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MLR Study of IC₅₀ values for Cephalosporin derivatives by MS Excel

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Abstract:

In this paper there is a study of multiple linear regression analysis (MLR) to develop a regression equation for prediction of IC₅₀ values of cephalosporin derivatives. IC₅₀ values are considered in their $-\log IC_{50}$ i.e. pIC₅₀ terms. MLR is applied in stepwise regression analysis by means of forward selection method. 22 compounds of cephalosporin were selected for present study. 3D structures of these compounds were prepared with the help of chemsketch and saved as a mol file. Various indices like winer, detour, randic, harary, balban, schultz molecular topological indices, topological distance indices T(N-N), T(N-S), T(N-O), 3D Morse indices, Sum of Keir-Hall electro topological state (S_k), various combinations of 3D Morse and Keir Hall topological state, (N_S)^x, α_{xx} were calculated with the help of Dragon software. The IC₅₀ values in terms of pIC₅₀ were collected from literature. Then a stepwise regression analysis between pIC₅₀ and selected indices was carried out by Microsoft excel software. A multiple linear regression equation was developed. There occurs strong correlation ($R^2 = 0.642$, pearson product moment correlation coefficient, $r^2 = 0.801$) between observed and predicted values of pIC₅₀ by developed regression equation. The developed equation/ model can be employed for suggesting some other cephalosporin molecules with improved IC₅₀ which can be proposed for further practical study/ verification.

Keywords: MLR, topological distances, β -lactum antibiotic, 2D and 3D indices, pIC₅₀.

INTRODUCTION

Cephalosporins are broad-spectrum antibiotics, applied for the treatment of bacterial infections caused by susceptible organisms. such as respiratory tract infections (pneumonia, strep throat, tonsillitis, and bronchitis), skin infections and urinary tract infections, surgical prophylaxis prevention of bacterial infection before, during, and after surgery, open, laparoscopic or endoscopic surgery intravenous prophylaxis etc.'s. They are sometimes given with other antibiotics. Cephalosporins [1] belong to class of β -lactum type antibiotic. β -Lactam antibiotics (beta-lactam antibiotics) are a broad class of antibiotics. Most β -lactam antibiotics work by inhibiting cell wall biosynthesis in the bacterial organism and are the most widely used group of antibiotics. Up to year

2003, in the view of sales, more than half of all commercially available antibiotics in use were β -lactam compounds. Penicillin and most other β -lactam antibiotics [2] act by inhibiting penicillin-binding proteins, which normally catalyze cross-linking of bacterial cell walls. In the absence of β -lactam antibiotics, the bacterial cell wall plays an important role in bacterial reproduction. Adding β -lactam antibiotics to the cell medium while bacteria are dividing will cause them to shed their cell walls and fail to divide, forming large, fragile spheroplasts.

β -lactam antibiotics are bacteriocidal [3], and act by inhibiting the synthesis of the peptidoglycan layer of bacterial cell walls. The peptidoglycan layer is important for cell wall structural integrity, especially in Gram-positive organisms, being the

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outermost and primary component of the wall. The final transpeptidation step in the synthesis of the peptidoglycan is facilitated by transpeptidases known as penicillin-binding proteins (PBPs). PBPs vary in their affinity for binding penicillin or other β -lactam antibiotics.

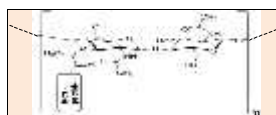


Figure 1: Chemical structure of peptidoglycan molecule.

Core structure of cephalosporin and related structure property relationship can be shown by following diagram:

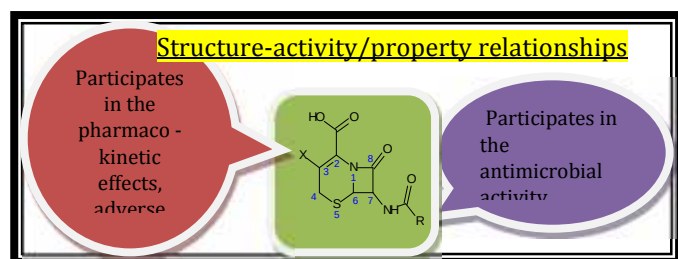


Figure 2: Structure-function relationships for cephalosporin core molecule

In the structure of cephalosporin as given in figure no. 2, nature of group $-R$ and $-X$ affects [4] activity as well as property of cephalosporin. Kinetic studies combined with absorption and nuclear magnetic resonance spectroscopy have shown the structure of the opening of the β -lactam ring of cephalosporin. Cephalosporin is the species formed by the aminolysis of β -lactam ring of cephalosporin due to reaction with amino acid's amino group present in cell wall of bacterial cell wall. Opening of β -lactam ring takes place either in a concerted fashion or in some stages. The opening of the β -lactam ring leads to elimination of the group $-X$ when this is configured as a leaving group. The process is well documented chemically and this property has been used as a strategy to obtain cephalosporins that can apply in a double action way. When the $-X$ is conformed as the inactive form of the drug, the action of the β -lactam in the cephalosporin implies the release of the drug in situ. The cephalosporin nucleus can be modified to gain different properties by insertion of suitable $-R$ group and $-X$ group to obtain desirable activity/property. This task can be completed by QSAR/QSPR.

Material and methods:

QSAR/ QSPR i.e. Quantitative Structure Activity Relationship/ Quantitative Structure Property Relationship Studies for series of cephalosporin compounds consist the following steps:

1. To select accurate experimental physicochemical properties from compilations and studies

(i.e. from experimental or journal.)

