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Quantitative Structure–Electrochemistry Relationship for Substituted Benzenoids Using Levenberg–Marquardt Artificial Neural Network[1]

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Abstract—Quantitative structure–property relationship models correlating the half-wave potentials ($E_{1/2}$) of the benzenoids and its derivatives were developed using both linear and non-linear modelling approaches. Descriptors calculated from molecular structures alone were used to represent the $E_{1/2}$ of the benzenoids. A set of 36 compounds were selected and suitable sets of molecular descriptors were calculated. A genetic algorithm-partial least square (GA-PLS) method was used to select the most appropriate molecular descriptors whilst a linear, quantitative structure–property relationship model was developed; using the selected descriptors, a Levenberg–Marquardt artificial neural network (L–M ANN) was employed for the non-linear model development. The stability and prediction ability of models were validated using leave-group-out cross-validation, external test set and Y-randomization techniques. The described model does not parameters require experimental and potentially provides useful prediction for $E_{1/2}$ of new benzenoids derivatives.

Keywords: benzenoids, half–wave potential, QSPR, genetic algorithm, Levenberg–Marquardt artificial neural network

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1. INTRODUCTION

Half-wave potential ($E_{1/2}$) is an important electrochemical property of organic compounds. This property which is a characteristic constant for a reversible oxidation–reduction system can be useful for predicting electrochemical properties of other organic compounds. There are some different electrochemical methods which permit determination of the half-wave potentials of a wide variety of organic and organomethalic compounds [1]. Quantitative structure–activity/property relationships (QSAR/QSPR) studies, as one of the most important areas in chemometrics, give information that is useful for molecular design and medicinal chemistry [2, 3]. QSAR/QSPR models are mathematical equations relating chemical structure to a wide variety of physical, chemical, biological and technological properties. The main task of QSPR is to obtain a reliable statistical model for the prediction of properties/behavior of new chemical substances and analytical systems. These relationships also take an approach to the identification and isolation of most important structural descriptors that affect physicochemical properties. Model development in QSAR/QSPR studies comprises different critical steps as (1) descriptor generation, (2) data splitting to calibration and prediction (or training) and validation (or test) sets, (3) variable selection, (4) finding appropriate model between selected variables and activity/property and (5) model validation.

In recent years, numerous quantitative QSAR/QSPR models have been introduced for calculating the physicochemical properties of molecules from chemical structure; the applications of QSAR/QSPR in electrochemistry are described [4]. A successful strategy for prediction of the reduction potential is the construction of the QSPR models, by which, structural features affecting $E_{1/2}$ will be understood too [4–7].

The electrochemical half-wave potential in some cases it could be directly correlated with biological properties of compound. Therefore, the aim of the present study is estimation of ability optimal descriptors calculated with linear multivariate regressions (e.g. the partial least squares (PLS)) as well as the non-linear regressions (Levenberg–Marquardt artificial neural network (L–M ANN)) in QSPR analysis of half-wave potentials of some benzenoids. The stability and predictive power of these models were validated using Leave-Group-Out Cross-Validation (LGO CV), external test set, and Y-randomization techniques.

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Table 1. The experimental, calculate, RE and RMSE values $E_{1/2}$ of benzenoids derivatives for training set by L–M ANN model

Benzenoids	Exp. (V)	Cal. (V)	RE	RMSE
Calibration Set				
1	−1.98	−1.97	0.50	0.002
2	−1.46	−1.35	7.69	0.025
3	−1.94	−1.86	3.93	0.017
4	−1.14	−1.08	5.14	0.013
5	−1.53	−1.51	1.09	0.004
6	−1.81	−1.77	2.38	0.009
7	−1.75	−1.65	5.43	0.021
8	−1.97	−1.78	9.82	0.042
9	−1.61	−1.58	1.79	0.006
10	−0.86	−0.81	5.56	0.010
11	−1.19	−1.14	3.85	0.010
12	−1.44	−1.41	2.08	0.007
13	−1.54	−1.53	0.78	0.003
14	−1.57	−1.53	2.62	0.009
15	−1.79	−1.64	8.23	0.032
16	−1.65	−1.55	5.95	0.021
17	−1.55	−1.54	0.65	0.002
18	−1.25	−1.24	0.83	0.002
19	−1.67	−1.57	5.90	0.022
20	−1.4	−1.39	1.06	0.003
21	−1.73	−1.57	9.42	0.036
Prediction Set				
22	−1.53	−1.48	3.19	0.018
23	−1.36	−1.28	6.21	0.032
24	−0.95	−0.96	1.05	0.004
25	−1.33	−1.26	4.97	0.025
26	−1.21	−1.17	2.91	0.013
27	−1.57	−1.60	1.91	0.011
28	−1.59	−1.48	6.96	0.042

2. COMPUTATIONAL

2.1. Data Set

All data of the present investigation was available from the literature reported by Bergman [8]. This dataset consists of 36 benzenoids derivatives. The chemical structures of studied compounds are similar. Through data collection, attention was made to choose electrochemical data obtained at similar experimental conditions. The molecular structures of studied compounds for the training and test sets are shown in Figs. 1, 2. A list of the studied compounds and their experimental $E_{1/2}$ values are shown in Tables 1, 2.

