

Predicting (Nk) factor of (CPT) test using (GP): Comparative Study of MEPX & GN7

Ahmed H. ELbosraty¹, Ahmed M. Ebid², Ayman L. Fayed³

Abstract— Static cone penetration test (CPT) is a broadly satisfactory and dependable geotechnical in-situ apparatus that gives brisk and honest substantial measure of data about soil classification, stratification and properties. Un-drained shear strength of clay (c_u) is one of the principle soil parameters that could be sensibly evaluated from the (CPT) results, as it is specifically connected to the tip resistance through the experimental cone factor (Nk). Earlier researches showed that (Nk) value depends on type of soil, nature and stress history conditions and many other variables. Construction development in some locations with thick deposits of soft to very soft clays motivates extensive researches to define the reasonable value of the (Nk) factor for such types of clay. The performed study concentrated on utilizing the genetic programming technique (GP) to predict (Nk) value of clay using the consistency limits that can be easily determined in the laboratory. A set of 102 records were gathered from the CPT site investigations and corresponding consistency limits and other physical properties experiments, were divided into training set of 72 records and validation set of 30 records. Both (GN7) & (MEPX) software were used to apply (GP) on the available data. Four trials for each software with different chromosome lengths were performed to correlate the (Nk) factor with the clay consistency limits, water content (wc) and unit weight (γ) using training data set, then, the produced relations were tested using the validation data set. The four generated formulas using (GN7) showed accuracies ranging between 93% and 97% and coefficient of determination (R^2) ranging between 0.7 and 0.9, while the other four formulas form (MEPX) showed accuracy not exceeding 95% and coefficient of determination (R^2) ranging between 0.45 and 0.75.

Index Terms— CPT, Consistency Limits, Genetic Programming (GP), Multi Expression Programming (MEP), Cone Factor (Nk).

1 INTRODUCTION

Classic static cone penetration test (CPT) is one of the well-known site tests which carried out to characterize the soil formations and estimate their mechanical proprieties based on their penetration resistance. Today, modern (CPT) equipment is capable to measure many more parameters than penetration resistance such as pore water pressure, lateral soil pressure at rest, lateral elastic modulus of soil. Figure (1) shows (CPT) test overview and sample of its output. [3, 10, 15].

Many theories were introduced to simulate the behavior of the soil during static penetration process such as the bearing capacity theory (Meyerhof 1961, Durgunoglu and Mitchell 1975), cavity expansion theory (Vesic 1972 and Yu and Houlsby 1991), the strain path method proposed by Baligh (1985), calibration chamber testing and the finite element analysis (Walker and Yu 2006). [1, 8, 9, 12, 17,19 and 20].

Although, many previous researches were carried out to correlate tip resistance from (CPT) with other soil properties specially the un-drained shear strength of clay (c_u), but none of them derives a proper correlation due to the sophisticated be-

havior of the clay which depends on many parameters such as initial stresses, pore-water pressure, penetration rate and over consolidation ratio. In addition, uncertainties in measured values make the correlation more difficult. [4, 14].

Previously suggested formulas to correlate (CPT) results with the un-drained shear strength of clay (c_u) are summarized in many publications [3, 6, 9, 10, 15, and 16]. Many of those researches considered that (c_u) proportional linearly with the corrected tip resistance of the cone as shown in equation (1)

$$c_u = \frac{q_c - \sigma_{vo}}{Nk} \quad \dots\dots (1)$$

Where,

- c_u : Un-drained shear strength of clay.
- q_c : Tip resistance of the cone.
- σ_{vo} : Total overburden pressure.
- Nk : Empirical cone factor.

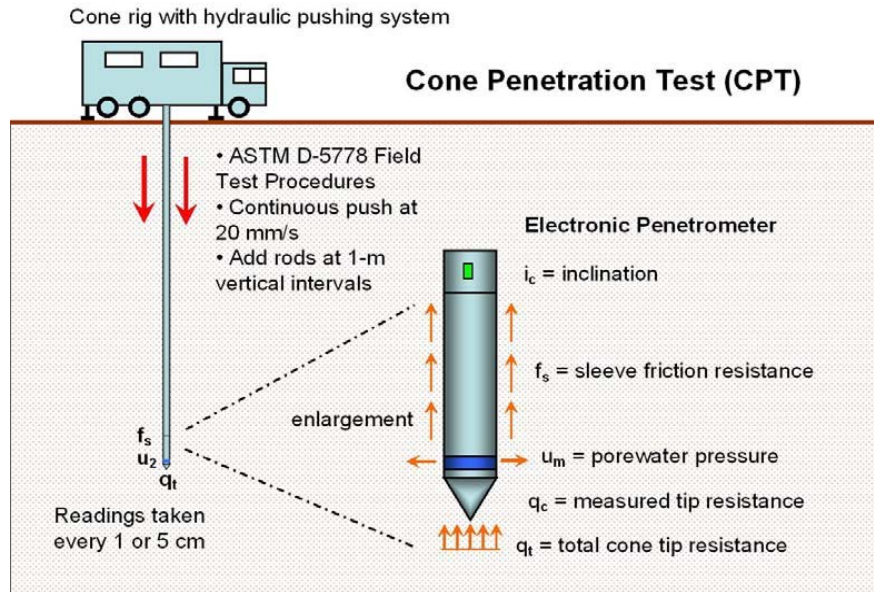
Accordingly, most of the previous researches were concerned in estimating (Nk) value which correlates (CPT) with (c_u).