2. To implement these properties and cephalosporin molecular descriptors to produce various

QSAR/ QSPR equations in terms of single or multiple regression equations [5], [6].

$$Y = aX_1 + bX_2 + cX_3 + \dots + nX_n$$

3. To determine the best QSPR equation on the basis of best prediction for each Physico-chemical property.

4. To propose a model i.e. MLRM (multi linear regression model).

Example of a QSAR/ QSPR model:

$$Y = aX_1 + bX_2 + cX_3 + \dots + nX_n + \epsilon$$

Where, Y = Physicochemical property as a dependent variable,

$X_1, X_2, X_3, \dots, X_n$ = Specific molecular descriptor as independent variables.

$a, b, c, \dots, n$ = Regression constants, ϵ = Error

When correlation is not strong between dependent and independent variable then any single independent variable can not be used for satisfactory prediction of dependent variable. So multiple linear regression analysis is to be applied to increase correlation by adding suitable one or more indices in various steps. This can be done in two ways [7], [8] –

(a) By forward selection method, in which each variable index is added in various steps one by one in regression analysis. In each step variable index is selected on the basis of lowest P-value. Regression analysis is carried out till the step at which all variable appears significant ($P < 0.05$) in any one or more regression equation.

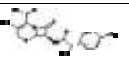
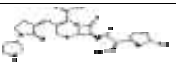
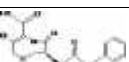
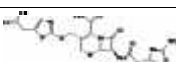
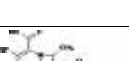
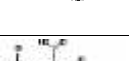
(b) By backward selection method, in which initially all variable indices are taken in regression analysis and variable indices are removed in step by step. Removal is done on the basis of P-value. In each step the variable index, whose removal results in highest significant regression equation, is removed.

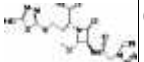
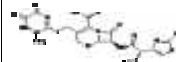
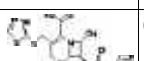
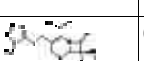
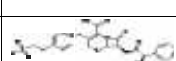
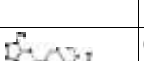
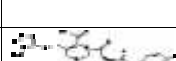
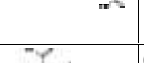
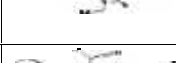
Various molecular descriptors choosed for selected set of molecular structure of cephalosporin type drugs and calculated

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with the help of Dragon software [9]. For this purpose 2D and 3D structures prepared by Chem sketch [10] and saved in the form of mol. files. Then some physico-chemical properties calculated by above software. The pharmacological property (activity) collected from reliable cheminformatics sources. Stepwise regression analysis was carried out for modeling the physico-chemical and pharmacological properties (activity) with the help of selected descriptors by Micro soft office 2007 software [11]. A regression equation and hence a regression model was developed. Then each physico-chemical and pharmacological property were predicted with the help of respective developed regression equations. Importance of regression equation was tested by calculating the correlation between observed and predicted values. Correlation between observed and predicted values were expressed by means of simple R^2 , Adjusted- R^2 , pearson product moment correlation coefficient $r^2 \equiv r$, PRESS. The detailed information of selected molecules for present study is given in table no.1 as follows:

Table no. 1 Structure of selected molecules for the study

Molecular Set	Name	Structure of molecule	Molecular Set	Name	Structure of molecule
C ₁	Cefadroxil		C ₁₂	Ceftibiprole	
C ₂	Cefalexin		C ₁₃	Cefminoxime	
C ₃	Cefaclor		C ₁₄	Cefpodizime	
C ₄	Cefradine		C ₁₅	Cefotaxime	
C ₅	Cefalothin		C ₁₆	Cefepime	
C ₆	Cefoxitin		C ₁₇	Ceftizoxime	

C ₇	Cefazolin		C ₁₈	Ceftriaxone	
C ₈	Ceftezole		C ₁₉	Cefexime	
C ₉	Cefmetazole		C ₂₀	Cefpimizole	
C ₁₀	Cefotetan		C ₂₁	Cefoperazone	
C ₁₁	Cefdinir		C ₂₂	Ceftazidime	

A description of selected pharmacological property (activity) are as follows:

Half maximal Inhibitory Concentration (IC₅₀):

It is a measure of the effectiveness of a compound in inhibiting biological or biochemical function. Often, the compound in question is a drug candidate. This quantitative measure indicates how much of a particular drug or other substance (inhibitor) is needed to inhibit a given biological process (or component of a process, i.e. an enzyme, cell, cell receptor or microorganism) by half. The IC₅₀ [12] of a drug can be determined by constructing a dose-response curve and examining the effect of different concentrations of antagonist on reversing agonist activity. IC₅₀ values can be calculated for a given antagonist by determining the concentration needed to inhibit half of the maximum biological response of the agonist.

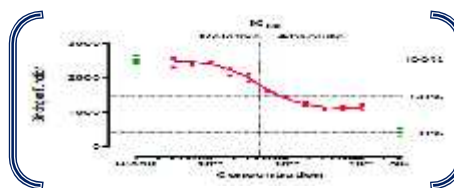


Figure 3: Illustration of IC₅₀ by graph.

