# Molecular Descriptors Family on Structure-Activity and Structure-Property Relationships: Results

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### Purpose

• To present the results obtained by utilization of an original approach called Molecular **Descriptors Family (MDF) on Structure-Property** (SPR) and Structure-Activity **Relationships** (SAR) applied on different classes of chemical compounds and its usefulness as precursors of models elaboration of new chemical compounds with better properties and/or activities.

### Methodology

**Molecular Descriptors Family** 

- Preparing chemical compounds for molecular modeling
- Generating the molecular descriptors family
- Finding the MDF SPR/SAR models
- Validating the MDF SPR/SAR models
- Comparing the MDF SPR/SAR models with previous reported model(s)

### **Materials**

Set name	Observed/Measured Property/Activity
IChr	retention chromatography index
PCB_rrf	relative response factor
23159	octanol/water partition coefficients
23159e	octanol/water partition coefficients
PCB_lkow	octanol/water partition coefficient
36638	water activated carbon adsorption
MR10	molar refraction
Ta395	cytotoxycity
52730	toxicity
Tox395	mutagenicity
41521	insecticidal activity
Triazines	herbicidal activity
52344	antioxidant efficacy
26449	antituberculotic activity
23151	antimalarial activity
22583	anti-HIV-1 potencies

### **Results: database**

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■ 23159e_xval	E	Tox395 data		14	MyLSAM	latin1_swedish_ci	11KB	
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### **Results: web interface**



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## **Results: MDF model**

Molecule filename: Distance operator: Topological distance, t Geometrical distance, g Cardinality, C Count of directly bounded hidrogen's, H Relative atomic mass, M Atomic electronegativity, E Group electronegativity, G Partial charge, Q	4
Descriptor (of interaction) formula:Distance, 'D' = dInverted distance, 'd' = 1/dFirst atom's property, 'O' = p1Inverted O, 'o' = 1/p1Product of atomic properties, 'P' = p1p2Inverted P, 'o' = 1/p1p2'1/2Inverted Q, 'o' = 1/p1p2'1/2Inverted Q, 'o' = 1/p1p2'1/2Inverted J, 'j' = 1/p1p2'1/2Inverted J, 'j' = 1/p1p2'1/2Inverted J, 'j' = 1/p1p2dProduct of atomic properties and distance, 'K' = p1p2dInverted L, 'i' = 1/p1p2dProduct of distance and squared atomic properties, 'L' = d(p1p2)'1/2Inverted L, 'I' = 1/p1p2dFirst atom's property potential, 'V' = p1/dFirst atom's property field, 'E' = p1/d'2First atom's property work, 'W' = p1'2/dProperties work, 'w' = p12/d'2Properties force, 'f' = p1p2/d'2First atom's property weak nuclear force, 'S' = p1'2/d'3Properties storg nuclear force, 't' = p1p2/d'4	el: tant relative to fragment's head, R tant relative to conventional origin, r sultant relative to fragment's head, M sultant relative to conventional origin, m ultant relative to conventional origin, d
Fragmentation criteria:       Molecular overall superposing formula         Minimal fragments, m       Cond., smallest m         Maximal fragments, M       Cond., highest absolute, N         Szeged distance based fragments, D       Avg., Avg.(Avg.(Avg.(atom)/count(atoms), B)         Raw, Sky (Avg., Sky (Count(bonds), b)       Geom., product, P         Geom., P'1/count(fragments), g       Geom., P'1/count(atoms), F         Geom., P'1/count(bonds), f       Harm., sum, s         Harm., H       Harm., Hearn.(Harm./atom)/count(atoms), I	a: Linearization operator: Identity (no change), I Inversed L, i Absolute I, A Inversed A, a Logarithm of A, L Logarithm of L, I

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### **Results: investigated datasets**

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### Browse or Query MDF SARs by sets from vl.academicdirect.org web server. Query database0 Browse database0 IChr10\_ Submit Query IChr10\_ Submit Query -IChr10 DevMTOp25\_ \* . 36638\_ RRC433\_lbr\_ PCB\_rrf\_ RRC433 Ikow 23159e RRC433 pka Ta395\_ 52730\_ Tox395\_ DHFR\_ 41521 a acids MR10\_ 34121bad 26449t 34121nopt\_ 52344 19654\_ DevMT0p00 3300\_

### **Results: training vs. test application**

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### **Training vs. Test Experiment**

Please select a data file from the list of available data. The experiment will performe a random split of experimental data in two sets: "trainig set" and "test set". The QSAR/QSPR model are calculate using the data from training set. The obtained QSAR equation are apply then on both sets, in order to calculate statistical parameters.