Table 2. The experimental, calculate, RE and RMSE values $E_{1/2}$ of benzenoids derivatives for test set by L–M ANN model

Benzenoids	Exp. (V)	Cal. (V)	RE	RMSE
29	−1.22	−1.26	3.20	0.014
30	−1.5	−1.45	3.16	0.017
31	−0.97	−0.93	4.21	0.014
32	−0.88	−0.93	5.68	0.018
33	−1.00	−1.01	0.68	0.002
34	−1.49	−1.64	10.07	0.053
35	−1.45	−1.39	3.81	0.020
36	−1.36	−1.45	6.77	0.033

2.2. Genetic Algorithm for Descriptor Selection

To select the most relevant descriptors with GA, the evolution of the population was simulated. Each individual of the population, defined by a chromosome of binary values, represented a subset of descriptors. The number of the genes at each chromosome was equal to the number of the descriptors. The population of the first generation was selected randomly. A gene was given the value of one, if its corresponding descriptor was included in the subset; otherwise, it was given the value of zero. The number of the genes with the value of one was kept relatively low to have a small subset of descriptors [9–11] that is the probability of generating zero for a gene was set greater. The operators used here were crossover and mutation. The application probability of these operators was varied linearly with a generation renewal. For a typical run, the evolution of the generation was stopped, when 90% of the generations had taken the same fitness. In this paper, size of the population is 30 chromosomes, the probability of initial variable selection is 5 : V (V is the number of independent variables), crossover is multi Point, the probability of crossover is 0.5, mutation is multi Point, the probability of mutation is 0.01 and the number of evolution generations is 1000. For each set of data, 3000 runs were performed.

2.3. Data Pre-processing

Each set of the calculated descriptors was collected in a separate data matrix D_i with a dimension of $(m \times n)$, where m and n are being the number of molecules and the number of descriptors, respectively. Grouping of descriptors was based on the classification achieved by Dragon software. In each group, the calculated descriptors were searched for constant or near constant values for all molecules and those detected were removed. Before applying the analysis methods, and due to the quality of data, a previous treatment of the data is required. Scaling and centering is one of the