IC₅₀ is not a direct indicator of affinity although the two can be related at least for competitive agonists and antagonists by the following Cheng-Prusoff equation [13]:

$$K_i = IC_{50} / \{1 + ([S]/K_m)\}$$

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Where, K_i is the binding affinity of the inhibitor, IC_{50} is the functional strength of the inhibitor, $[S]$ is substrate concentration and K_m is the affinity of the substrate for the enzyme. Whereas the IC_{50} value for a compound may vary between experiments depending on radioligand concentration, the K_i is an absolute value. K_i is the inhibition constant for a drug. The concentration of competing ligand in a competition assay which would occupy 50% of the receptors if no radioligand were present. IC_{50} values can be determined through journal searching and cheminformatics as well as estimated also by various softwares calculations available online or in purchased version. These softwares require 3D structures of considered molecules.

Brief descriptions of selected descriptors [14], [15], [16] are as follows:

Wiener Index (W): Wiener index (also Wiener number, introduced by H. Wiener in 1947) is a topological index of a molecule, defined as half the sum of the numbers of edges in the shortest path in a chemical graph between all pairs of non-hydrogen atoms in a molecule. Chemical graph or molecular graph is the collection of points and lines connecting these points. This index was introduced by H. Wiener in 1947. Wiener index may be calculated using distance matrices.

Harray Index (H): Harray Index H is defined as half sum of the element of the inverse distance matrix.

$$H = \frac{1}{2} \sum_{i=1}^{j=1} (d^{-1})_{ij}$$

Where, $(d^{-1})_{ij} = ij^{\text{th}}$ element of inverse distance matrix.

Schultz Molecular Topological Index (SMTI): This index was given by Harry P. Schultz,

SMTI is defined as the summation of all the terms obtained by multiplying valence row matrix (V) to sum of adjacency matrix (A) to distance matrix (D).

$$\text{SMTI} = \sum_{i=1}^N [V(A+D)]$$

Randic Index (X): This Index was proposed by Randic in 1975 and shows the effect of vertices i.e. shape of molecule over properties and activity. This is defined as summation of all terms obtained by taking inverse root of each term's derived by multiplication of column and horizon element of matrix for connectivity. $X = \sum [d_i d_j]^{-\frac{1}{2}}$

d_i, d_j are valences of vertices i and j which is equal to number of bonds connected to atom i and j .

Balban Index (J):

$$J = \left[\frac{M}{(\mu+1)} \right] \sum (D_i D_j)^{-1}$$

M = No. of bonds (edges) .

μ = Cyclometric no.

$D_i D_j$ = Sum of row i column j of a distance matrix respectively.

Detour Index (W')

It is half the sum of all matrix elements present in Detour matrix (DD). Entries of the Detour matrix (DD) represent the maximum topological distances between two given vertices.

$$W' = \frac{1}{2} \sum_{i,j}^{N_{SA}} dd_{ij}$$

dd_{ij} – the number of bonds in the longest path connecting the pair of atoms i and j

N_{SA} – the number of non-hydrogen atom in the molecule. This was first introduced by Harary in 1969, in the context of Graph theory. When there is no cycle present in the considered molecular structure, the distance and the detour matrixes are identical. This can characterize one or more rings in the molecule. Detour matrix has been proposed as a tool to characterize cyclic structures.

T(N-O): Sum of Topological Distances between Nitrogen and Oxygen atom.

T(N-N): Sum of Topological Distances between Nitrogen and Nitrogen atom.

T(N-S): Sum of Topological Distances between Nitrogen and Sulphur atom.

Topological Distances used in T(N-O), T(N-N), T(N-S):

This was given by Bonchev (1991) Trinajstić (1992). Let $\{x_1 \dots x_k\}$ be the atoms of a particular chemical element x in the molecule. Similarly, $\{y_1 \dots y_m\}$ are the atoms of a

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particular chemical element y in the molecule. We permit the case of $x = y$ as well. Then the atom pair topological distance between the chemical elements x and y is given by:

$$\frac{1}{2} \left(\sum_{i=1}^k \sum_{j=1}^m d_{ij} \right)$$

where, d_{ij} is the topological distance between x_i and y_j .

3D MoRSE Descriptors:

3D MoRSE descriptors (3Dimensional Molecule Representation of Structures based on Electron diffraction) are derived from infrared spectra simulation using a generalized scattering function. A typical MoRSE descriptor is denoted by $Mor(s, w)$, where s and w take the values $1 \leq s \leq 32$ and

$$w \in (u, m, v, e, p)$$

where, u is unweighted

m is weighted by mass

v is weighted by van der Waals volume

e is weighted by electronegativity

p is weighted by polarizability

The MoRSE descriptor is defined as follows:

$$Mor(s, w) = I(s, w) = \sum_{i=2}^n \sum_{j=1}^{i-1} w_i w_j \sin \left(\frac{sr_{ij}}{(sr_{ij})} \right)$$

where, r_{ij} is the Euclidean distance between the atoms i and j ,

and w_i and w_j are the weights of the atoms i and j respectively.

Keir and Hall valence connectivity indices: The molecular connectivity valence delta-values have been defined in terms of the count of no hydrogen. Non valence electrons on a valence-state atom as screened from the nucleus by the core electrons.

Z_k - Total number of electrons present on atom k .

Z_k^v - Number of valence electrons in the k^{th} atom

H_k - Number of hydrogen atoms directly attached to the k^{th} non-hydrogen atom

$m = 0$ - Atomic valence connectivity indices

$m = 1$ - One bond path valence connectivity indices

$m = 2$ - Two bond fragment valence connectivity indices

$m = 3$ Three contiguous bond fragment valence connectivity indices etc.