As summarized by Zsolt Rémai (2013) [17], typical values for (Nk) for different soil types has been suggested by many researchers. Lunne and Kleven (1981) [13] suggested that (Nk) varies between 11 and 19 for normally consolidated, Scandinavian marine clays. Jörss (1998) [7] suggested that (Nk) equals 20 for marine clays and 15 for boulder clays. Gebreselassie (2003) [5] proposed that (NK) value is ranged between 7.6 and 28.4 for different soil types. Finally, Chen (2001) [4] recommended (Nk) values varying between 5 and 12.

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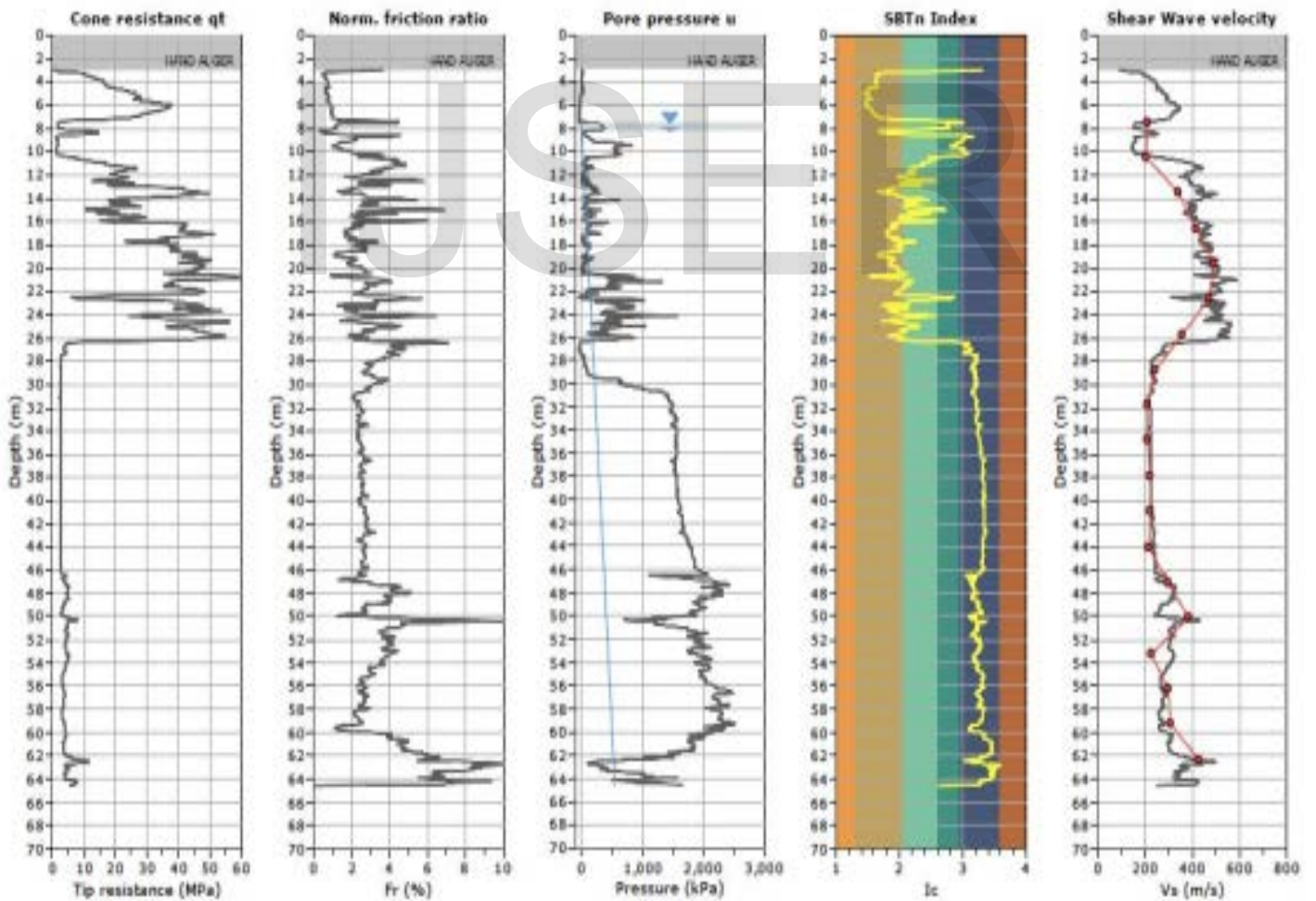