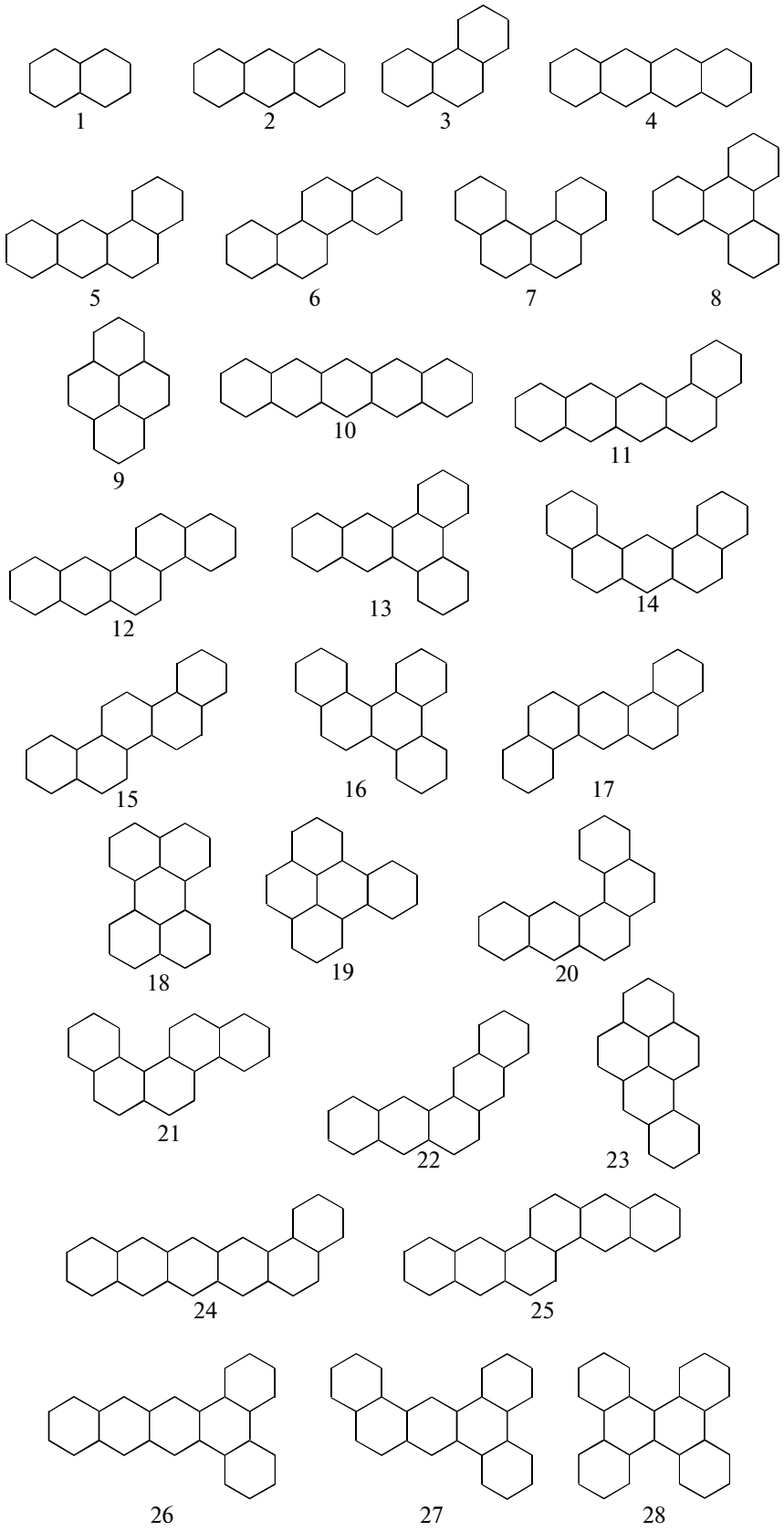

Fig. 1. The structure of the benzenoid hydrocarbons in the training set.

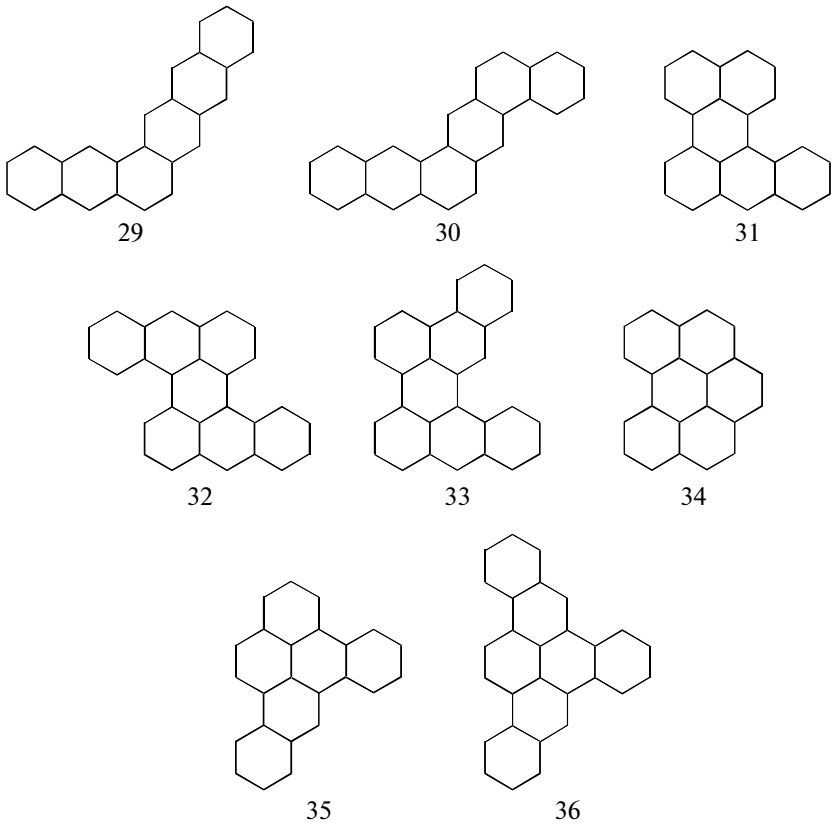

Fig. 2. The structure of the benzenoid hydrocarbons in the test set.

pre-processing methods we need before performing the regression methods combined with FE. The results of projection methods depend on the normalization of the data. Descriptors with small absolute values have a small contribution to overall variances; this biases towards other descriptors with higher values. With appropriate scaling, equal weights are assigned to each descriptor, so that the important variables in the model can be focused. In order to give all variables the same importance, they are standardized to unit variance and zero mean (autoscaling).