Valence connectivity for the k^{th} atom in the molecular graph,

$$\delta_k^v = \frac{(Z_k^v - H_k)}{(Z_k - Z_k^v - 1)}$$

Above all descriptors [17], [18] some other indicator indices representing the no. of particular atom in particular group or structure like no. of S atoms in group $-X$ etc. are also counted and applied in MLR. The combination of 3D Morse and sum of Keir hall topological distances are applied shown in table no. 4 Other indices like $(EN_{orb})^{*O=C<}$, Donar sites and α_{xx} calculated by Dragon shown in table no. 5 considered for MLR analysis. For determining microscopic contribution of group $-X$ the common indices like W , H , X^1 , W' , $T(N-N)$, $T(N-S)$, $T(N-O)$ also calculated for selected set of molecules by removing $-R$ group as shown in table no. 7

Experimental:

IC_{50} values in terms of pIC_{50} values searched out from literature. Selected molecules 2D and 3D structures were prepared by chem sketch software and saved in mol file format. The various molecular descriptors were calculated by Dragon software (given in table no. 2, 3, 4, 5, 6 and 7)

In order to derive relationship of dependent variable (activity/property) and independent variables (descriptors/ indices) different approaches for QSAR have been offered in the literature. These approaches range from simple linear regression (LR) and multiple linear regression trained by a variety of methods. MLR techniques can be used to determine the most relevant features for a given model.

Multiple regression carried out by MS excel 2007 through the method (a) out of above discussed methods.

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Table no. 2 Topological, connectivity and geometrical indices of selected set of molecular structures for QSAR study.

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Indices → Molecular Set ↓	plC_{50}	Weiner (W)	Randic (X^1)	Balban (J)	Detour (W')	Harary (H)	T(N-N)	T(N-S)	T(N-O)	SMTI
C ₁	4.96	1570	11.81	1.57	2690	46.77	12	9	76	6763
C ₂	4.64	1242	11.00	1.56	2222	42.42	12	9	53	5319
C ₃	4.66	1383	11.41	1.58	2443	44.73	12	9	53	5882
C ₄	4.94	1383	11.41	1.58	2443	44.73	12	9	44	5882
C ₅	6.2	1790	12.38	1.56	2946	48.00	3	14	52	7526
C ₆	5.63	1837	12.79	1.7	3045	51.36	16	31	79	7670
C ₇	5.96	2468	13.94	1.3	4075	55.01	19	172	22	10736
C ₈	0.89	2223	13.54	1.31	3727	52.95	19	172	17	9732
C ₉	6.28	2591	14.35	1.64	4105	56.63	14	130	25	10706
C ₁₀	5.16	4350	17.01	1.37	6438	70.53	15	196	51	18294
C ₁₁	6.69	1701	12.38	1.62	2835	48.94	46	42	14	7128
C ₁₂	6.06	4333	17.29	1.19	7008	71.76	22	48	36	18914
C ₁₃	6.01	3413	15.81	1.35	5431	63.76	27	177	33	14566
C ₁₄	5.77	4530	17.19	1.31	6928	69.30	10	162	35	19112
C ₁₅	5.66	2584	14.24	1.62	4020	56.56	46	42	24	10666
C ₁₆	5.68	3029	15.24	1.40	4863	62.51	91	58	18	12948
C ₁₇	5.58	1531	11.94	1.61	2562	46.52	46	42	14	6456
C ₁₈	5.74	4386	17.12	1.35	6872	70.17	21	152	43	18532
C ₁₉	5.05	2560	14.24	1.63	3930	56.47	46	42	21	10576
C ₂₀	4.8	8803	21.84	1.17	1286	91.97	99	116	55	37294
C ₂₁	4.91	7383	21.01	1.23	1112	88.41	29	108	64	31520
C ₂₂	4.84	4573	17.49	1.4	6924	72.45	91	58	28	19281

Table no. 3: Values of 3D indices (3D Morse and Keir Hall) for selected set of molecular 3D- structures.

Molecular Set	$(S_6)^{wor}$	$(Mor_{01u})^{wor}$	$(Mor_{01am})^{wor}$	$(Mor_{01v})^{wor}$	$(Mor_{01en})^{wor}$	$(Mor_{01p})^{wor}$	$(S_6)^{wor}$	$(Mor_{01u})^{wor}$	$(Mor_{01am})^{wor}$	$(Mor_{01v})^{wor}$	$(Mor_{01en})^{wor}$	$(Mor_{01p})^{wor}$
C ₁	68.8	741	405.6	307.8	791.7	304.2	48.2	325	190.5	129.8	353.5	146.1
C ₂	63.2	703	368.6	295.1	739.9	328.4	46.5	253	168.1	105.3	280.8	117.5
C ₃	63.2	703	368.6	295.1	739.9	328.4	50.3	253.0	222.4	115.5	288.3	130.7
C ₄	62.2	780	368.6	295.1	739.9	328.4	48.2	325	190.5	129.8	353.5	146.1
C ₅	57.2	528	346.2	237.2	562.9	275.5	61.8	496	296.8	194.8	548.6	215.8
C ₆	62.6	666	415.5	285.5	713.1	330.2	65.8	561	328.2	215.0	620.4	237.4
C ₇	60.7	465	317.6	197.9	519.2	212.3	62.7	595	459.9	270.5	646.1	324.4
C ₈	60.7	465	317.6	197.9	519.2	212.3	61.0	496	422.9	234.6	546.5	278.2
C ₉	64.9	595	389.2	248.6	647.2	286.7	69.6	741	496.1	304.8	816.0	343.6
C ₁₀	87.2	820	667.3	362.3	925.6	418.8	69.6	741	496.1	304.8	816.0	343.6
C ₁₁	71.0	595	452.1	266.5	662.8	298.5	51.2	351	210.6	146.3	380.6	163.7
C ₁₂	71.8	630	412.3	264.6	700.7	283.8	71.8	1081	514.6	420.7	1136	468.9
C ₁₃	70.6	703	488.2	304.8	772.1	343.2	64.2	595	420.1	254.8	654.8	287.8
C ₁₄	70.6	703	488.2	304.8	772.1	343.2	75.8	741	573.4	335.1	815.3	392.7
C ₁₅	70.6	703	488.2	304.8	772.1	343.2	61.8	496	296.8	495.8	548.5	215.8
C ₁₆	71.5	666	485.5	297.4	735.5	333.2	58.2	820	350.9	300.4	850.4	342.4

