have been selected based on some previously suggested values and also after several runs of trial and error in multiple replications and monitoring the training and testing performance of each model.

Several runs are conducted to come up with an optimal parameterization of MEP. The MEP parameters are changed for different runs, a parameter changed in its logical range while the other parameter settings were set to a constant value suggested by Oltean and Grosan [47], and the values of the fitness function and error for each model are extracted [50]. A relatively large number of generations are tested on each run to find models with minimum error. In this method, the results were compared in each model to select the optimal value for each parameter setting. Finally, for the MBBR and nitrate model, the population size was set to 500 and 600, the chromosome length was set to 57 and 47, the crossover probability was set to 0.7 and 0.8, and the mutation probability was set to 0.01 and 0.02, respectively. Table 1 shows the various parameter settings involved in the MEP model and the resulted setting obtained in the replications trial and error.

After finding the specified values for the parameter settings, the final model was executed with the possibility of generating a large number of generations (i.e., 15,000 generations).

5.3. MEP-based prediction models for COD and nitrate

To evaluate the capabilities of the proposed MEP models, coefficient of determination (r^2) and root mean square error (RMSE) was used as follows:

$$R^2 = \left[\frac{\sum_{i=1}^{n} (x_i - \bar{x}_i)(y_i - \bar{y}_i)}{\sqrt{\sum_{i=1}^{n} (x_i - \bar{x})^2 \sum_{i=1}^{n} \left(y_i - \bar{y}_i^{\,2} \right)}} \right]^2 \tag{5}$$

$$\text{RMSE} = \sqrt{\frac{\sum_{i=1}^{n} \left(x_i - y_i \right)^2}{n}} \tag{6}$$

where n is the number of data, x_i, y_i are measured and predicted output values, and $\bar{x}$ is the average of the measured outputs. The coefficient of determination, in statistics, R^2 (or r^2), is a measure that assesses the ability of a model to predict or explain an outcome in the linear regression setting. R^2 ranges from 0 to 1. The RMSE is a frequently used measure of the difference between values predicted by a model, and the values observed from the environment that is being modeled. RMSE can range from 0 to ∞ and is indifferent to the direction of errors.

The prediction equations for COD and nitrate, for the best results by the MEP algorithm, are as given below:

$$\text{COD}_{\text{final}} = \text{COD}_{\text{initial}} - 2 \times \left(\begin{array}{l} \text{HRT} + X + \text{FR} - Z + \dfrac{\text{FR}}{\text{HRT}} + \dfrac{0.0008\text{HRT}^2\text{FR}}{3} \\ - \dfrac{2}{0.020624 \times \text{HRT}} \end{array} \right) - Z + 0.000425\text{HRT}^2\text{X}^2 \tag{7}$$

where Z and T are:

$$Z = 0.020624 \times \text{FR}^2 \times \left(1 + 0.020624 \times \frac{\text{FR}}{\text{HRT}} \right) \tag{8}$$

$$X = Z - \text{FR} - 2\frac{\text{FR}}{\text{HRT}} + 0.020624\frac{\text{FR}^2}{\text{HRT}} \tag{9}$$

$$\text{Nitrate}_{\text{final}} = \text{Nitrate}_{\text{initial}} - \frac{\dfrac{0.976232A}{-AX_1 + X_0 - 0.0884} + AX_0 - 0.0884A}{0.887832 \times \left(-AX_1 + 2X_0 - 1.064632 \right)} \tag{10}$$

where A is:

$$A = \frac{X_0 - 0.976232}{0.976232X_1} \tag{11}$$

In these equations, filling rate FR is in percentage, and hydraulic resistance time HRT is in an hour.

The best evolved MEP-based model for COD produced the least errors (R^2 = 0.994, and RMSE = 1.42) for the training data (Fig. 8) and for the test data (R^2 = 0.997, and RMSE = 0.965) (Fig. 9). Also, the nitrate model yields (R^2 = 0.8609, and RMSE = 0.957) for the training data (Fig. 10) and for the test data (R^2 = 0.896, and RMSE = 1.0864) (Fig. 11).