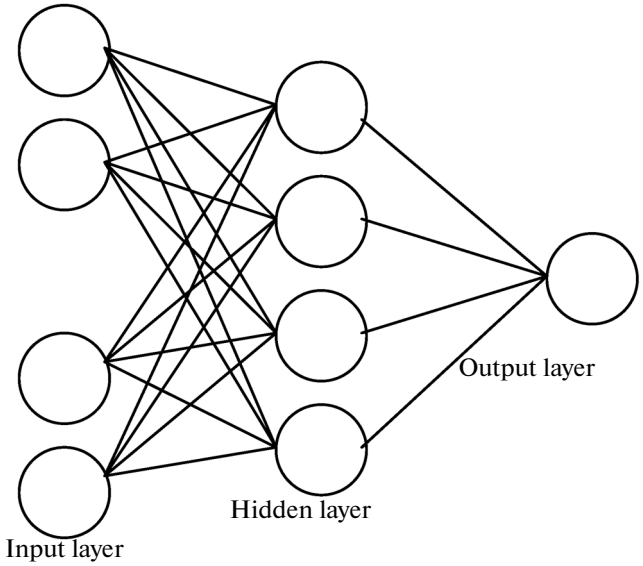

Fig. 3. Used three layer ANN.

2.4. Y-randomization or Chance Correlations

Part of validating the models is to check for the possibility of chance correlations. This can be done by performing the entire sequence of computations over but with the dependent variables scrambled. This scrambling destroys any relationship between the descriptors and the dependent variable. No model that exceeds chance performance should be found. The results obtained are compared to the results achieved with the actual computations to demonstrate that the actual results were achieved by finding relationships rather than by finding chance correlations.

2.5. Nonlinear Model

2.5.1. Artificial neural network. A three-layer back propagation artificial neural network ANN (Fig. 3) with a sigmoid transfer function was used in the investigation of feature sets. The descriptors from the cali-

bration set were used for the model generation whereas the descriptors from the prediction set were used to stop the overtraining of network. And the descriptors from the test set were used to verify the predictivity of the model. Before training the networks, the input and output values were normalized with auto-scaling of all data [12, 13]. The initial weights were selected randomly between –0.3 and 0.3. For the purpose of comparison of results, the same number of hidden layer nodes was used for the ANN models from all other feature sets of each database. The goal of training the network is to minimize the output errors by changing the weights between the layers.

$$\Delta W_{ij,n} = F_n + \alpha \Delta W_{ij,n-1}, \quad (1)$$

in this, ΔW_{ij} is the change in the weight factor for each network node, α is the momentum factor, and F is a weight update function, which indicates how weights are changed during the learning process. The weights of hidden layer were optimized using the Levenberg–Marquardt algorithm, a second derivative optimization method [14].

2.5.2. Levenberg–Marquardt algorithm. In Levenberg–Marquardt algorithm, the update function, F_n, is calculated using equations.

$$F_0 = -g_0, \quad (2)$$

$$g = J^T e, \quad (3)$$

$$F_n = -[J^T \times J + \mu I]^{-1} \times J^T \times e, \quad (4)$$

where g is gradient and J is the Jacobian matrix that contains first derivatives of the network errors with respect to the weights, and e is a vector of network errors. The parameter μ is multiplied by some factor (λ) whenever a step would result in an increased e and when a step reduces e, μ is divided by λ [15, 16].

3. RESULTS AND DISCUSSION

3.1. Linear Model

3.1.1. Results of the GA-PLS model. PLS is a linear modeling technique where information in the descriptor matrix X is projected onto a small number of underlying ("latent") variables called PLS components, referred to as latent variables. The Matrix Y is simultaneously used in estimating the "latent" variables in X that will be most relevant for predicting the Y variables. The number of significant factors for the PLS algorithm was determined using the cross-validation method. The prediction error sum of squares (PRESS) obtained in the cross-validation was calculated each time that a new principal component (PC) was added to the model. The optimum number of PLS factors is the one that minimizes PRESS [17, 18]. Figure 4a shows the plot of PRESS versus the number of factors (components) for the PLS model. As can be seen from this figure, the best PLS model contained 3 components. The best GA-PLS model contains