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C ₁₇	70.6	703	488.2	304.8	772.1	343.2	46.5	253	168.1	105.3	280.8	117.5
C ₁₈	70.5	703	488.2	304.8	772.1	343.2	46.5	253	168.1	105.3	280.8	117.5
C ₁₉	84.6	820	609.6	356.8	922.1	395.9	51.2	351	210.6	146.3	380.6	163.7
C ₂₀	95.8	1275	747.4	538.5	1334	578.3	84.2	990	610.1	406.7	825.0	355.4
C ₂₁	86.5	1225	666.1	509.1	1311	555.1	64.2	595	420.1	254.8	654.8	287.8
C ₂₂	89.4	1035	691.3	438.4	1141	488.6	60.7	595	337.4	257.5	633.0	284.7

> (Mor_{1u})^{wor}, and (Mor_{1am})^{wor}, (Mor_{1v})^{wor}, (Mor_{1en})^{wor}
(Mor_{1p})^{wor} = 3D MoRSE descriptors for Cep training set molecules with out -x group unweighted and weighted by atomic mass, vander waal volume, electronegativity, polarizability respectively.

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> (S_s)^{wor}, (S_s)^{wor} = Keir-Hall electro topological state for Cep training set molecules with out -x group and -R group respectively.

(Superscript 'wor' and 'wor' shows values for structures with out -x group and with -R group respectively.)

C ₃	113.45	12.89	2435.05	4167.10	6602.15	-1732.1
C ₄	111.34	15.0	2439.73	4176.46	6616.19	-1736.7
C ₅	119.0	-4.66	1949.90	3371.80	5321.7	-1421.9
C ₆	128.33	-3.17	2410.38	4154.76	6565.14	-1744.4
C ₇	123.34	-2.0	1711.97	2958.94	4670.91	-1247.0
C ₈	121.67	-0.33	1711.97	2958.94	4670.91	-1247.0
C ₉	134.50	-4.66	2166.76	3738.52	5905.28	-1571.8
C ₁₀	156.83	17.67	3194.12	5568.24	8762.36	-2374.1
C ₁₁	122.17	19.83	2274.93	3954.86	6229.79	-1679.9
C ₁₂	143.66	0.0	2291.44	3952.88	6244.32	-1661.4
C ₁₃	134.72	6.38	2611.31	4519.62	7130.93	-1908.3
C ₁₄	146.38	-5.28	2611.31	4519.62	7130.93	-1908.3
C ₁₅	132.38	8.72	2611.31	4519.62	7130.93	-1908.3
C ₁₆	129.67	13.33	2517.60	4369.20	6886.80	-1851.6
C ₁₇	117.05	24.05	2611.31	4519.62	7130.93	-1908.3
C ₁₈	148.55	-7.45	2611.31	4519.62	7130.93	-1908.3
C ₁₉	135.84	33.50	3104.48	5388.96	8493.44	-2284.5
C ₂₀	180.08	11.58	4472.80	7670.60	12143.40	-3197.8
C ₂₁	150.67	22.33	4266.44	7307.88	11574.30	-3041.4
C ₂₂	150.09	28.75	3794.64	6554.28	10348.90	-2759.6

Where, (S_s)^{wor}, (S_s)^{wor} = Keir-Hall electro topological state for Cep training set molecules with out -x group and -R group respectively.
Sum of all 3D MoRSE descriptors unweighted and weighted atomic by mass, vander waal volume, electronegativity, polarizability respectively
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Table no. 4: Descriptors generated by combination of Keir-Hall electro topological state and 3D MoRSE

Molecular Set	(S _s) ^{wor} + (S _s) ^{wor}	(S _s) ^{wor} - (S _s) ^{wor}	(MoRSE) ^{wor}			
			A	B	C	D
C ₁	117.0	20.66	2550.27	4359.54	6909.81	-1809.3
C ₂	109.67	16.67	2435.05	4167.10	6602.15	-1732.1

