



Journal of Applicable Chemistry

2018, 7 (6): 1829-1842
(International Peer Reviewed Journal)



New Chemistry News $\text{N}=\text{C}=\text{N}$	
New News of Chem (NNC)	ChemNewsNew (CNN)

Genetic expression in Omnimetrics	Information Source (is) Sci.direct.com (SD):
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Gene Expression Program	Books
Gene Expression Programming Ferreira, C	Mathematical Modeling by an Artificial Intelligence. 2nd Edition, 2006, Springer-Verlag, Germany
Gene Expression Programming Ferreira, C	Gene Expression Programming: Mathematical Modeling by an Artificial Intelligence, 2002, Online version
Gene Expression Programming: Mathematical Modeling by an Artificial Intelligence (Studies in Computational Intelligence) Candida Ferreira	Springer, Oct 14, 2014,

SAR/SPR	Gene Expression Prog.	GEP >> MLR	SI-01
Task		X: Descriptors	

<p>➔ Potential screening mechanism for a series of 1,4-dihydropyridine calcium channel antagonist</p>	<ul style="list-style-type: none"> ■ HOMO, HOMO energy; ■ MIC, Moment of inertia C; XYSR, XY ■ Shadow/XY Rectangle; YZSR, YZ ■ Shadow/YZ Rectangle; ■ MSA, Molecular surface area; ■ THCMD, Tot hybridization component of the molecular dipole 	<ul style="list-style-type: none"> ■ CODESSA ■ 600 descriptors ■ 45 compounds
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SXR	Gene Expression Prog.
<p>QSAR study of 1,4-dihydropyridine calcium channel antagonists based on gene expression programming</p>	<p>Bioorganic & Medicinal Chemistry 14(14)(2006) 4834 - 4841</p>
<p>Hong Zong Si and Tao Wang and Ke Jun Zhang and Zhi De Hu and Bo Tao Fan</p>	

SXR	Gene Expression Prog.	SI-02
Task	X	
<p>➔ Predict EC50 of nucleoside</p>	<p>Descriptors</p> <ul style="list-style-type: none"> ■ Constitutional, topological, geometrical, electrostatic ■ Quantum-chemical 	
<p>➔ Five descriptor model</p> <p>➔ GEP >SVM</p>	<p>Training CC : 0.91; ESS:0.41</p> <p>Test CC : 0.63; ESS:0.67</p>	
<p>Quantitative structure activity relationship study on EC50 of anti-HIV drugs</p>	<p>Chemomet. Intelligent Laboratory Systems, 90(1)(2008)15-24</p>	
<p>Hongzong Si and Shuping Yuan and Kejun Zhang and Aiping Fu and Yun-Bo Duan and Zhide Hu</p>		

SXR	Gene Expression Prog.
Task	Inference
<p>➔ QSAR</p> <p>➔ #compounds: 39</p>	<ul style="list-style-type: none"> ■ GEP >SVM
<p>QSAR Model for Prediction Capacity Factor of Molecular Imprinting Polymer Based on Gene Expression Programming</p>	<p>QSAR & Combinatorial Science Volume 26, Issue 1 First published: 29 January 2007</p>
<p>H. Z. Si, K. J. Zhang, , B. T. Fan</p>	