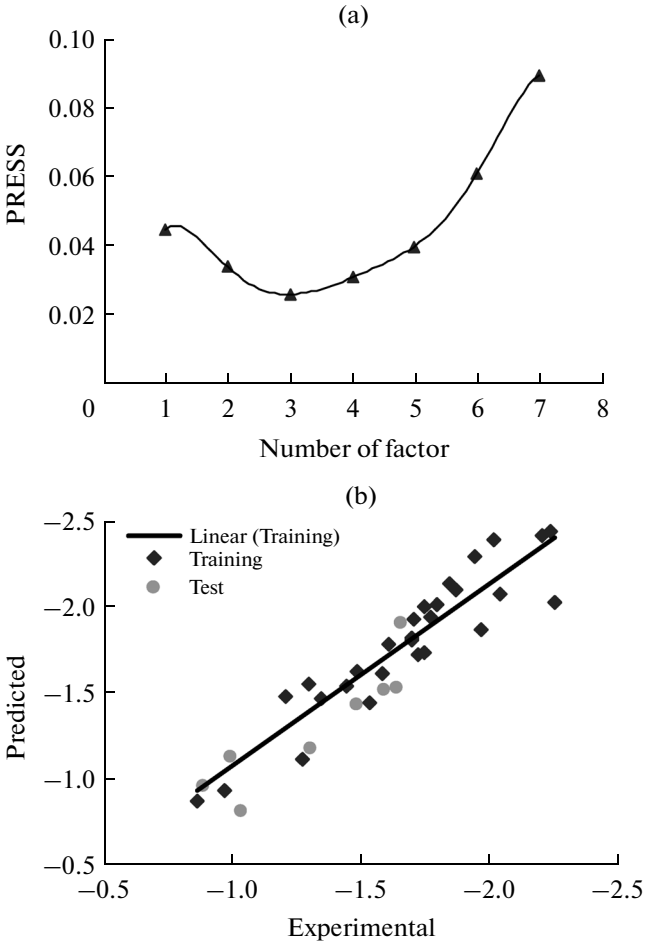

Fig. 4. (a) PRESS versus the number of factors (b) Plots of predicted against the experimental $E_{1/2}$ values by GA-PLS model.

9 selected descriptors. For this in general, the number of components (latent variables) is less than number of independent variables in PLS analysis. The predicted values of $E_{1/2}$ are plotted against the experimental values for training and test sets in Fig. 4b. The statistical parameters square correlation coefficient (R^2), root-mean-square error (RMSE) and relative error (RE) were obtained for proposed models. Each of the statistical parameters mentioned above were used for assessing the statistical significance of the QSPR model. The R^2, mean relative error and RMSE for training and test sets were (0.866, 10.95, 0.031) and (0.802, 16.01, 0.056), respectively. The PLS model uses higher number of descriptors that allow the model to extract better structural information from descriptors to result in a lower prediction error.

3.2. Nonlinear Model

3.2.1. Results of the L–M ANN model. With the aim of improving the predictive performance of nonlinear QSPR model, L–M ANN modeling was per-

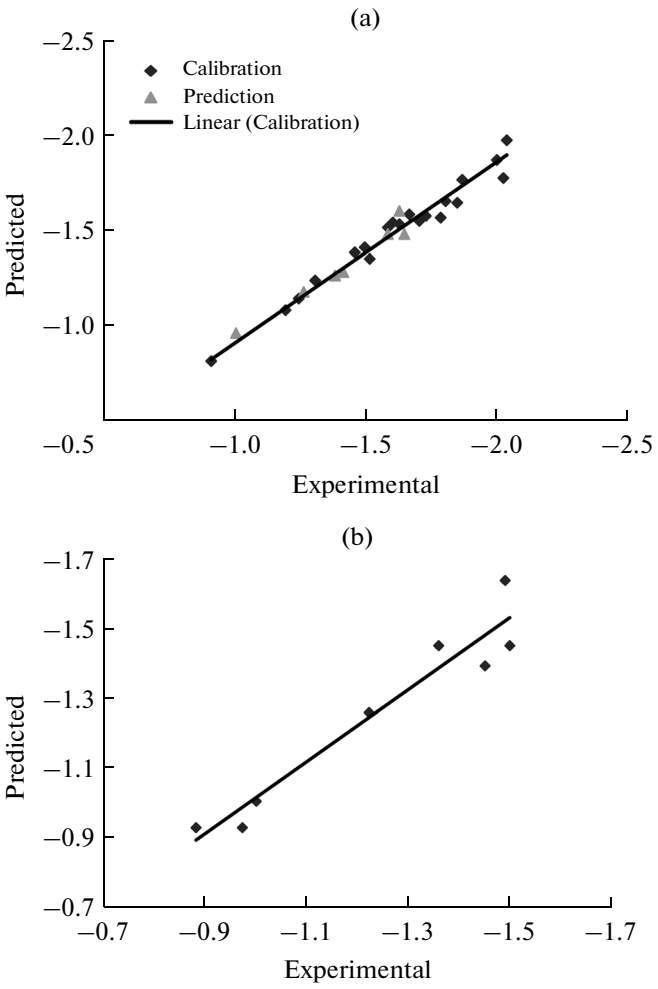

Fig. 5. Plot of predicted $E_{1/2}$ obtained by L–M ANN against the experimental values (a) for training set and (b) test set.

