

NEW APPROACH FOR QSAR AND QSTR TREND ANALYSIS ON LARGE SAMPLE DATA SET BY THE KY-METHODS O Kohtaro Yuta In Silico Data, Ltd. (http://www.insilicodata.com)

Objection : Big data analysis by the KY-method on QSAR oriented research works

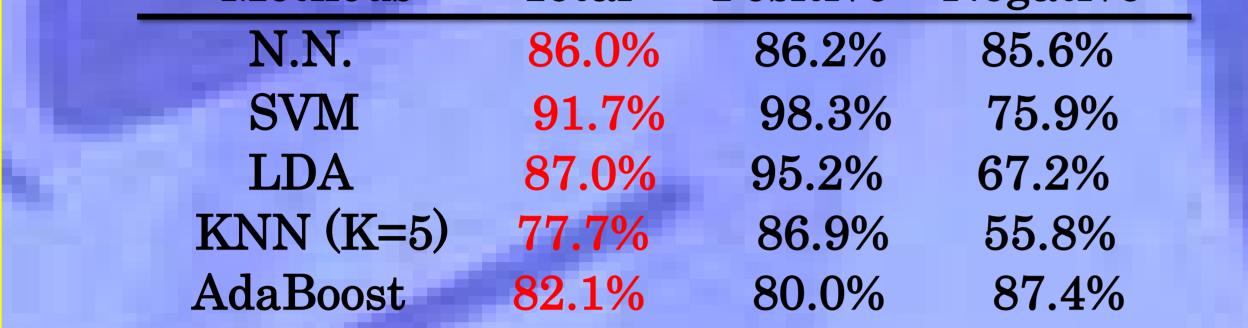
Used samples : Skin sensitization data Total; 593, Positive 419, Negative; 174

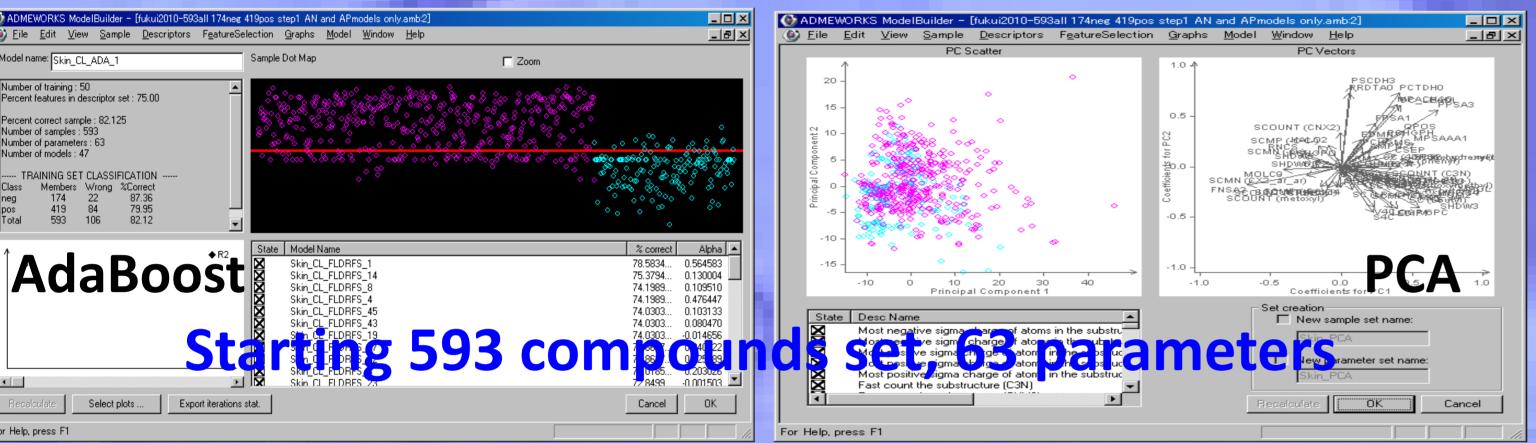
 Classification Results by various methods (63params) Total Positive Negative Methods