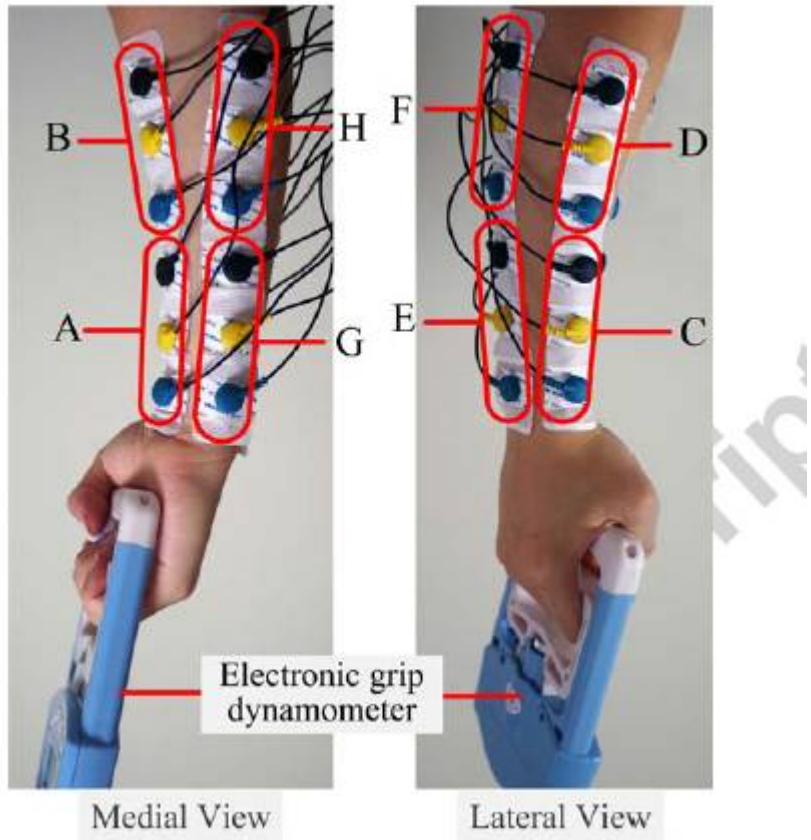
SXR	Gene Expression Prog.												
Task	X												
<p>➔ Insights into structural factors in design of new drug molecules</p> <p>➔ #Compounds : 47;</p> <p>Inhibitors 5-arylidene-2thioxoimidazolidin-4-ones derivatives</p>	<ul style="list-style-type: none"> ■ # Descriptors from CODESSA : 384 ■ # Selected : 5 ■ Response : IC₅₀ (μM) values <table border="0" style="width: 100%; border-collapse: collapse;"> <tr> <td align="center" colspan="2">-----</td> </tr> <tr> <td align="center">Method</td> <td align="center">R2</td> </tr> <tr> <td align="center" colspan="2">-----</td> </tr> <tr> <td align="center">Heuristic</td> <td align="center">0.82</td> </tr> <tr> <td align="center">GEP</td> <td align="center">0.92</td> </tr> <tr> <td align="center" colspan="2">.</td> </tr> </table>	-----		Method	R2	-----		Heuristic	0.82	GEP	0.92	.	

Method	R2												

Heuristic	0.82												
GEP	0.92												
.													

SXR		Gene Expression Prog.
Task		X
<p>➔ EC50 prediction</p>	<p>➔ HIV-1 Inhibitors</p> <p>➔ O-(2-phthalimidoethyl)-N-substituted thiocarbamates and their ring-opened congeners</p>	<p>➔ Molecular descriptors</p> <ul style="list-style-type: none"> ○ Radial distribution function (RDF)
<p>Methods</p> <ul style="list-style-type: none"> ■ Improved GEP ■ GEP, MC_GEP IGEP ■ SVM ■ MLR 	<p>➔ Software: Java</p> <p>➔ Hardware Intel(R) Pentium(R) 4 PC (3.20 GHz, 1.00GB RAM).</p>	<p>➔ IGEP >> MLR, SVM, GEP MC_GEP.</p>
<p>Improved gene expression programming and its application to QSAR</p>		<p>2010 Sixth International Conference on Natural Computation (ICNC 2010) 4057-4061</p>
<p>Weizhong Fu, Yuntao Zhang, Zhengjun Cheng</p>		

SXR		Gene Expression Prog.
Task		X
<p>➔ To predict depletion percentage of glutathione (DPG) compounds</p>		<ul style="list-style-type: none"> ■ Structural descriptors <ul style="list-style-type: none"> ○ Constitutional, topological, geometrical ■ Electrostatic ■ Quantum-chemical
<p>➔ GEP method produced a nonlinear and five-descriptor quantitative model</p> <p>➔ mean error 10.52</p> <p>➔ correlation coefficient 0.94</p>		<ul style="list-style-type: none"> ■ GEP prediction >> [experimental; heuristic method]
<p>Quantitative structure activity relationship model for predicting the depletion percentage of skin allergic chemical substances of glutathione</p>		<p>Analytica Chimica Acta 591(2)(2007)255-264</p>
<p>Hongzong Si and Tao Wang and Kejun Zhang and Yun-Bo Duan and Shuping Yuan and Aiping Fu and Zhide Hu</p>		