Figure (1) Cone Penetration Test (CPT): a) Test Overview, b) Output Example (after Paul W. Mayne and Jon M. Williams (2007))

2 (GP) & (MEP)

2.1 Genetic programming (GP)

(GP) is a direct application of genetic algorithm (GA) optimization technique on a population of mathematical formulas to generate the most fitting formula for certain given points in a hyper-space. Accordingly, (GP) may be described as Multivariable Regression Procedure. (Koza,1994)

(GP) is big title includes several techniques such as Linear GP, Cartesian GP, Compacted GP and many others. [2 ,11,18].

Classic (GP) procedure starts with randomly generating a population of mathematical formulas which are encoded in genetic form (chromosome form) and testing each formula using the training data set to calculate its fitness. Only the most fitting formulas (survivors) will be selected to generate the next cycle (or generation) using crossover and mutation operators, then the new population to be tested again to calculate their fitness and so on until accepted accuracy is achieved.

2.2 Multi Expression Programming (MEP)

(MEP) is a technique to automatic generation of computer programs. Accordingly, it could be used to generate fitting mathematical formulas for certain data set. MEP differentiates from classic (GP) techniques by encoding multiple solutions in the same chromosome. Same as classic (GP), crossover is applied in (MEP) using one Point Crossover technique, where one crossover point is randomly chosen and the parent chromosomes exchange the sequences at the right side of the crossover point. Also, both classic (GP) and (MEP) are sharing the same mutation technique where randomly selected gens (or symbols) are changed. Unlike classic (GP), the output of the (MEP) is a series of programming commands, if all these commands are mathematical expressions, then the output could be simplified in one mathematical expression just like classical (GP).

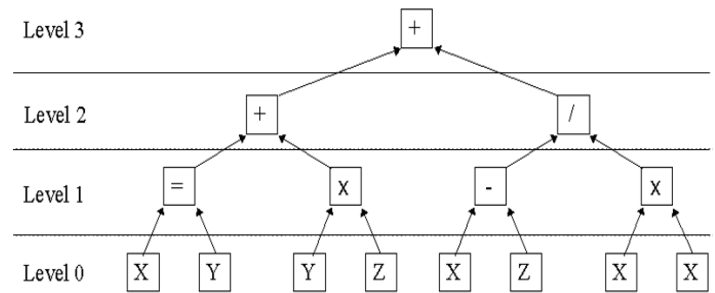
3 (GN7) & (MEPX)

3.1 (GN7) software

(GN7) is the 7th version of classic (GP) software which was developed by the author in (2004) in C++[2]. Figure (2) shows the encoding technique and the principal of tree levels to measure the complexity of the mathematical formula. It is clear that complex of the formulas needs more levels to represent it than simple ones. As shown in Figure (2). The chromosome consists of two parts, "operators" and "variables". The "operators" part contains the entire tree except the level 0 and has $(2^{No. of levels - 1})$ genes. The "variables" part contains only the level 0 of the tree and has $(2^{No of levels})$ genes. Therefore, the total number of genes in the chromosome is $(2^{No. of levels + 1})$ genes [2].

(GN7) supports eight operators which are (=, +, -, x, /, X^y, e[^], Ln) and support up to 7 levels of complexity. Regarding crossover procedure, it doesn't support the classic one-point crossover technique, instated, it supports random crossover technique which was proposed by author, 2004 [2] to generate the new chromosomes by randomly selecting each gene from similar surviving chromosomes as shown from figure (3). Mutation is applied by replacing some randomly selected genes with random operator (in the "operators" part) or variable (in "variables" part). Since most mathematical formula have con-

stant values, hence variables with constant values are used to present those constants. Usually, the following set of constants is used (1, 3, 5, 7 and 11). (GN7) uses the sum of squared errors (SSR) method to measure the fitness.