Classifica	tion resul	t by	the KY-met	thod	(100%	% corr	ect)
Step1;	Positive	187	Negative	88	Grey	zone	318
Step2;	Positive	177	Negative	34	Grey	zone	107
Step3;	Positive	55	Negative	52	Grey	zone	0

Classification results of compounds which are included in the "High reliability" space of the "KY-methods"

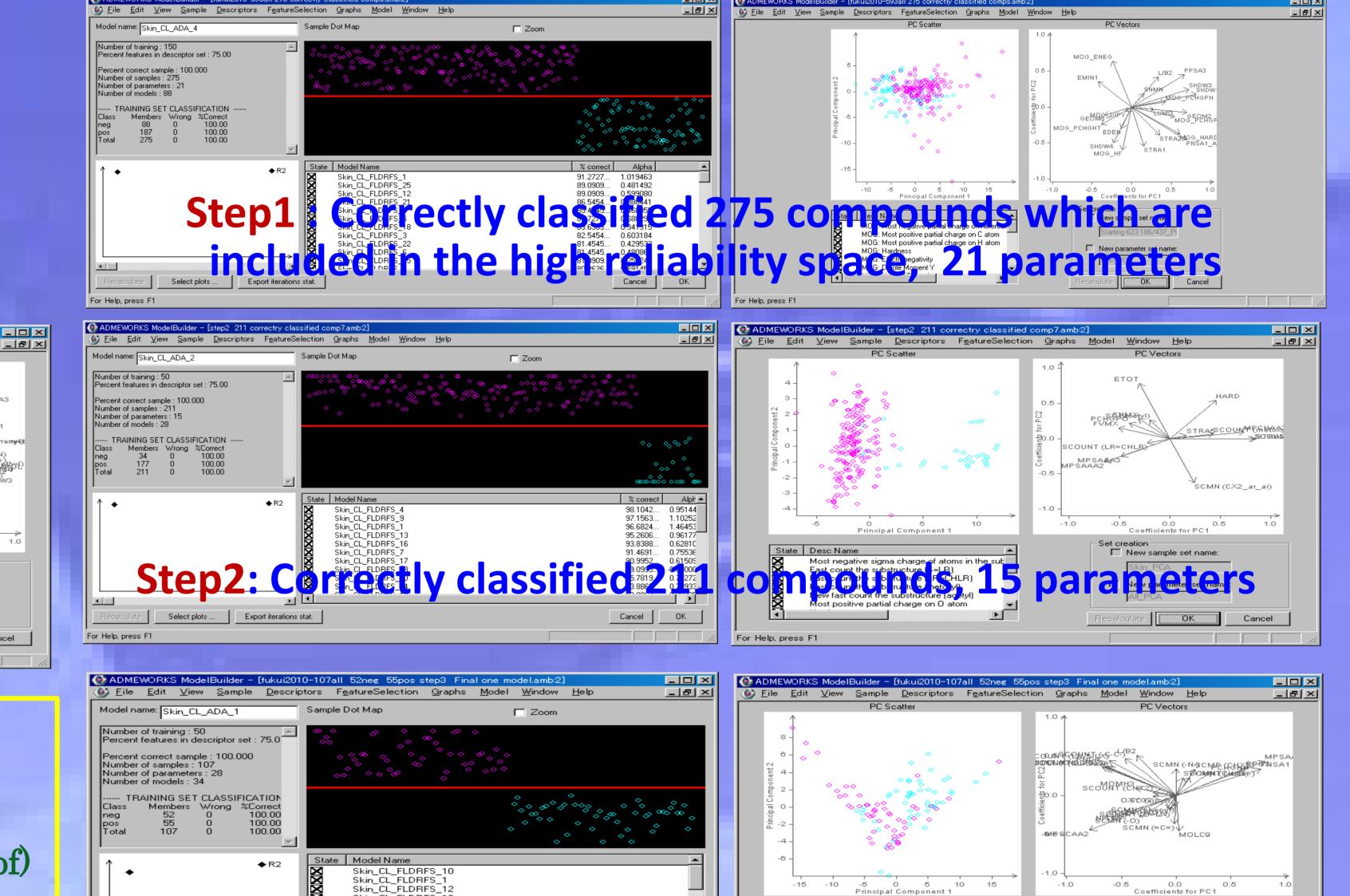
ADMEWORKS ModelBuilder - [fukui2010-593all 275 correctly classified comps.amb;2]											
<u>F</u> ile	<u>E</u> dit	⊻iew	<u>S</u> ample	<u>D</u> escriptors	F <u>e</u> atureSelection	<u>G</u> raphs	<u>M</u> odel	<u>₩</u> indow	<u>H</u> elp		
del anno Destato											