Biology muscle forces	Gene Expression Prog.	SI-03
<p>➔ Task : Precise prediction of muscle forces for hand gesture recognition</p>  <p>Hand posture and electrodes placements (on one subject) of 8 channels (A-H) of sEMG sensors</p>		<ul style="list-style-type: none"> ■ Subjects: 6 healthy ■ 4 levels of maximum % of voluntary contraction ■ 10 features of sEMG time domain <p>Method : MLP-BP-SVM</p>
Surface EMG based handgrip force predictions using gene expression programming		Neurocomputing", 207(2016)568-579 doi.org/10.1016/j.neucom.2016.05.038
Zhongliang Yang and Yumiao Chen and Zhichuan Tang and Jianping Wang		

SXR	Gene Expression Prog.	SI-04
Quantitative structure–activity relationship and molecular docking studies on designing inhibitors of the perforin		Chemical Biology & Drug Design 90(4)(2017) doi:10.1111/cbdd.12975
Fucheng Song, Lianhua Cui, Jinmei Piao, Hui Liang, Yunbo Duan, Honglin Zhai		

Bio. inhibition	Gene Expression,Prog.	SI-05
Prediction on the Inhibition Ratio of Pyrrolidine Derivatives on Matrix Metalloproteinase Based on Gene Expression Programming		BioMed Research International; 2014:1-8. dx.doi.org/10.1155/2014/210672
Li Y.Q., You C.R., Jia B.X., Si H.Z., Yao X.J.		

Bio. Enzymes	Gene Expression Prog.	SI-06
<p>➔ Task: To predict Km of 47 human dopamine sulfotransferases</p>		
<p>Study of Human Dopamine Sulfotransferases Based on Gene Expression Programming</p>		<p>Chem Biol Drug Des; 78.. (2011) 370–377. doi.org/10.1111/j.1747-0285.2011.01155.x</p>
<p>Si H.Z., Zhao J.G., Cui L.H., Lian N., Feng H.L., Duan Y.B., Hu Z.D</p>		

Evapotranspiration	Gene Expression Prog.
	X
<p>Task To predict long-term monthly reference evapotranspiration (ET0)</p> <p>Methods: MLP-NN, ANFIS-GP, ANFIS-SC</p>	<p>Data: 50 stations in Iran</p> <ul style="list-style-type: none"> ■ Periodicity component, ■ Station latitude, longitude, altitude inputs
<p>Long-term monthly evapotranspiration modeling by several data-driven methods without climatic data</p>	<p>Computers and Electronics in Agriculture 115(2015)66-77</p>
<p>Ozgur Kisi, Hadi Sanikhani, Mohammad Zounemat-Kermani, Faegheh Niazi</p>	

Performance of detention dams	Gene Expression Prog.
Task	Methods
<p>➔ Trap efficiency (TE) of detention dams</p>	<ul style="list-style-type: none"> ■ Multivariate adaptive regression splines (MARS) ■ Group method of data handling (GMDH) ■ Gene expression programming (GEP) ■ MARS (more accurate)
<p>Physical and numerical modeling of performance of detention dams</p>	<p>Journal of Hydrology (2017) doi.org/10.1016/j.jhydrol.2017.01.018</p>
<p>Abbas Parsaie and Hazi Mohammad Azamathulla and Amir Hamzeh Haghiabi</p>	

Agriculture. Irrigation	Gene Expression Prog.
Task	X
<p>Infiltrated water volume (Z) under furrow irrigation</p> <p>➔ GEP resulted in an explicit equation for estimation of the Z</p>	<ul style="list-style-type: none"> ■ Inflow rate ■ Furrow length ■ Waterfront advance time at the end of the furrow ■ Infiltration opportunity time ■ Cross-sectional area of the inflow
Agriculture. Irrigation. furrow	Gene Expression Prog.
<p>A new predictive model for furrow irrigation infiltration using gene expression programming</p>	<p>Computers and Electronics in Agriculture 122(2016)168-175</p>
<p>Mohamed A. Yassin and A.A. Alazba and Mohamed A. Mattar</p>	

Distribution Networks. Water	Gene Expression Prog.
Gene Expression Programming Algorithms for Optimization of Water Distribution Networks	Procedia Engineering, 37(2012) 359-364 doi.org/10.1016/j.proeng.2012.04.253
Huanhuan Wang and Shuming Liu and Fanlin Meng and Mingming Li	