Table 1
Parameter settings for the MBBR and nitrate models

Parameter	Range of changing setting	MBBR setting	Nitrate setting
Population size	10–1,000	500	500
Chromosome length	10–100	31	35
Crossover type	Uniform		
Crossover probability (%)	0–100	70	70
Mutation probability (%)	0–100	1	1
Function set	+, –, ×, /		

5.4. Parametric sensitivity analysis

In this study, a parametric sensitivity analysis was performed for verifications of the MEP-based prediction equations. This technique determines how independent variable values will impact the predicted COD and Nitrate from MEP models under a given set of input data and assumptions. The simplest way to approach parametric sensitivity analysis is to vary each factor one at a time. In this approach, while one factor is being varied from –100% to 100% of its average value, the others are kept constant at the average values of their entire datasets. After obtaining a set of synthetic data for a single varied parameter, the percentage

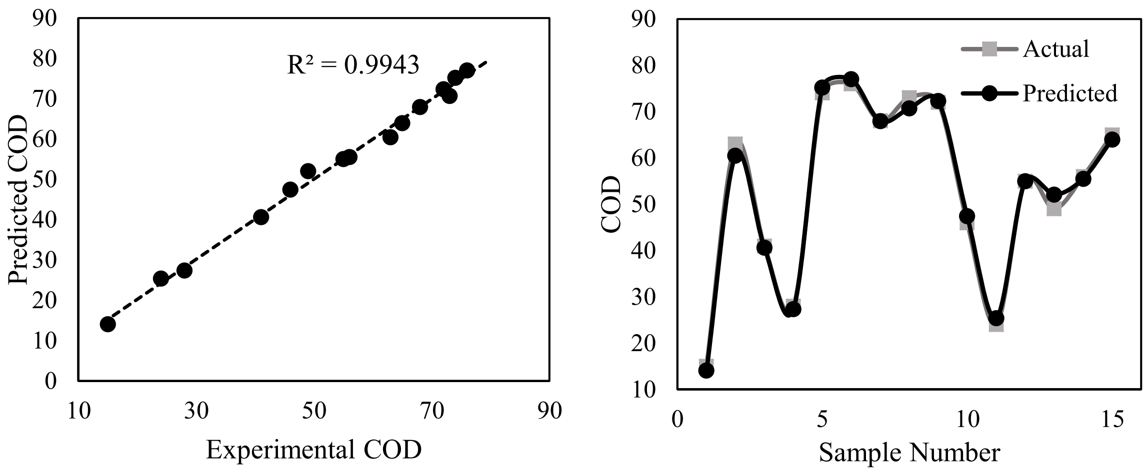

Fig. 8. Comparison of the predicted COD values with the experimental measured for training data.

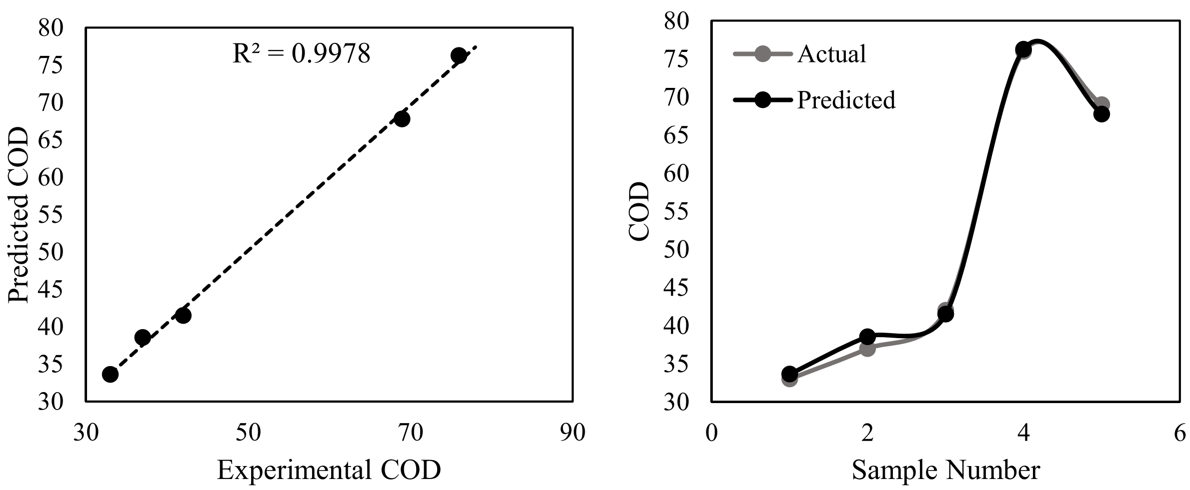

Fig. 9. Comparison of the predicted COD values with the experimental measured for testing data.