Table no. 5: Values of (EN_{orb})^{*O=C<}, Donar sites and α_{xx}

Molecular Set	(EN _{orb}) ^{*O=C<}	(Sites)	(Sites)	(3D-Surfacearea) ^{V.W.}	α _{xx}	Training Set	(EN _{orb}) ^{*O=C<}	(Sites)	(Sites)	(3D-Surfacearea) ^{V.W.}	α _{xx}
C ₁	12.5	9	5	438.6	36.2	C ₁₂	11.4	15	6	590.5	49.5
C ₂	12.3	8	4	396.6	34.2	C ₁₃	12.9	13	4	561.9	74.6
C ₃	12.3	9	4	409.9	50.1	C ₁₄	12.9	13	5	614.7	88.4

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C ₄	12.3	8	4	424.2	50.3	C ₁₅	12.9	12	4	522.3	62.5
C ₅	12.7	8	2	467.2	37.4	C ₁₆	12.8	10	3	592.9	70.3
C ₆	12.8	9	4	436.5	42.2	C ₁₇	12.8	10	4	418.9	48.6
C ₇	12.9	11	2	490.9	70.4	C ₁₈	12.9	16	5	603.8	80.6
C ₈	12.9	11	2	457.6	65.8	C ₁₉	12.9	13	5	485.6	59.1
C ₉	12.9	12	2	535.9	48.4	C ₂₀	12.9	18	5	788.9	70.8
C ₁₀	13.1	16	5	590.6	590.6	C ₂₁	12.9	17	4	759.2	73.3
C ₁₁	12.9	10	5	408.1	54.0	C ₂₂	12.9	13	4	623.1	57.9

Table no. 6: Index showing the no. of different types atoms present in particular structure.

Molecule set	Total no. of atoms in group -X, (N _T) ^x	No. of C atoms in group X, (N _C) ^x	No. of N atoms in group -X, (N _N) ^x	No. of S atoms in group X, (N _S) ^x	No. of O atoms in group X, (N _O) ^x	Total no. of atoms in group R, (N _T) ^R	No. of C atoms in group -R, (N _C) ^R	No. of N atoms in group -R, (N _N) ^R	No. of S atoms in group -R, (N _S) ^R	No. of O atoms in group -R, (N _O) ^R
C ₁	1	0	0	0	0	9	7	1	0	0
C ₂	0	0	0	0	0	8	7	1	0	0
C ₃	1	0	0	0	0	8	7	1	0	0
C ₄	1	1	0	0	0	8	7	1	0	0
C ₅	5	3	0	0	2	6	5	0	1	0
C ₆	4	1	1	0	1	6	5	0	1	0
C ₇	6	2	2	2	0	6	2	4	0	0
C ₈	8	3	2	3	0	6	2	4	0	0
C ₉	8	3	4	1	0	5	3	1	1	0

C ₁₀	8	2	4	1	0	11	5	1	2	3
C ₁₁	2	2	0	0	0	9	4	3	1	1
C ₁₂	12	9	2	0	1	9	4	4	0	1
C ₁₃	8	3	4	1	0	9	4	3	1	1
C ₁₄	11	6	1	2	2	9	4	3	1	1
C ₁₅	5	3	0	0	2	9	4	3	1	1
C ₁₆	7	6	1	0	0	9	4	3	1	1
C ₁₇	0	0	0	0	0	9	4	3	1	1
C ₁₈	10	4	3	1	2	9	4	3	1	1
C ₁₉	2	2	0	0	0	12	5	3	1	3
C ₂₀	13	8	1	1	3	17	12	3	3	3
C ₂₁	8	3	4	1	0	14	7	3	0	4
C ₂₂	7	6	1	0	0	15	8	3	1	3

Table no. 7: Topological, connectivity and geometrical indices of selected set of molecular structures without -R group for QSAR

Molecule Set	(W) ^{wor}	(X) ^{wor}	(J) ^{wor}	(W) ^{wor}	(H) ^{wor}	{T(N-N)} ^{wor}	{T(N-S)} ^{wor}	{T(N-O)} ^{wor}	(SMTI) ^{wor}
C ₁	415	7.58	2.07	839	28.01	3	3	26	1718
C ₂	1242	11.00	1.55	2222	42.42	12	9	53	5319
C ₃	415	7.58	2.07	839	28.01	3	3	26	1718
C ₄	415	7.58	2.07	839	20.01	3	3	26	1718
C ₅	812	9.47	2.02	1444	35.44	3	3	12	3284
C ₆	866	9.89	2.19	1554	38.48	16	8	79	3468
C ₇	1079	10.63	1.6	1971	40.33	35	45	96	4624
C ₈	1486	11.96	1.68	2635	42.27	67	46	207	6224
C ₉	1486	11.96	1.68	2635	42.27	67	46	207	6244
C ₁₀	492	8.11	2.09	968	29.94	3	3	26	2018
C ₁₁	1873	13.02	1.39	3404	52.26	42	18	124	8160
C ₁₂	1218	11.04	1.60	2221	42.49	67	46	166	5180
C ₁₃	1822	12.42	1.52	3022	47.93	18	35	115	7626

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C ₁₄	812	9.47	2.022	1444	35.44	3	3	52	3284
C ₁₅	1015	10.47	1.71	1907	41.26	14	7	51	4324
C ₁₆	354	7.16	2.01	726	25.78	3	3	26	1482
C ₁₇	1728	12.34	1.57	3056	48.77	53	36	182	7246
C ₁₈	492	8.11	2.09	968	29.94	3	3	26	2018
C ₁₉	2276	13.21	1.51	3624	52.12	14	36	147	9460
C ₂₀	1218	11.04	1.61	2221	42.49	67	46	166	5180
C ₂₁	1048	10.63	1.65	2012	40.65	14	7	51	4480
C ₂₂	492	8.11	2.09	968	29.94	3	3	26	2018