The above tree representing the formula :

$$X + YZ + \frac{X-Z}{X^2}$$

The genetic representation (as a chromosome) is:

(+ + / = x - x X Y Y Z X Z X X)
Operators part Variables part

Figure (2) Mathematical and Genetic Representation of Binary Tree (after A. Ebid 2004)

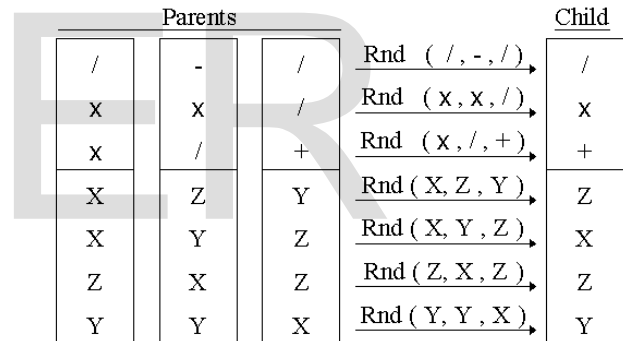


Figure (3) Random Crossover Technique (after A. Ebid 2004)

3.2 (MEPX) software

(MEPX) is free and open source software that uses (MEP) technique. This project started in 2001 and the first end-user for windows is released in 2015. Unlike (GN7), current version of (MEPX) has a graphical user interface (GUI). Both source code and compiled software could be freely downloaded from <http://www.mepx.org>. The software is easy to learn and offers many options to control the searching process as shown in figure (4), these options could be summarized in the following points:

- Three types of problems (regression, binary classification and multi-class classification)
- Two methods to measure error (mean absolute error and mean squared error)
- 26 different mathematical, logical, statistical and trigonometrical operators.
- Two methods of crossover (uniform and one point crossover)
- Two methods to generate constants (user defined and automatically generated)

- Code length, is the number of genes on each chromosome, it is a measurement for the complexity of the solution which is equivalent to number of levels in (GN7).

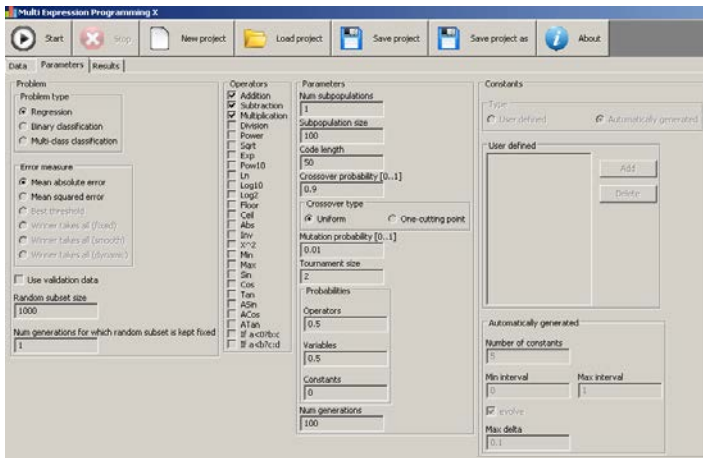


Figure (4) screenshot of (GUI) of (MEPX) software

3.3 Comparison Bases

In order to fairly compare the results of the two programs, the following points were considered:

- Using same set of variables, liquid limit (L.L), plastic limit (P.L), plasticity index (P.I), water content (wc) and unit weight of clay (γ).
- Using same constant values (1,3,5,7,11)
- Using the same training and validation data sets
- Using the same population size
- Using same number of generations
- Using same method to measure error (SSR)
- Using same complexity level (code length)
- Since the output should be mathematical formula, only mathematical operators were used in (MEPX)
- Unaccepted too complicated expressions such as multi-power (x^(y^z)) and multi logarithms (log(log(x))) were eliminated from both programs.
- For the best fitting formula of each trial, its accuracy was determine using equation (2), the predicted values of (Nk) were plotted against the experimental ones and the coefficient of determination (R²) was determined.

$$Accuracy (\%) = 100 - \sum \left| \frac{Nk_{cal} - Nk_{exp}}{Nk_{exp}} \right| \times \frac{100}{N_{rec}} \quad \dots(2)$$

4 PREDICTION OF (Nk) USING (GN7)

Four trials were carried out using (GN7) to predict the value of (Nk) factor using the training data set as follows:

- 1st trial had only two levels of complexity (chromosome length is 8 genes), Population size was 5000 chromosome, number of generations was 50 and the best formula was equation (3)

$$Nk = 27.3 - \frac{3.6 \times L.L}{P.L} \quad \dots(3)$$

- 2nd trial had three levels of complexity (chromosome length is 16 genes), Population size was 10000 chromosome, number of generations was 50 and the best formula was equation (4)

$$Nk = 1.16 \times \left[\ln(P.I - \gamma) \frac{12P.L}{L.L} \right] - 2.56 \quad \dots(4)$$

- 3rd trial had four levels of complexity (chromosome length is 32 genes), Population size was 20000 chromosome, number of generations was 50 and the best formula was equation (5)

$$Nk = 1.11 \times \left[\frac{21 + P.L^2}{L.L} + \frac{20}{\ln(P.L)} \right] - 1.79 \quad \dots(5)$$

- 4th trial had five levels of complexity (chromosome length is 64 genes), Population size was 40000 chromosome, number of generations was 50 and the best formula was equation (6)

$$Nk = 1.3 \times \left[\frac{P.L + (5/\gamma) + 3}{\ln(4 + 0.14PI)} - \ln(P.I - 2\gamma)(\ln(L.L) - 5) \right] - 5.19 \quad \dots(6)$$

Accuracies and coefficient of determination (R²) of training and validations sets for each one of the four trials are summarized in table (1). Figure (5) represent the correlation between the predicted (Nk) values using the equations (3),(4),(5),(6) and the measured ones.

TABLE (1): SUMMARY OF ACCURACIES AND (R²) VALUES FOR EQUATIONS (3),(4),(5),(6)

Trial No.	No. of Levels	Proposed Formula	Accuracy %			R ²		
			Training	Validation	Total	Training	Validation	Total
1	2	Eq. (3)	93	95	94	0.72	0.71	0.71
2	3	Eq. (4)	96	97	96	0.87	0.89	0.87
3	4	Eq. (5)	96	96	96	0.82	0.88	0.84
4	5	Eq. (6)	96	97	97	0.91	0.88	0.87

The following points could be noted from table (1):

- Accuracies of all proposed formulas are ranged between 93% to 97%, while (R²) values are ranged between 0.71 to 0.91 which indicates good fitting
- The enhancement in fitting between equations (4),(5),(6) is negligible, on other hand, the remarkable complexity difference between them makes equation (4) more favorable than the others.
- None of the four proposed formulas contains water content (wc) which indicates that (Nk) doesn't depend on it.