Distribution Networks. Water	Gene Expression Prog.
Task	
➔ Optimization of Water Distribution Networks	<ul style="list-style-type: none"> ■ Methods: GA ACO SA GEP ■ Hanoi benchmark network, result of 6.081 million costs and 15,000 evaluations is combined with that obtained with GA and SA
Modeling of local scour depth downstream hydraulic structures in trapezoidal channel using GEP and ANNs	Ain Shams Engineering Journal 4(4)(2013)717-722 doi.org/10.1016/j.asej.2013.04.005
Yasser Abdallah Mohamed Moussa	

Soil.Piles	Gene Expression Prog.	SI-07
Predicting axial capacity of driven piles in cohesive soils using intelligent computing	Engineering Applications of Artificial Intelligence 25(3)(2012) 618-627 doi.org/10.1016/j.engappai.2011.08.009	
Iyad Alkroosh and Hamid Nikraz		

Soil. Pile dynamic capacity	Gene Expression Prog.	SI-08
Predicting pile dynamic capacity via application of an evolutionary algorithm	Soils and Foundations, 54(2)(2014)233-244 doi.org/10.1016/j.sandf.2014.02.013	
I. Alkroosh and H. Nikraz		

Fault detection	Gene Expression Prog.
Task	Methods
<ul style="list-style-type: none"> ➔ Fault detection of centrifugal pump and isolation in rotating machinery ➔ Classification accuracy <ul style="list-style-type: none"> ○ Normal, bearing fault, impeller fault, seal fault, impeller and bearing fault 	<ul style="list-style-type: none"> ➔ SVM, Wavelet-GEP ➔ Proximal PSVM ■ Decision tree algorithm is used to select the features <p style="text-align: center;">Inference</p> <ul style="list-style-type: none"> ■ [GEP == SVM] >> classifiers [PSVM; Wavelet-GEP]
Soft computing approach to fault diagnosis of centrifugal pump	Applied Soft Computing 2(5)(2012) 1568-4946 doi.org/10.1016/j.asoc.2011.12.009
N.R. Sakthivel and Binoy.B.Nair and V. Sugumaran	

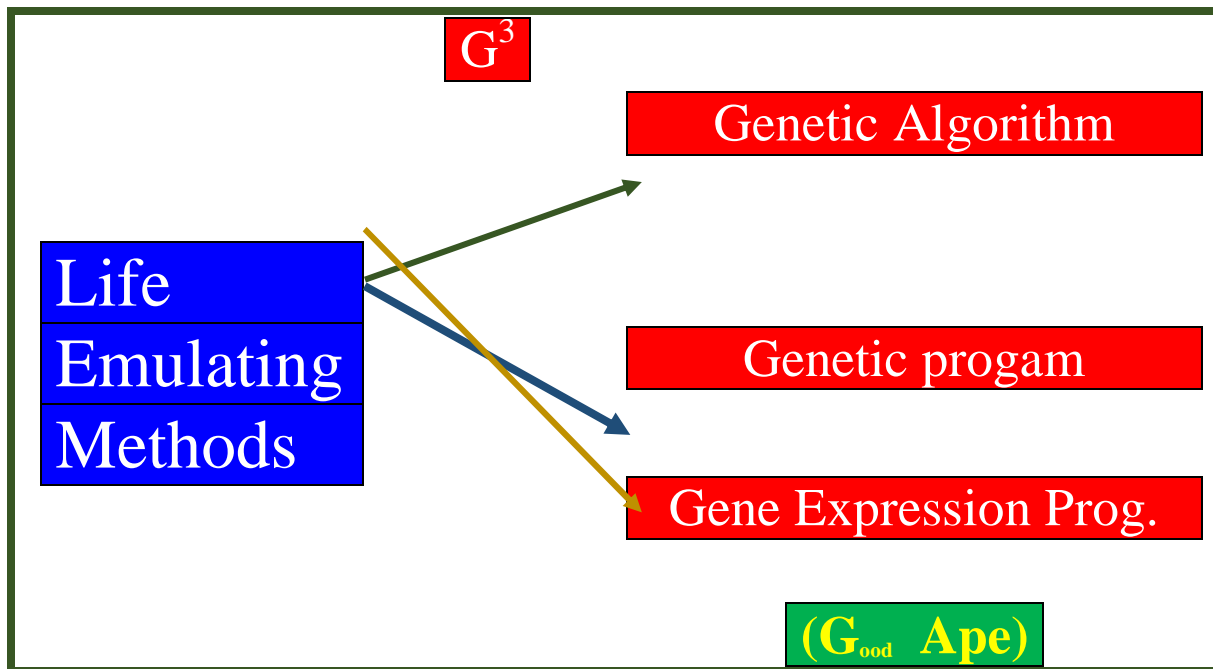
Cutting force	Gene Expression Prog.
A new approach for predicting and collaborative evaluating the cutting force in face milling based on gene expression programming	Journal of Network and Computer Applications 36(6)(2013)15 doi.org/10.1016/j.jnca.2013.02.00440-1550
Yang Yang and Xinyu Li and Liang Gao and Xinyu Shao	