formed. The networks were generated using the nine descriptors appearing in the GA-PLS models as their inputs and $E_{1/2}$ as their output. For ANN generation, data set was separated into three groups: calibration and prediction (training) and test sets. All molecules were randomly placed in these sets. A three-layer network with a sigmoid transfer function was designed for each ANN. Before training the networks the input and output values were normalized between –1 and 1. The network was then trained using the training set by the back propagation strategy for optimization of the weights and bias values [19]. The proper number of nodes in the hidden layer was determined by training the network with different number of nodes in the hidden layer. The root-mean-square error (RMSE) value measures how good the outputs are in comparison with the target values. It should be noted that for evaluating the overfitting, the training of the network for the prediction of $E_{1/2}$ must stop when the RMSE of the prediction set begins to increase while RMSE of calibration set continues to decrease. Therefore, training of the network was stopped when overtraining began. All of the above mentioned steps were carried out using basic back propagation, conjugate gradient and Levenberge–Marquardt weight update functions. It was realized that the RMSE for the training and test sets are minimum when three neurons were selected in the hidden layer. Finally, the number of iterations was optimized with the optimum values for the variables. It was realized that after 18 iterations, the RMSE for prediction set were minimum. The values of experimental, calculated, percent relative error and RMSE for training and test sets are shown in Tables 1 and 2. The RMSE, mean relative error and R^2 for calibration, prediction and test sets were (0.014, 4.03, 0.964), (0.021, 3.88, 0.952) and (0.025, 4.69, 0.928), respectively. Comparison between these values and other statistical parameter reveals the superiority of the L–M ANN model over other model. The key strength of neural networks, unlike regression analysis, is their ability to flexible mapping of the selected features by manipulating their functional dependence implicitly. The statistical parameters reveal the high predictive ability of L–M ANN model. The whole of these data clearly displays a significant improvement of the QSPR model consequent to nonlinear statistical treatment. Plot of predicted $E_{1/2}$ versus experimental $E_{1/2}$ values by L–M ANN for training and test sets are shown in Figs. 5a and 5b. Obviously, there is a close agreement between the experimental and predicted $E_{1/2}$ and the data represent a very low scattering around a straight line with respective slope and intercept close to one and zero. As can be seen in this section, the L–M ANN is more reproducible than GA-PLS for modeling the half-wave potentials of benzenoids molecules. Finally, in order to ensure the robustness of the L–M ANN model, the Y-randomization test was performed in this contribution. The dependent variable vector ($E_{1/2}$) was randomly shuffled and a new QSPR model was developed using the original independent variable matrix. The new QSPR model is expected to have low R^2 and Q^2 values. Several random shuffles of the y vector were performed and the results are shown in Table 3. If the R^2 and Q^2 values of these models were much lower than those of the original model, it could be considered that the model was reasonable and had not been obtained by the chance.

3.3. Discussions of the Input Parameters

By interpreting the descriptors in the model, it is possible to gain some insight into factors affecting the half-wave potential value and find out which structural factor plays an important role during the reduction reaction. The electron transfer process constitutes the basic feature of chemical, biochemical and, especially, electrochemical reactions. Thus, the ability of calculating redox potentials accurately using the theoretical methods would be advantageous in a number of different areas, particularly where the experimental mea-

surements are difficult, due to complex chemical equilibria and reactions of the chemical species involved.

Constitutional descriptors are most simple and commonly used descriptors, reflecting the molecular composition of a compound without any information about its molecular geometry.

The GETAWAY (GEometry, Topology, and Atom-Weights AssemblY) descriptors try to match 3Dmolecular geometry provided by the molecular influence matrix and atom relatedness by molecular topology, with chemical information by using different atomic weights (atomic mass, polarizability, van der Waals volume, and electronegativity).

The WHIM descriptors are built in such a way as to capture the relevant molecular 3-D information regarding the molecular size, shape, symmetry, and atom distribution with respect to some invariant reference frame. Both WHIM and GETAWAY descriptors are quickly computed from the atomic positions of the molecule atoms (hydrogens included). WHIM descriptors are based on principal component analysis of the weighted covariance matrix obtained from the atomic Cartesian coordinates. In relation to the kind of weights selected for the atoms different sets of WHIM descriptors can be obtained. Unitary weights (u), atomic mass (m), atomic van der Waals volume (v), atomic electronegativity (e), atomic polarizability (p) and atomic electrotopological state (s) are the available weighting schemes globally providing 66 directional and 33 global WHIM descriptors.

3D-MoRSE (3D-MOlecule Representation of Structures based on Electron diffraction) descriptors are based on the idea of obtaining information from the 3D atomic coordinates by the transform used in electron diffraction studies. These descriptors are calculated by summing atom weights viewed by a divergent angular scattering function.

Although these descriptors are often successful in $E_{1/2}$ of benzenoids compounds, they cannot account for conformational changes and they do not provide information about electronic influence through bonds or across space. For that reason, quantum chemical descriptors are used in developing QSPR.