23167.bt Submit Query		You selected: Set file: 23167.txt •
26449tbt 31572.bt 33504.bt		Please select: Training set count: 18 -
36638_2.2.bd 36638_2.2.bd	Set file: 23167.	18 19 20 Submit Query 21
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Set file: 23167.txt Training set count: 18 Training set: a Endegulfon 1.3.5 CP 1.3 CP a p1 DDT 1.2.3.5 CP p p1	CB PCB 2-2p-4-4p-5-5p-PCB 1-2-	
CB PCB 2-2p-4-4p-5-5p-PCB 1-2-4-CB 1-2-4-5-CB Heptachlor 1-2-3-C	Test set list:	v
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### **Results: leave one out application**

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Leave one out analysis require a tabutated data in html format as input data with followings:	
Data example:	
Mol iSMmEQt iSMMWHg LADmkQt INPRJQg Y_Est Y Y_Pre	
t1 2.0396e-2 7.0397e-4 1.4830 1.6344e-1 3.8295 3.82 3.8619	
t2 1.9849e-2 5.212e-4 -1.5099 3.1038e-2 5.2003 5.2 5.2009	
t3 1.7683e-2 4.2792e-4 1.8269 1.5977e-2 5.3298 5.34 5.3267	
t4 1.5673e-2 3.2419e-4 2.3702 1.8778e-2 5.8340 5.83 5.8348	
t5 1.9487e-2 4.0228e-4 1.0849 1.3049e-2 5.9636 6.01 5.9436	

### **Results: comparisons**

	Previous reported SAR				MDF SA	R	
Set name	<b>r</b> <sup>2</sup>	n	v	<b>r</b> <sup>2</sup>	r <sup>2</sup> <sub>cv(loo)</sub>	n	v
IChr10	0.900	10	2	0.999	0.999	10	2
				0.628	0.619	209	1
				0.693	0.682	209	2
PCB_rrf	-	-	-	0.737	0.717	209	4
				0.873	0.87	206	1
				0.89	0.885	206	2
PCB_lkow	-	-	-	0.917	0.909	206	4
36638	0.967	16		0.994	0.991	16	3
	0.388	18	1	0.755	0.684	18	1
23159	0.839	18	3	0.982	0.974	18	2
				0.899	0.758	8	1
23159e	-	-	-	0.968	0.898	8	2
Ta395	0.870	13	2	0.977	0.961	15	2
Tox395	0.800	13	2	0.957	0.934	14	2

### **Results: comparisons**

	Previous reported SAR			MDF SAR			
Set name	<b>r</b> <sup>2</sup>	n	V	<b>r</b> <sup>2</sup>	r <sup>2</sup> <sub>cv(loo)</sub>	n	v
	0.913	8	3				
41521	0.985	8	5	0.999	0.998	8	2
	0.991		1	0.961	0.954	10	1
	0.998		2	0.99	0.988	10	2
26449	0.993	10	4	0.998	0.997	10	4
<b>MR10</b>	0.976	10	2	0.999	0.999	10	2
	0.741	16	4				
23151	0.985	13	4	0.997	0.995	16	3
	0.780	8	1	0.904	0.832	8	1
	0.710	8	1	0.999	0.999	8	2
	0.810	8	2	0.999	0.999	8	2
52344	0.970	8	4	0.999	0.999	8	2

### **Results: comparisons**

	Previous reported SAR			MDF SAR			
Set name	r <sup>2</sup>	n	V	r <sup>2</sup>	r <sup>2</sup> <sub>cv(loo)</sub>	n	v
				0.966	0.947	10	1
52730	-	-	-	0.998	0.996	10	2
				0.951	0.946	30	1
				0.975	0.971	30	2
				0.983	0.976	30	3
Triazines	0.970	30	3	0.989	0.985	30	4
	0.888	37	5	0.783	0.766	57	2
	0.885	20	5	0.835	0.809	57	3
	0.883	57	5	0.9	0.884	57	4
22583				0.918	0.9	57	5



### **Conclusions: SPR**

• Molecular Descriptors Family on Structure-Property Relationships obtained very good performances in estimation and prediction of compound's properties as are for example retention chromatographic index, molar refraction and water activated carbon organics adsorption.

### **Conclusions: SAR**

• Good performances are also obtained by Molecular Descriptors Family on Structure-Activity Relationships in estimation and prediction of compound's activities as are for example toxicity of alkyl metal compounds, insecticidal activity of neonicotinoid compounds, antituberculotic activity of polyhydroxyxanthones, antioxidant efficacy of 3-indolyl derivates, or antimalarial activity of some 2,4-diamino-6-quinazoline sulfonamide derivates.

### **Conclusions: new compounds virtual building**

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Predict activity based on <ul> <li>a learning set and</li> <li>a set of previous obtained MDF SAR models for</li> <li>any molecule submitted as HIN file by the user.</li> </ul>	*
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### Conclusions

- The MDF SPR/SAR methodology opens a new pathway in:
  - Sunderstanding the relationships between compounds structure and property/activity,
  - **\⇔**characterization,
  - **\\$** investigation,
  - **b**development of new compounds,
  - more competitive as costs and property/activity.

### Acknowledgments

- Research was partially supported by the M. Ed. & Res., through ET/36/2005(-2008) project.
- AcademicDirect.Org domain is sponsored by Register.Com registrar.
- Servers IP's are from T.U. C-N addresses space.

## Thank you for your attention!