Eng.Civil	Gene Expression Prog.
Soft computing for modeling punching shear of reinforced concrete flat slabs	Ain Shams Engineering Journal 6(2)(2015)439-448 doi.org/10.1016/j.asej.2014.12.001
Iyad Alkroosh and Hayder Ammash	

Eng.Civil. concrete	Gene Expression Prog.
Soft computing for modeling punching shear of reinforced concrete flat slabs	Ain Shams Engineering Journal 6(2)(2015)439-448
Iyad Alkroosh and Hayder Ammash	

Greek index	Gene Expression Prog.	SI-09
Modelling and trading the Greek stock market with gene expression and genetic programming algorithms.	Journal of Forecasting, 33(8), 596-610 doi:10.1002/for.2290	
Karathanasopoulos, A., Sermpinis, G., Laws, J., and Dunis, C		

TS.financial Frankfurt stock exchanges	Gene Expression Prog.
➔ New short-term financial forecasting	➔ Forecast RW MACD ARMA ➔ MLP RNN ➔ Higher Order NN ➔ GP GEP Trader Tool
Modelling and trading the London, New York and Frankfurt stock exchanges with a new gene expression programming trader tool.	Intelligent Systems in Accounting, Finance and Management, 24(1), (2016) 3-11. doi:10.1002/isaf.1401
Karathanasopoulos, A.	



Supplementary Information (SI)

SI-01: SXR

Heuristic (MLR) Method

$$\begin{aligned} \text{Log}(1/\text{IC}_{50}) = & 0.31 - 2.55\text{HOMOE} + 2.80 \\ & \times 10^2\text{MIC} + 7.07\text{XYSR} - 1.60 \\ & \times 10^{-1}\text{YZSR} - 3.04 \times 10^{-2}\text{MSA} \\ & - 1.16\text{THCMD} \end{aligned}$$

R^2	S^2
0:90	0:22

GEP

y =

$$\begin{aligned} & \sin\left(9.76 \times x_3 - x_6 - \frac{x_1}{x_4 - x_2} + x_2\right) \\ & + \sin(\sin(\sin(\sin((\sinh(\text{ceil}(\sqrt{x_5}))))))) \\ & + \sin\left(x_1 - \frac{\cos(x_5)}{f\left(\frac{x_2}{x_6} - x_3\right)}\right) \sin(\cos(\sqrt{x_5})) + e^{x^3} \\ & + p\left(\ln_{x_5}\left(\lg\left(\frac{f(x_4)}{x_6}\right)\right)\right) + x_2 + p\left(\frac{\sinh(x_2)}{\sin\left(\frac{1}{\sin(x_5)}\right)}\right) \\ & + \sin(\sin(x_1)) \end{aligned}$$

R^2	S^2
0:80	0:43

SI-02: SXR

186th generation (GEP)

$$y = \sin(x_3) \times \frac{1}{\sin((\cos(x_1 x_2 x_3) + \ln(x_3 + x_2 - \log_{10}(x_3))))} \times x_2$$

$$+ \sin\left(\tan(x_1) + \frac{1}{\sin(x_2^{x_4})} + x_4\right) + x_1 + (x_2 - x_3) \times x_3$$

$$+ \frac{\log_{10}^{(x_1)}}{x_4 \times (\sqrt{\tan(x_2)} \sin(\frac{x_4}{x_3}) - \frac{1}{\sin(x_1 - x_2)} + x_5)}$$

$$+ (x_1 - x_2) \times \frac{\tan(x_1 x_2 x_3) - x_4}{10^{\sin(\frac{1}{x_2})}}$$