Features of the KY (K-step Yard sampling) methods

- 1. Always achieve perfect (100%) classification under any conditions • Highly overlapped class sample data set
 - •Quite large number of sample data set (tens and several thousands of)
- 2. Starting sample set was divided into
 - small and clean sample set



small and hierarchical sample set

3. Applicable not only the discriminant but multi-regression analysis

"Two model KY-method for Discriminant analysis" No classification **High reliability High reliability** ×× **Positive Zone Negative Zone Gray Zone** Step O X OD $\mathbf{Q} \times \mathbf{A}$ **Gray Zone** Step 2 **Gray Zone**

Cancel For Help, press F1 For Help, press F1

Step3: Skin_CL_FLBBFS_15 Skin_CL_FLBBFS_3 Skin_CL_FLBBFS_3 Skin_CL_FLBBFS_3 Skin_CL_FLBBFS_3 Skin_CL_FLBBFS_3 Skin_CL_FLBBFS_3 Classified 107 com for equile graphing of atoms in the Step3: Skin_CL_FLBBFS_16 Most negative sigma charge of atoms in the Step3: Skin_CL_FLBBFS_16 Step3: Skin_CL_FLBBFS_17 Step3: Step3: Skin_CL_FLBBFS_17 Step3: Step3: Skin_CL_FLBBFS_17 Step3: Skin_CL_FLBBFS_17 Step3: Skin_CL_FLBBFS_17 Step3: Skin_CL_FLBBFS_17 Step3: Step3: Skin_CL_FLBBFS_17 Step3: Step3: Skin_CL_FLBBFS_17 Step3: Skin_CL_FLB

Parameters used in the original and each steps in KY-method

Parameter Name (Starting 593 compounds, 63 parameters) 4th order cluster MC Simple 4th order cluster MC Valence 6th order path-cluster MC Valence **Balabans** topological index **Combined symmetry** Charge of the most positive at Electric dipol moment Shadow area 3 (YZ plane) Shadow area 5 (normalized SHDW Shadow area 6 (normalized SHDW3 Dist between most (+) and most (-) cha rge in structure Minimum autopolarizability value Minimum electron density value Max. free radical superdelocalizabil Length-to-breath ration (Mini Mass weighted Width Molecular polarizability Atomic charge weighted PPSA Fractional positive charged partial SA Fractional negative charged partial SA Relative negative charged SA HBP: Sum of (surface area*charge) don. hydr. / To a mol. surface area HBP: Count of donatable hydrogen atoms HBP: Ratio of number donors to number ac HBM: Sum of surface area of acceptor atoms HBM: Ave. chg. diff. between donor and accepto Molecular distance edge between all sec quat C Molecular distance edge between all tert tert C Molecular distance edge between all tert quat C Average E-State value over all hetero-atoms Difference between Max and Min E-State values X: Total charge weighted atomic surface area X: Partial at. surf. area/Tot. mol. surf. area **Distance weighted flexibility Dipole Moment Z** Most positive partial charge on H atom Mean partial charge on C atoms Most positive partial charge on O Number of H-bond donors New fast count the substructure (t-butyl) New fast count the substructure (phenyl) New fast count the substructure (2-hydroxyethyl) New fast count the substructure (4-hydroxyphenyl) New fast count the substructure (n-butoxyl New fast count the substructure (carboxymethyl) New fast count the substructure (-ester-New fast count the substructure (-N=) New fast count the substructure (LR=CH2) New fast count the substructure (LR-NH Fast count the substructure (ethyl) Fast count the substructure (metoxyl) Fast count the substructure (-ester-) Fast count the substructure (-N-) Fast count the substructure (CH3LX) igma charge of atoms in the substructure (-O-) Most negative sigma charge of atoms in the substructure (CX2 ar ar CONSTANT