Table no. 8: Correlation of some selected indices with pIC₅₀ values

Indices	Correlation	Indices	Correlation	Indices	Correlation	Indices	Correlation
W	-0.01	T(N-S)	-0.14	(Mor _{1v}) ^{wox}	-0.03	(Mor _{1v}) ^{wor}	0.15
χ ¹	0.02	T(N-O)	0.05	(Mor _{1en}) ^{wox}	-0.05	(Mor _{1en}) ^{wor}	0.18
J	0.20	SMTI	-0.01	(Mor _{1p}) ^{wox}	0.001	(Mor _{1p}) ^{wor}	0.10
W'	-0.01	(S _s) ^{wox}	-0.004	(S _s) ^{wor}	0.14	(N _s) ^x	-0.47
H	0.03	(Mor _{1u}) ^w	-0.64	(Mor _{1u}) ^{wor}	0.19	(S _s) ^{wox} - (S _s) ^{wor}	-0.12
T(N-N)	-0.06	(Mor _{1am}) ^{wox}	0.05	(Mor _{1am}) ^{wor}	0.03	α _{xx}	-0.03

Table no. 9: Summary of stepwise multilinear regression for developing a model equation for prediction of pIC₅₀

Step no.	Developed MLR equation	R ²	PRESS	SE
1	Step -1 pIC ₅₀ = 5.6473 - 1.6499 (±0.2638) (N _s)	0.219	21.327	1.03

2	Step -2	pIC ₅₀ = 4.9708 - 1.6499(±0.4288) (N _s) ^x + 0.0157(±0.0056) T(N-S)	0.449	15.041	0.89
3	Step -3	pIC ₅₀ = 5.5383 - 1.9456(±0.3916) (N _s) ^x + 0.0160(±0.0049) T(N-S) - 0.0413(±0.0158) {(S _s) ^{wox} - (S _s) ^{wor} }	0.601	10.894	0.78
4	Step -4	pIC ₅₀ = 5.4085 - 2.1864(±0.4190) (N _s) ^x + 0.0213 (±0.0061) T(N-S) - 0.0353(±0.0159) {(S _s) ^{wox} - (S _s) ^{wor} } - 0.0027(±0.0019) α _{xx}	0.642	9.778	0.76
5	Step -5 (Final)	No variable can be added satisfactory.	-	-	-

Results and discussions: By multiple linear regression equation analysis regression equation developed for prediction of IC₅₀ can be represented by the following equation:

$$pIC_{50} = 5.4085 - 2.1864(\pm 0.4190) (N_s)^x + 0.02133 (\pm 0.0061) T(N-S) - 0.0353(\pm 0.0159) \{(S_s)^{wox} - (S_s)^{wor}\} - 0.0027(\pm 0.0019) \alpha_{xx}$$

Statistics of the developed regression equation is as follows:

n	R ² -Adj.	Pearson R ²	F-ratio	Overall significance-F	SE	PRESS
22	0.558	0.642	0.801	7.624	0.001	0.76 9.778

Predicted value related to observed value by the following equation:

$$pIC_{50}(\text{pred.}) = 0.642(pIC_{50}(\text{obs.}) - 1.889)$$

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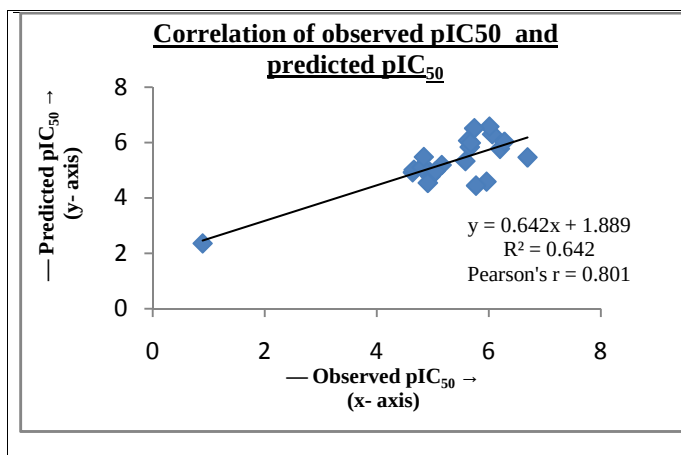


Figure no. 4 Graph showing predicted and observed pIC₅₀ for selected set of molecules

Table no. 10: Predicted and observed values of pIC₅₀

Molecular Set	Observed pIC ₅₀	Predicted pIC ₅₀	Molecular Set	Observed pIC ₅₀	Predicted pIC ₅₀
C ₁	4.96	4.77	C ₁₂	6.06	6.29
C ₂	4.64	4.91	C ₁₃	6.01	6.57
C ₃	4.66	5.01	C ₁₄	5.77	4.44
C ₄	4.94	4.94	C ₁₅	5.66	5.83
C ₅	6.2	5.77	C ₁₆	5.68	5.98
C ₆	5.63	6.07	C ₁₇	5.58	5.32
C ₇	5.96	4.58	C ₁₈	5.74	6.51
C ₈	0.89	2.35	C ₁₉	5.05	4.96
C ₉	6.28	6.03	C ₂₀	4.8	5.09
C ₁₀	5.16	5.18	C ₂₁	4.91	4.54
C ₁₁	6.69	5.46	C ₂₂	4.84	5.47