Quantum chemical descriptors can give great insight into structure and reactivity and can be used to establish and compare the conformational stability, chemical reactivity and inter-molecular interactions. They include thermodynamic properties (system energies) and electronic property (HOMO energy). Quantum chemical descriptors were defined in terms of atomic charges and used to describe electronic aspects both of the whole molecule and of particular regions, such atoms, bonds, and molecular fragments. Electronic properties may play a role in the magnitude in a biological activity, along with structural features encoded in indexes. Roughly, the HOMO level is to *organic semiconductors* what the *valence band* is to inorganic *semiconductors* and *quantum dots*. The eigenvalues of HOMO as an electron donor represents the ability to donate an electron. The HOMO energy plays a very important role in the nucleophylic behavior and it represents molecular reactivity as a nucleophyle. Good nucleophyles are those where the electron residue is high lying orbital.

Table 3. R^2 and Q^2 values for L–M ANN model after several Y-randomization tests

Model	R^2	Q^2
1	0.357	0.215
2	0.081	0.161
3	0.267	0.024
4	0.234	0.009
5	0.175	0.070
6	0.011	0.005
7	0.079	0.064
8	0.022	0.075
9	0.168	0.219
10	0.137	0.024

Charge descriptor are electronic descriptor defined in terms of atomic charges and used to describe electronic aspects both of the whole molecule and of particular regions, such a atoms, bonds, and molecular fragments. Charge descriptor calculated by computational chemistry and therefore can be consider among quantum chemical descriptor. Electrical charges in the molecule are the driving force of electrostatic interactions, and it is well known that local electron densities or charge play a fundamental role in many chemical reactions, physic-chemical properties and receptors-ligand binding affinity.

3.4. Model Validation and Statistical Parameters

The applied internal (leave-group-out cross validation (LGO-CV)) and external (test set) validation methods were used for the predictive power of models. In addition, chance correlation procedure is a useful method for investigating the accuracy of the resulted model, by which one can make sure if the results were obtained by chance or not.

Cross validation is a popular technique used to explore the reliability of statistical models. Based on this technique, a number of modified data sets are created by deleting in each case one or a small group (leave-some-out) of objects. For each data set, an input–output model is developed, based on the utilized modeling technique. Each model is evaluated, by measuring its accuracy in predicting the responses of the remaining data (the ones or group data that have not been utilized in the development of the model). In particular, the LGO-CV procedure was utilized in this study. A QSPR model was then constructed on the

basis of this reduced data set and subsequently used to predict the removed data. This procedure was repeated until a complete set of predicted was obtained. The statistical significance of the screened model was judged by the correlation coefficient (Q^2). The predictive ability was evaluated by the cross validation coefficient (Q^2 or R^2_{cv}). The accuracy of cross validation results is extensively accepted in the literature considering the Q^2 value. In this sense, a high value of the statistical characteristic ($Q^2 > 0.5$) is considered as proof of the high predictive ability of the model.

The data set should be divided into three new subdata sets, one for calibration and prediction (training), and the other one for testing. The calibration set was used for model generation. The prediction set was applied deal with overfitting of the network, whereas test set which its molecules have no role in model building was used for the evaluation of the predictive ability of the models for external set.

In the other hand by means of training set, the best model is found and then, the prediction power of it is checked by test set, as an external data set. In this work, in each running program, from all 36 compounds, 21 components are in calibration set, 7 components are in prediction set and 8 components are in test set).

The result clearly displays a significant improvement of the QSPR model consequent to non-linear statistical treatment and a substantial independence of model prediction from the structure of the test molecule. In the above analysis, the descriptive power of a given model has been measured by its ability to predict half-wave potentials of unknown benzenoids molecules.

For the constructed models, some general statistical parameters were selected to evaluate the predictive ability of the models for $E_{1/2}$ values. In this case, the predicted $E_{1/2}$of each sample in prediction step was compared with the experimental acidity constant. The PRESS (predicted residual sum of squares) statistic appears to be the most important parameter accounting for a good estimate of the real predictive error of the models. Its small value indicates that the model predicts better than chance and can be considered statistically significant.

$$\mathrm{PREES} = \sum_{i=1}^{n} (\hat{y_i} - y_i)^2. \quad (5)$$

Root mean square error (RMSE) is a measurement of the average difference between predicted and experimental values, at the prediction step. RMSE can be interpreted as the average prediction error, expressed in the same units as the original response values. The RMSE was obtained by the following formula:

$$\mathrm{RMSE} = \left[\frac{1}{n}\sum_{i=1}^{n} (y_i - \hat{y_i})^2\right]^{\frac{1}{2}}. \quad (6)$$

The other statistical parameter was relative error (RE) that shows the predictive ability of each component, and is calculated as:

$$\mathrm{RE}\ (\%) = 100\left[\frac{1}{n}\sum_{i=1}^{n} \frac{(\hat{y_i} - y_i)}{y_i}\right]. \quad (7)$$

The predictive ability was evaluated by the cross validation coefficient (Q^2 or R^2_{cv}) which is based on the prediction error sum of squares (PRESS) and was calculated by following equation:

$$R^2_{cv} \equiv Q^2 = 1 - \frac{\sum_{i=1}^{n} (y_i - \hat{y}_i)^2}{\sum_{i=1}^{n} (y_i - \bar{y})^2}. \quad (8)$$

Where y_i is the experimental $E_{1/2}$ in the sample i, $\hat{y}_i$ represented the predicted $E_{1/2}$ in the sample i, $\bar{y}$ is the mean of experimental $E_{1/2}$ in the prediction set and n is the total number of samples used in the test set [20].