of the change in the output of the model was obtained by introducing this variable to the prediction equations of the COD and nitrate models. This procedure is repeated using another variable until the model response is tested for the entire predictor variables. Results for parametric sensitivity analysis of COD and nitrate models are presented in Fig. 12. According to Fig. 12b, COD decreases due to the increasing FR and HRT. As can be seen in Fig. 12a, Nitrate increases due to the increasing HRT. Also, it decreases with increasing FR.

The results of the parametric analysis for FR and HRT have generally expected cases as was described in section 2.7.

6. Conclusions

In this paper, sugar industry wastewater was successfully treated by a combined process integrating an MBBR and membrane separation processes (namely SSF and RO). The separation systems were utilized to separate the formed biomass from obtaining a suitable effluent. The MEP-based models for predicting COD and nitrate were derived by the data obtained from treating sugar wastewater. Parameter settings of the models were obtained by several runs of trial and error and considering a large number of generations as the stopping criteria. The following conclusions can be drawn from the findings of this study:

- Sequential MBBR/SSF/RO treatment process proposed in this study is significantly compact and allows the production of the high-quality effluent with the reduction of 99.25%, 98%, and 99.2% in COD and nitrate, and TSS concentration, respectively.
- Performance measures (RMSE, R^2) of prediction models indicate good results in the training and testing dataset.
- Parametric sensitivity analysis was used for verification of the COD and nitrate models. The result showed that, for the COD model in the least HRT (i.e., 6 h) and the lowest FR (i.e., 40%) and for the nitrate model the in the most HRT (i.e., 12 h) and the lowest FR (i.e., 40%) the most removal occurred.

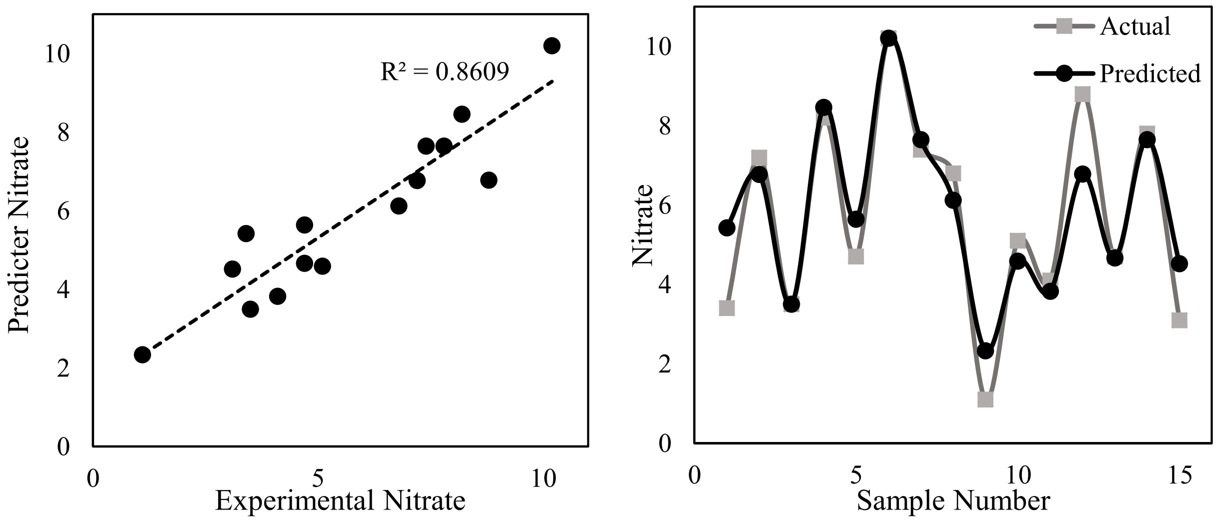

Fig. 10. Comparison of the predicted nitrate values with the experimental measured for training data.