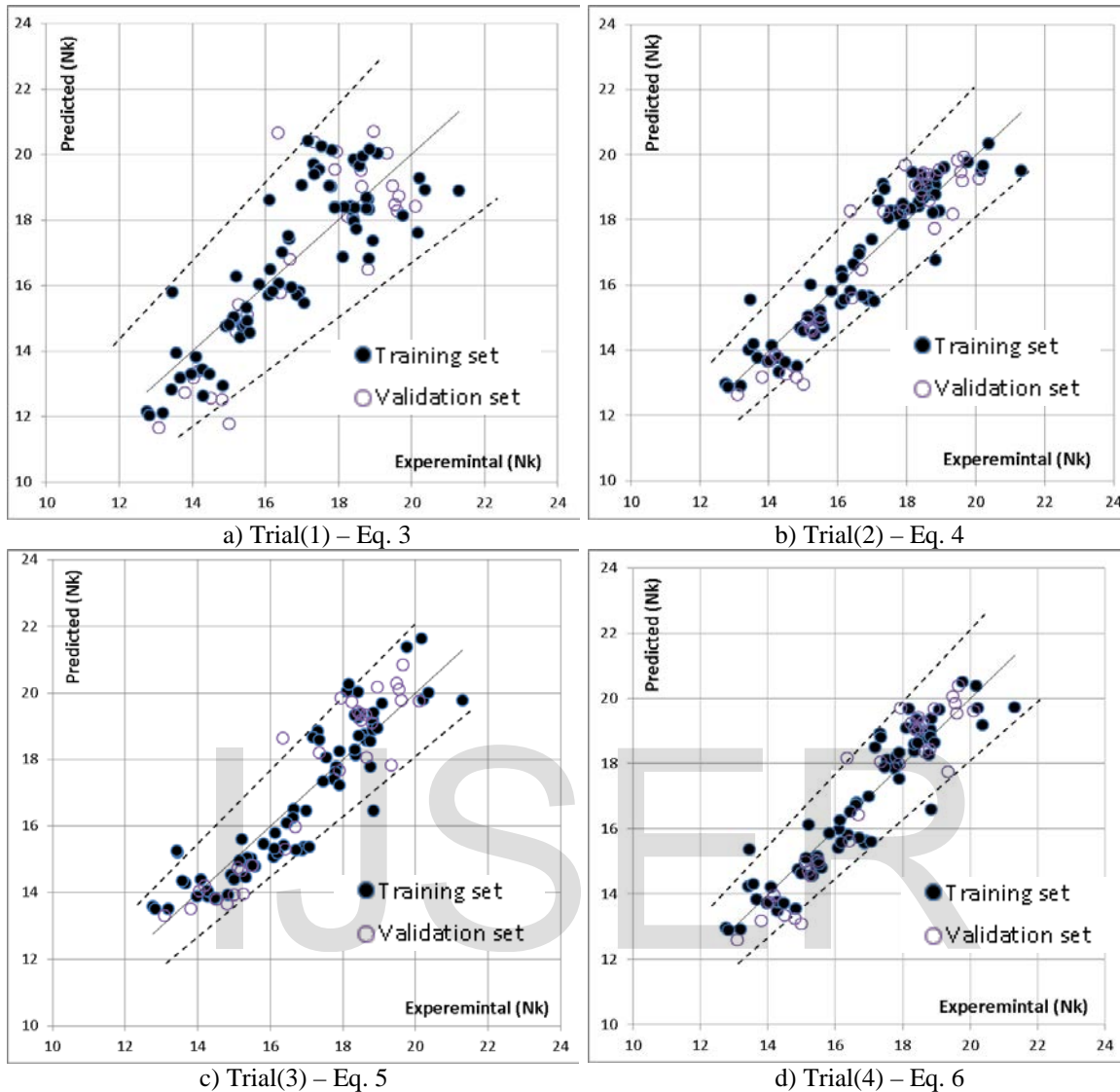


Figure (5) Relation between the Predicted and Measured (Nk) values for Developed Correlations using (GN7)

5 PREDICTION OF (Nk) USING (MEPX)

Four equivalent trials were carried out using (MEPX) to predict the value of (Nk) factor using the training data set as follows:

- 1st trial had chromosome length of 8 genes, Population size was 5000 chromosome, number of generations was 50 and the best formula was equation (7)

$$Nk = \frac{11L.L - 55}{P.I} \quad \dots(7)$$

- 2nd trial had chromosome length is 16 genes, Population size was 10000 chromosome, number of generations was 50 and the best formula was equation (8)

$$Nk = \frac{11}{11 + P.I} [11 + P.L + P.I + \ln(P.I)] \quad \dots(8)$$

- 3rd trial had chromosome length is 32 genes, Population size was 20000 chromosome, number of generations was 50 and the best formula was equation (9)

$$Nk = \frac{7 / P.I}{\ln(7 / P.I)} + \frac{7}{P.I} + [(1.6 + \ln(P.I))(7 - \ln(P.I))] \quad \dots(9)$$

- 4th trial had chromosome length is 64 genes, Population size was 40000 chromosome, number of generations was 50 and the best formula was equation (10)

$$Nk = \frac{11L.L + 11\ln(5\gamma)}{P.I + \frac{(5\gamma)^2}{P.I - 11}} \quad \dots(10)$$

Accuracies and coefficient of determination (R^2) of training and validations sets for each one of the four trials are summarized in table (2). Figure (6) represent the correlation between the predicted (Nk) values using the equations (7),(8),(9),(10) and the measured ones.