Parameter Name (Step 1; 275 compounds, 21 parameters Shadow area 1 (XY plane) Shadow area 3 (YZ plane) low area 4 (normalized SHDW1) otal electron density of atoms in structure owest unoccupied molecular orbitation Vin. nucleophilic superdelocalizabili ength-to-breath ration (Minimum area Angle strain energy of molecule Bond strain energy of molecule Mass weighted Widtl Mass weighted Width/Thikcness Atomic charge weighted PPSA Minimum E-State value Partial negative surface area (AM1) MOG: Heat of Formation MOG: Dipole Moment Y **MOG: Electronegativity MOG: Hardness** MOG: Most positive partial charge on H atom MOG: Most positive partial charge on C atom MOG: Most negative partial charge on heteroatom CONSTANT Parameter Name (Step2; 211 compounds, 15 parameters) Total energy Maximum free valence value Max. nucleophilic superdelocalizability Bond strain energy of molecule Other strain energy of molecule IBM: Sum of surface area of acc. atoms / Number of acc. at HBM: Sum of surface area of acc. atoms / Total mol. surface area HBM: Sum of charge on acc. atoms / Number of acc. atoms Hardness Most positive partial charge on O atom fast count the substructure (acetyl) ast count the substructure (metoxy) Fast count the substructure (LR=CHLR) Fast count the substructure (S=LR) Nost negative sigma charge of atoms in the substructure (CX2_ar_ar) CONSTANT r Name (Step 3 ; 107 compounds, 28 parameters th order path-cluster MC Valence Whird moment of inertia with H ength-to-breath ration (Minimum ractional negative charged partial S **Relative positive charged SA** HBM: Sum of surface area of acc. atoms / Number of acc. a IBM: Sum of (surface area*charge) acc. atoms / Number of acc. atoms Superpendentivity index Sulfur only N: Atomic chg. weighted at. surf. area/Tot. mol. surf. area **O:** Total charge weighted atomic surface area Most negative partial charge on I New fast count the substructure (the substructure (CH2LRI ast count the substructure (CLR3L) ubstructure (LR-S-L) Fast count the Most positive sigma charge of atoms in the substructure (CHX) Most negative sigma charge of atoms in the substructure (pheny Most negative sigma charge of atoms in the substructure (=C=) Most negative sigma charge of atoms in the substructure (-O) Nost negative sigma charge of atoms in the substructure (-C(O)-Most negative sigma charge of atoms in the substructure (-N-) Most negative sigma charge of atoms in the substructure (CHX3

* Number of parameters used in common with other sample set

Set creation New sample set name

parameters

Starting set: 63 params To step 1; 3 params To step 2; 3 params To step 3; 5 params

Step 1: 21 params Starting ; 3 params To step 2; 1 params To step 3; 1 params

Step 2: 15 params Starting ; 3 params To step 1; 1 params To step 3; 1 params

Step 3: 28 params Starting ; 5 params



Variation of the "KY (K-step Yard sampling) methods" List of the available "KY methods" : Total 6 approaches

Sinary classification ; 3approaches 1. Two model KY- discriminant method 2. One model KY- discriminant method 3. Model free KY- discriminant method

Fitting (multi regression); 3approaches 1. KY-fitting with discriminant method 2. Three zone KY-fitting method 3. Model free KY-fitting method

* All six KY-methods are patented and pending applications in JP, USA and EU

To step 1; 1 params To step 2; 1 params

Conclusions:

- 1. Sophisticated and detailed QSAR analysis has been done by the KY-method even if used sample number was large.
- 2. Perfect (100%) classification ratio was achieved by the KY-method
- Other traditional methods could not be achieved perfect classification ratio
- **3.** The KY-method applicable not only classification but QSAR works

All research works and screen displays were executed and generated by the ADMEWORKS : ModelBuilder program developed by FJQS (Fujitsu Kyushu Systems Ltd.)