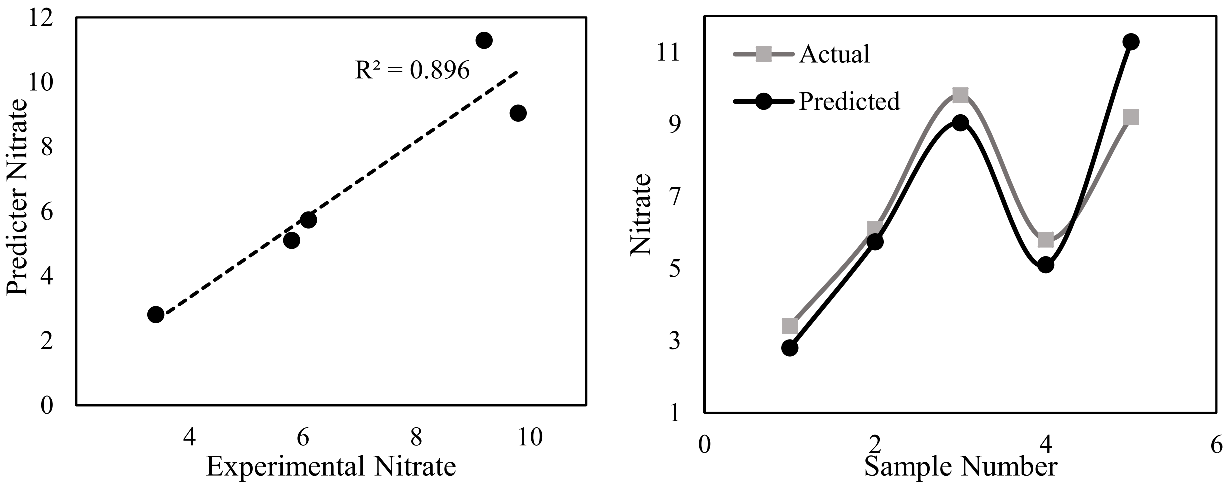

Fig. 11. Comparison of the predicted nitrate values with the experimental measured for testing data.

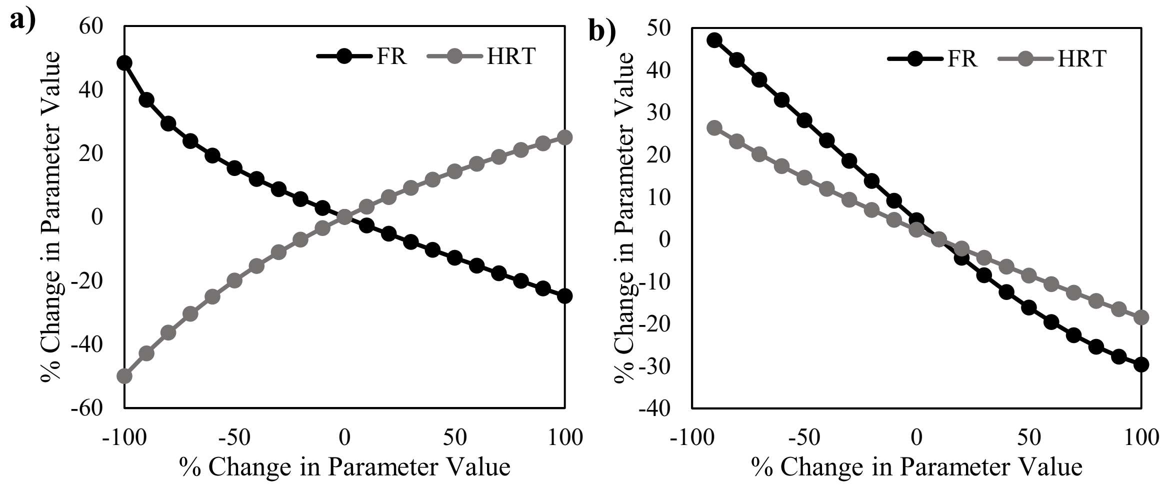

Fig. 12. Sensitivity analysis results for the two parameters used in the (a) nitrate model and (b) COD model.

- Using the derived MEP models, the removal level of the COD and nitrate can readily be estimated, which eliminates the needs of complicated and time-consuming laboratory tests.

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