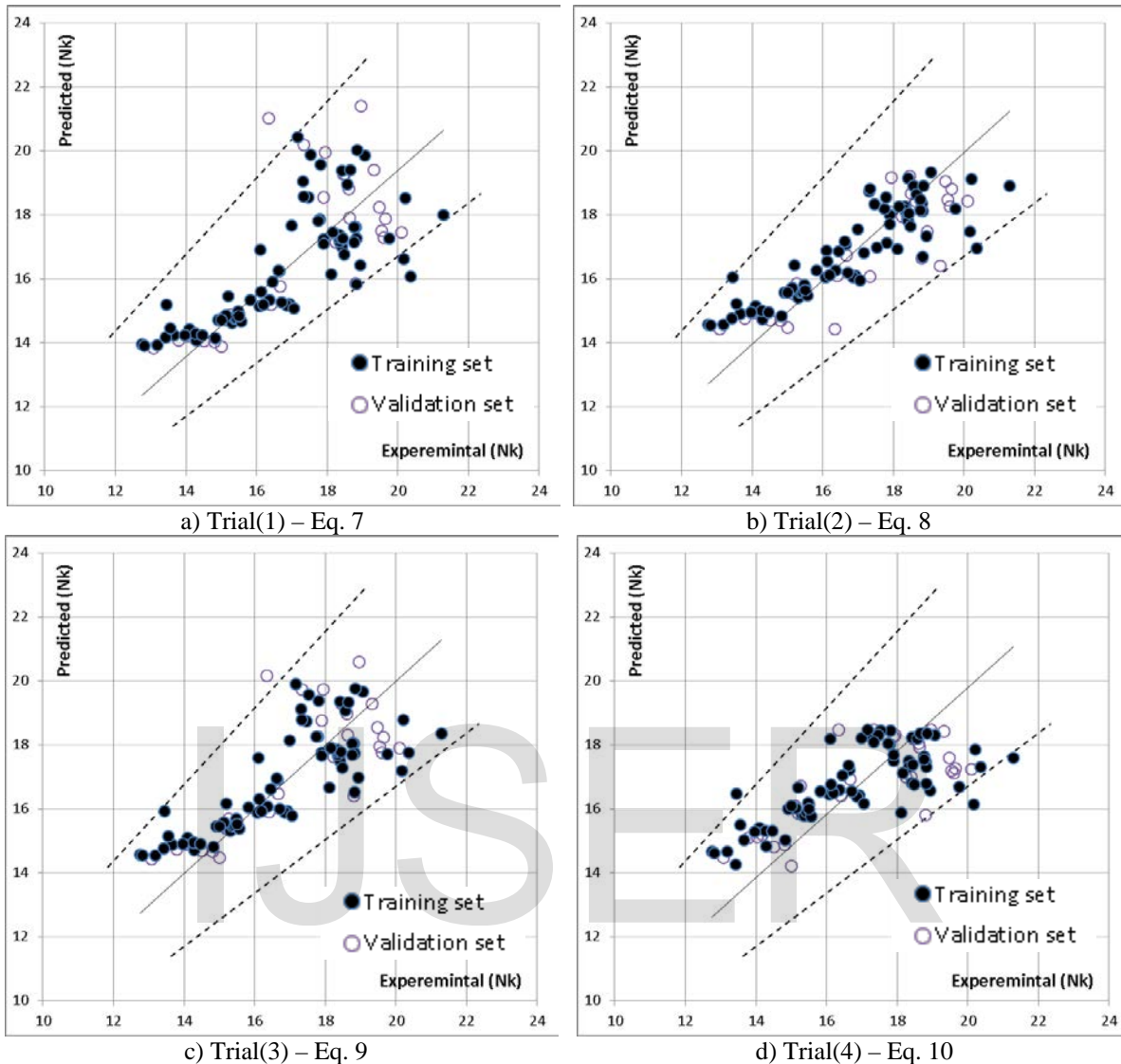


Figure (6) Relation between the Predicted and Measured (Nk) values for Developed Correlations using (MEPX)

TABLE (2): SUMMARY OF ACCURACIES AND (R^2) VALUES FOR EQUATIONS (7),(8),(9),(10)

Trial No.	Code Length	Proposed Formula	Accuracy %			R^2		
			Training	Validation	Total	Training	Validation	Total
1	8	Eq. (7)	93	93	93	0.44	0.54	0.52
2	16	Eq. (8)	94	94	94	0.53	0.63	0.58
3	32	Eq. (9)	93	94	94	0.53	0.58	0.56
4	64	Eq. (10)	95	95	95	0.63	0.76	0.67

The following points could be noted from table (2):

- Accuracies of all proposed formulas are ranged between 93% to 95%, while (R^2) values are ranged between 0.44 to 0.76 which indicates fair fitting
- Equation (10) is the most accurate one and the only one that used unit weight (γ) variable which indicates the importance and the impact of this variable.
- None of the four proposed formulas contains water content (w_c) which indicates that (Nk) doesn't depend on it.

6 CONCLUSIONS

By comparing the summarized results in tables (1),(2), the following points could be noted:

- Although equation (4) is not the most accurate proposed formula, but considering its simplicity, it is still the most favorable one.

- Formulas contains unit weight (γ) variable are more accurate than others regardless the used software, this reflects the high correlations between (N_k) and (γ).
- None of the proposed formulas regardless the used software contains water content (w_c) which indicates that (N_k) doesn't depend on it.
- Although proposed formulas from (GN7) & (MEPX) almost have same accuracies for same level of complexity (code length), but coefficients of determination (R^2) of (GN7) formulas are higher than those of (MEPX) which indicates the random crossover technique of (GN7) is more efficient than the one point crossover technique of (MEPX).
- It is also noted that (MEPX) is almost twice faster than (GN7), this may be because (MEPX) uses multi threads.