Variable	Descriptor
X1	ABOOA
X2	MBOHA
X3	MTICB
X4	PRCS
X5	HACA-2/TMSA

Parameter names	Values
Number of generations	1000
Population sizes	50
Number of fitting cases	37
Function set	{+, -, *, /, ^}
Gene head size	15
Number of genes	8
Linking function	+
Mutation rate	0.044
1-Point recombination rate	0.3
2-Point recombination rate	0.3
Gene recombination rate	0.1
IS transposition rate	0.1
IS elements length	1,2,3
RIS transposition rate	0.1
RIS elements length	1,2,3
Gene transposition rate	0.1
Selection range	100
Precision	0.01

R ²	S ²
0.91	0.41

SI-03

EMG based handgrip force predictions

x1	RMSmax	channel B
x2	RMSmean	channel B
x8	RMSmean	channel G
x9	RMSmax	channel H

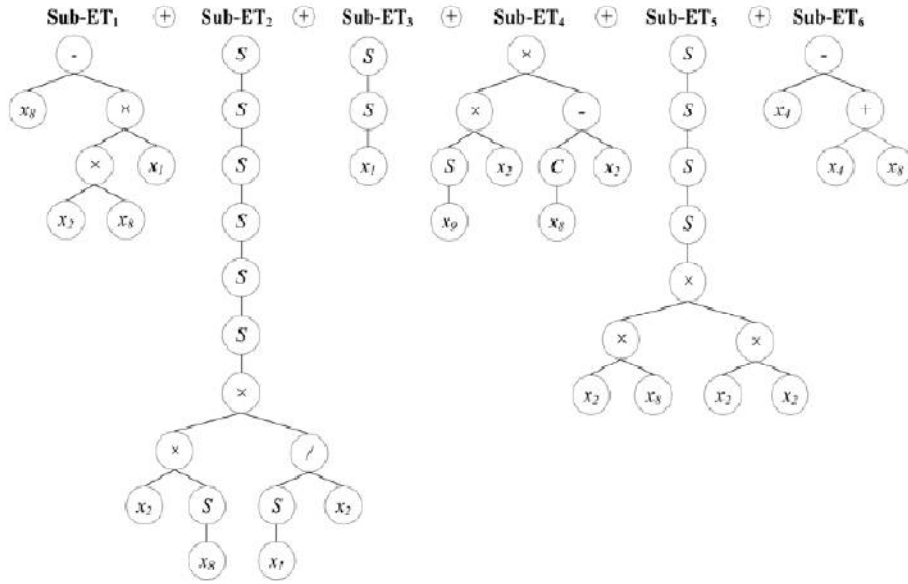
Number of Chromosomes	200
Function Set F	{+; -; *; /; ^; S; C}
Terminal	T = [x1x10]
Number of Genes,	6
Head Size	15
Gene Size	31
Linking Function	Addition
Fitness Function	Error Type MSE
Mutation Rate	0.044
Inversion Rate	0.05
IS/RIS/Gene	0.05
Transposition Rate	
One-Point/ Two-Point	0.2
Recombination Rate	
Gene Recombination Rate	0.05

Data Model	RMSE	CC
Training set		
GEP	0.0233	0.9965
BPNN	0.0763	0.9664
SVM	0.5074	0.8017
Test set		
GEP	0.0476	0.9893
BPNN	0.1318	0.9278
SVM	0.4379	0.7750

GEP Model

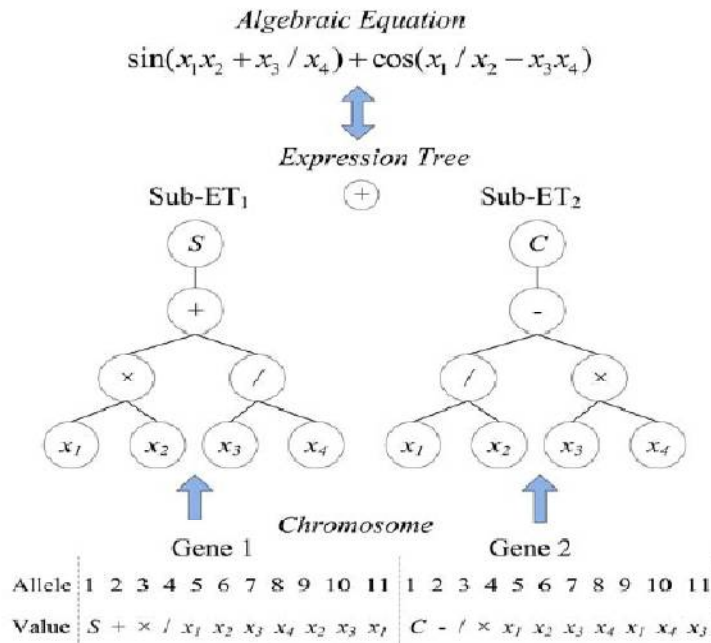
$$F(x) = \sin(\sin(\sin(\sin(\sin(\sin(\sin(x_1) \sin(x_8))))))) + \sin(\sin(x_1)) + x_2 \sin(x_9)(\cos(x_8) - x_2) + \sin(\sin(\sin(\sin(x_3 2x_8)))) - x_1 x_2 x_8$$