The main aim of the present work was to assess the performances of GA-PLS and L–M ANN for modeling the half-wave potentials of compounds. The procedures of modeling including descriptor generation, splitting of the data, variable selection and validation were the same as those performed for modeling of the half-wave potentials of benzenoids derivatives.

4. CONCLUSIONS

The GA-PLS and L–M ANN modeling was applied for the prediction of the half-wave potentials values of 36 substituted benzenoid hydrocarbons. Two methods seemed to be useful, although a comparison between these methods revealed the slight superiority of the L–M ANN over the GA-PLS model. High correlation coefficients and low prediction errors confirmed the good predictability of two models. Application of the developed model to a testing set of 8 compounds demonstrates that the new model is reliable with good predictive accuracy and simple formulation. The QSPR procedure allowed us to achieve a precise and relatively fast method for determination of $E_{1/2}$ of different series of benzenoids derivatives to predict with sufficient accuracy the $E_{1/2}$ of new substituted compounds.

REFERENCES

1. Krivenko, A.G., Kotkin, A.S., and Kurmaz, V.A., *Russ. J. Electrochem.*, 2005, vol. 41, p. 122.
2. Kornhuber, J., Terfloth, L., Bleich, S., Wiltfang, G., and Rupprecht, R., *Eur. J. Med. Chem.*, 2009, vol. 44, p. 2667.
3. Tang, W.Z., and Wang, F., *Chemosphere*, 2010, vol. 78, p. 914.
4. Yuan, S., Xiao, M., Zheng, G., Tian, M., and Lu, X., *SAR QSAR Environ. Res.*, 2006, vol. 17, p. 473.
5. Nesmerak, K., Nemec, I., Sticha, M., Waisser, K., and Palat, K., *Electrochim. Acta*, 2005, vol. 50, p. 1431.
6. Tompe, P., Clementis, G., Petnehazy, I., Jaszay, Z.M., and Toke, L., *Anal. Chim. Acta*, 1995, vol. 305, p. 295.
7. Nesmerak, K., Nemec, I., Sticha, M., Waisser, K., and Palat, K., *Electrochim. Acta*, 2005, vol. 50, p. 1431.
8. Bergman, I., *Trans. Faraday Soc.*, 1954, vol. 50, p. 829.
9. Todeschini, R., Consonni, V., Mauri, A., and Pavan, M., *DRAGON-Software for the Calculation of Molecular Descriptors; Version 3.0 for Windows*, 2003.
10. Zhou, X., Li, Z., Dai, Z., and Zou, X., *J. Mol. Graphics Modell.*, 2010, vol. 29, p. 188.
11. Sarıpınar, E., Geçen, N., Şahin, K., and Yanmaz, E., *Eur. J. Med. Chem.*, 2010, vol. 45, p. 4157.
12. Singh, K.P., Ojha, P., Malik, A., and Jain, G., *Chemom. Intell. Lab. Sys.*, 2009, vol. 99, p. 150.
13. Parthiban, T., Ravi, R., and Kalaiselvi, N., *Electrochimica Acta*, 2007, vol. 53, p. 1877.
14. Jalali-Heravi, M., Asadollahi-Baboli, M., and Shahbazikhah, P., *Eur. J. Med. Chem.*, 2008, vol. 43, p. 548.
15. Singh, K.P., Basant, N., Malik, A., and Jain, G., *Anal. Chim. Acta*, 2010, vol. 658, p. 1.
16. Noorizadeh, H. and Farmany, A., *Russ. J. Electrochem.*, 2014, in press.
17. Roy, K. and Roy, P.P., *Eur. J. Med. Chem.*, 2009, vol. 44, p. 1941.
18. Gupta, V.K., Khani, H., Ahmadi-Roudi, B., Mirakhorli, S., Fereyduni, E., and Agarwal, S., *Talanta*, 2011, vol. 83, p. 1014.
19. Frapiccini, A.L., Gasaneo, G., Colavecchia, F.D., and Mitnik, D., *J. Electron. Spectrosc. Relat. Phenom.*, 2007, vol. 161, p. 199.
20. Chamjangali, A., Beglari, M., and Bagherian, G., *J. Mol. Graphics Modell.*, 2007, vol. 26, p. 360.