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APPENDIX: DATA SETS

Validation data set

L.L. (%)	P.L. (%)	P.I. (%)	wc (%)	γ (t/m ³)	N_k
60	26	34	46	1.7	18.6
134	33	101	69	1.6	14.8
95	30	65	66	1.6	16.4
83	28	54	56	1.7	16.7
109	31	78	64	1.6	15.2
136	33	103	69	1.6	14.5
40	21	19	41	1.8	17.3
82	34	47	60	1.6	19.7
86	34	52	58	1.8	18.4
58	27	31	59	1.8	18.6
84	34	50	59	1.6	19.6
51	26	26	57	1.7	17.9
118	40	78	68	1.5	18.8
53	26	27	49	1.8	18.5
128	32	96	57	1.7	13.8
84	26	58	67	1.6	15.3
146	34	112	57	1.7	13.1
43	24	20	40	1.7	18.9
49	23	26	43	1.8	17.9
54	26	28	62	1.7	18.5
72	32	40	60	1.7	19.5
101	30	71	59	1.6	15.5
128	33	95	66	1.6	14.0
81	33	48	56	1.6	20.1
82	34	49	55	1.6	19.6
102	30	72	74	1.6	15.1
87	34	53	36	1.8	18.2
43	21	22	33	1.9	19.3
38	21	17	36	1.8	16.3
126	33	93	72	1.6	14.2
156	36	120	69	1.6	15.0

Training data set

L.L. (%)	P.L. (%)	P.I. (%)	wc (%)	Y (t/m ³)	Nk
94	30	64	53	1.7	16.9
132	34	98	57	1.7	13.7
93	29	63	36	1.8	13.4
109	31	79	66	1.6	15.3
136	34	103	83	1.5	14.3
76	28	48	35	1.8	16.6
100	30	70	47	1.7	15.5
90	29	61	63	1.6	16.4
141	34	107	56	1.7	12.7
92	36	56	59	1.9	18.4
41	21	20	41	1.7	17.8
72	27	45	52	1.7	16.6
73	31	43	58	1.8	18.8
93	35	58	57	1.7	18.5
97	38	59	61	1.6	19.8
80	28	52	52	1.7	16.5
140	33	107	59	1.6	13.2
142	34	108	59	1.6	12.8
95	30	66	57	1.7	16.9
120	32	88	59	1.6	14.1
53	26	27	60	1.7	18.4
72	29	43	64	1.7	18.3
112	42	71	68	1.6	20.2
41	21	20	49	1.7	17.5
53	25	28	49	1.7	18.6
72	29	42	58	1.6	18.3
53	25	28	48	1.8	17.3
48	24	24	52	1.7	18.6
68	29	40	51	1.7	18.8
49	22	28	26	1.8	17.0
51	26	26	46	1.7	19.1
65	29	35	47	1.7	20.2
72	31	41	59	1.6	21.3
131	33	98	62	1.6	14.8
41	22	20	44	1.7	17.2
48	25	24	49	1.7	18.8
117	41	77	58	1.6	18.1
77	31	46	45	1.7	18.8
97	35	62	57	1.6	18.9
93	29	64	59	1.6	16.1
111	32	79	72	1.6	15.4
104	30	74	63	1.6	14.9
91	29	62	70	1.6	16.7
92	29	63	70	1.6	16.2
107	31	76	76	1.7	15.4
57	25	32	67	1.6	17.8
78	32	46	37	1.8	18.3
157	39	118	54	1.7	13.4
72	29	43	38	1.8	17.9
75	30	45	37	1.8	18.4
85	34	50	36	1.8	18.2
56	24	31	41	1.7	17.8

70	28	41	66	1.6	18.8
48	20	28	44	1.8	16.1
65	27	39	33	1.9	17.9
87	30	57	37	1.8	18.8
48	22	25	50	1.6	17.5
56	26	31	47	1.7	17.3
73	31	46	38	1.8	20.4
122	32	90	50	1.7	14.3
88	29	59	67	1.5	15.2
104	31	73	63	1.6	15.1
86	29	57	69	1.6	16.1
111	32	80	69	1.6	15.6
122	32	90	71	1.6	14.5
101	31	70	73	1.6	17.1
105	31	74	55	1.7	15.5
91	29	62	69	1.6	15.8
123	32	91	68	1.6	14.0
101	29	72	62	1.6	15.0
117	32	86	70	1.6	13.6

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