Expression Tree:



Example

Decoding process of individual with one chromosome



SI-04

Heuristic (MLR) method

IC50=
406
- 356.38 * MAH
+ 9.4125 * ACIC
-16.65 * AVO
+ 8809.4 * MERIN
-53.197 * ASIC (2)

R ²	0.82
S ²	2.74
CV	0.70

Compounds: 5-Arylidene-2thioxoimidazolidin-4-ones
CODESSA : 384 descriptors

GEP Model

$$IC_{50} = \frac{\tan\left(\log\left(\frac{\chi_3 \times \chi_4}{\chi_1 + \chi_4}\right)\right)}{\chi_1 + \chi_4} + \frac{2 \times \tan(\sin \chi_2) \times \chi_2 \times \log\left(\frac{\chi_1}{\chi_4}\right)}{\chi_4} + \frac{\sin\left(\tan\left(\text{aps log i}\left(\frac{\chi_4}{\chi_3}\right)\right)\right) \times \chi_4}{\text{aps log i} \chi_0} + \tan\left(\log\left(\frac{\chi_1 \times \chi_3}{\chi_2}\right)\right) + \frac{1}{\sin(\sin(\log(\tan(\tan \chi_0))))} + \frac{\text{aps log i}\left(\tan\left(\tan\left(\frac{\chi_0 \times \chi_2}{\chi_4}\right)\right)\right)}{2 \times \chi_4} + \chi_1 + 1$$

SI-05

Heuristic (MLR) method

$\log(IC_{50}) = -1.9501 \times 10^2 + 2.4570 \text{ LUMO}$
 $- 3.6715 \text{ MRECO} - 2.0681 \times 10^{-1} \text{ KSIND}$
 $- 7.0757 \text{ ZX} + 8.4804 \times 10^{-1} \text{ MASEOAT.}$

R ²	S ²
0.93	0.23

GEP Model

```
double dblTemp = 0.0,
dblTemp = sin (tan((tan (d[1])/sin (d[4])))),
dblTemp += sin (sin(((tan (d[1])/d[0])-d[3]))),
dblTemp += d[0],
dblTemp += pow (d[4],[pow (d[4],d[0])/d[2]]),
dblTemp += sin (sqrt((d[2]-tan (sin(tan((d[2]*-
7.653931))))))),
```

Training

R ²	0.94
S ²	0.12

D[0]	Intercept	
d(1)	LUMO	Energy
d(1)	MRECO	Min resonance energy for a C-O bond
d(2)	KSIND	Kier shape index (order 3)
d(3)	ZX and	Shadow/ZX Rectangle
d(4)	MASEOAT	Min atomic state energy for a O atom

SI-06

Linear SXR model

$$\log(1/Km) = -3.04 - 20.40MIA + 66.10AERIC - 35.40RNTB + 11.30RNCG + 226.00(HDSA-1) - 209.00HBCA$$

R ²	0.88
S ²	0.12
CV	0.83

GEP Model

$$\begin{aligned} \log(1/Km) = & \left((RNCG - HDSA1) \times MIA - \frac{MIA}{RNCG} \right) \\ & \times (RNTB + RNCG) + \frac{AERIC}{RNCG} - \frac{AERIC}{MIA} - MIA \\ & - 2AERIC - RNTB + \frac{4MIA}{2RNTB - RNCG} + HDSA1 \\ & \times (2RNCG - MIA) \times AERIC + RNCG \times AERIC \\ & \times (2HDSA1 + RNTB - MIA) \end{aligned}$$