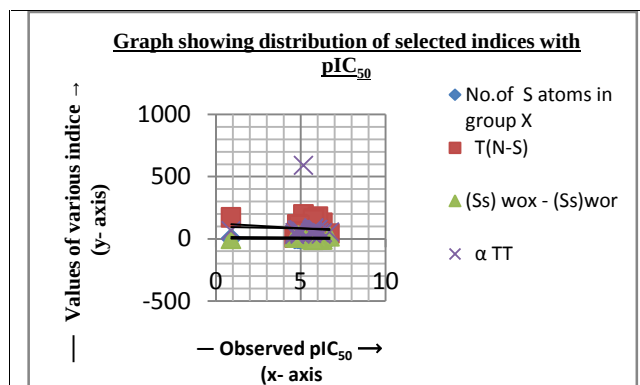


Figure 5: Distribution of selected indices with pIC₅₀

CONCLUSIONS:

From the developed equation this can be concluded that IC₅₀ value is predicted by (N_S)^x in larger proportion than others. Since, (N_S)^x appears in negative contribution so to decrease pIC₅₀ no. of S atoms in group -X of cephalosporin core structure should be minimized and vice versa. However, T(N-S) appears in positive factor so to increase pIC₅₀ sum of topological distances between nitrogen and sulphur should be maximized. Another fact which should be considered during designing of new molecule may be that for larger pIC₅₀ new molecule. However, polarizability in XX direction also helpful till little extent to propose new molecules with desired IC₅₀ value.

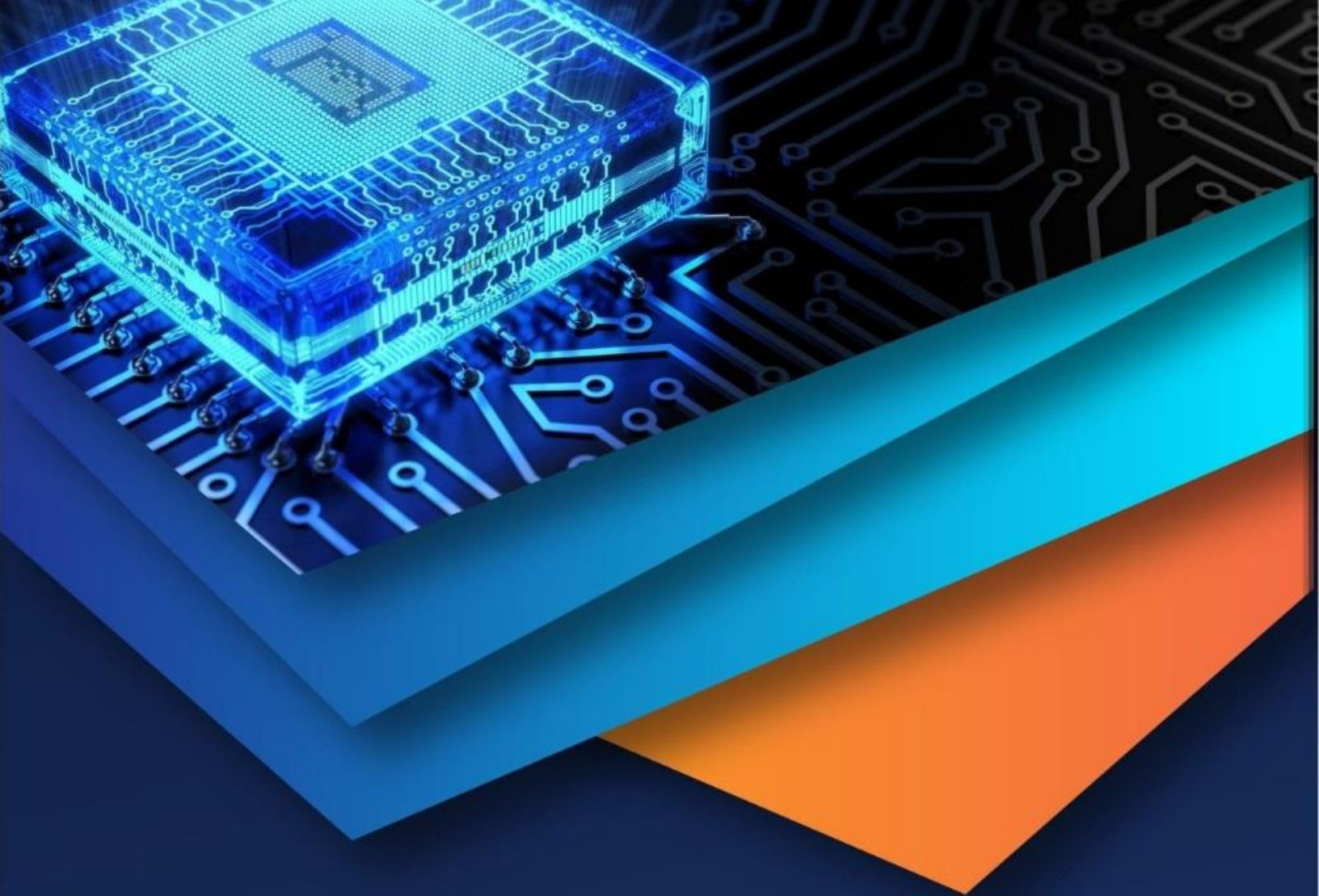
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