R ²	0.91
S ²	0.096

MIA	Moment of inertia A
AERIC	Avg. electroph. react. index for a C atom
RNTB	Relative number of triple bonds
RNCG	Relative negative charge (QMNEG / QTMINUS)
HDSA-1	HA-dependent HDSA-1
HBCA	HBCA H-bonding charged surface area

Training samples
Test samples 13

SI-07

$$\begin{aligned} Q_p = & \bar{f}_s(2 + Mat^{(2)}) + D_{eq} \left(\frac{\bar{f}_s}{Mat} \right)^{1/3} + L(L + 4.74\bar{q}_{c-tip}) - \left(\frac{52^{(3)}}{D_{eq}} \right) \\ & - E(1 + Mat) + \bar{q}_{c-shaft}(1 + Ln(D_{eq})) \end{aligned}$$

#chromosome	22
s	
#genes	3
Head size	10
Function set	p , Power, Ln : (natural logarithm)
Fitness function	MeanSquaredError
Linking function	p
Mutation rate	0.05
Recombination rate	0.3

SI-08

$$Q_{sp} = (N_s)^2 \sqrt[3]{m_1} + \sqrt{E(N_b^{m_2})^3} + \frac{l/d}{m_3} - 0.034$$

$$m_1 = (l/d) \exp^3 \sqrt{N_b}$$

$$m_2 = 7.5E + S - (l/d)$$

$$m_3 = \exp(l/d) + \exp(s) - (l/d) + 2E$$

Data sets: 24

#chromosome	22
s	
#genes	3
Head size	9
Function set	p , Power, Exp
Fitness function	MeanSquaredError
Linking function	p
Mutation rate	0.06
Recombination rate	0.4

Qsp	Scaled predicted pile capacity;
Ns	Average of SPT blows along shaft;
Nb	Average of SPT blows within pile base;
l/d	Penetration ratio;
S	Setting;
E	Hammer energy

SI-09

➔ ASE 20 Greek index

Methods

Gene expression programming (GEP)
Integrated genetic programming (GP)

Period	Trading Days	Time period	
		Beginning	End
Total Dataset	2087	21 January 2001	31 December 2008
Training Dataset	1719	29 January 2001	30 August 2007
Out- of- sample Dataset(Validation Set)	349	31 August 2007	31 December 2008

GEP Output	GP Output
$\tan(\exp((x1+x2)^{1/2}) + [(\cos(0.9395))^3]) / (\exp((2.2580)^3) * (((x6)^2) / (\sin(x11)) * (\tan(\exp((-0.6441)^{((x7) / (x4))}) - (\sin((\tan((-0.9604)^{(\cos(\cos(x7))) / (x5+x8)))) + (1.9056)) - ((x3)^{1/3}))^2))))^2)^{1/2})) * (x7)$	$\cos((x7) / ((-2.862)^{(1.0119)} - (((x11+x8)^{x1}) * (\exp((-2.8624) + (\exp(((-1.9846) / ((0.8175) * (1.2320))) + (1.2320)) - ((x2+x9) * (-2.8624) + ((x4) * ((-2.3000) / ((-1.9846) * ((x5)^{1/2}))) + (\tan(x3+x7))))^2)^{1/2})) * ((-2.3000)^2))^3) / (\tan(x9+x7))) * (x6+x10))$

Population Size:	1000	GEP	Population Size:	200	; GP
Head length:	6		Max tree depth:	6	
Constants' range:	[-3, 3]		Constants' range:	[-3, 3]	
Function Set:	+, -, *, /, ^, ^2, ^3, ^1/2, ^1/3 , Exp, If, sin, cos, tan		Function Set:	+, -, *, /, ^, ^2, ^3, ^1/2, ^1/3, Exp, If, sin, cos, tan	
Fitness evaluation function:	Mean Squared Error		Fitness evaluation function:	Mean Squared Error	
Tournament Size:	20		Tournament Size:	4	
Type of recombination:	Two point		Crossover trials:	1	
Mutation Probability:	0,75		Mutation Probability:	0,75	

Sci.direct.com (SD): Information Source (is)

**R. Sambasiva Rao, School of Chemistry
Andhra University, Visakhapatnam
rsr.chem@gmail.com**