

# System for Prediction of Pharmacokinetic Properties and Toxicity of Drug Compounds

**Radchenko E.V., Karpov P.V., Sosnin S.B., Dyabina A.S.,  
Sosnina E.A., Palyulin V.A., Zefirov N.S.**

*Department of Chemistry,  
Lomonosov Moscow State University*



*Institute of Physiologically Active  
Compounds RAS*



# Pharmacokinetic properties and toxicity (ADMET)

Absorption  
Distribution

Metabolism  
Excretion

**Toxicity**

- Critically affect the efficacy, pharmacological profile, administration protocol and safety of drugs
- Optimization of these properties is an important aspect of drug discovery and development
- Ability to **predict them for new structures** can substantially improve the speed and efficiency of drug development

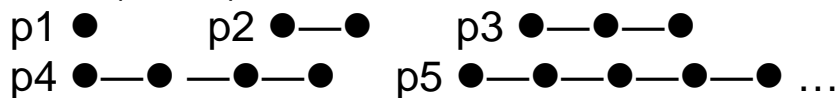
# Prediction of ADMET properties

## General prediction methodology based on the QSAR/QSPR approaches

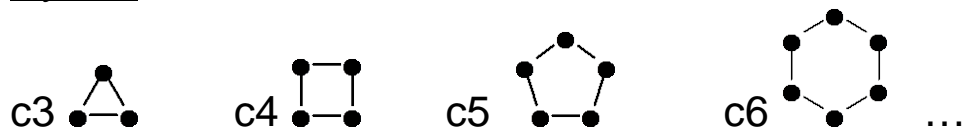
- Extensive and verified experimental data sets
- Nonlinear modeling of the structure-property relationships using artificial neural networks
- Flexible structure description based on the fragmental descriptors
- High prediction accuracy and efficiency
- Broad applicability domain
- Even for diverse compounds with varying (and/or incompletely characterized) mechanisms of action

# Fragmental (substructural) descriptors

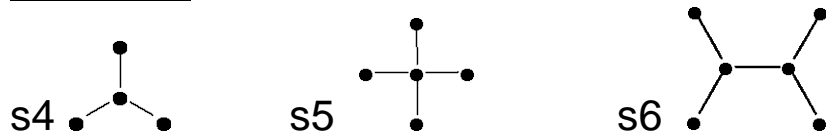
## Path (linear)



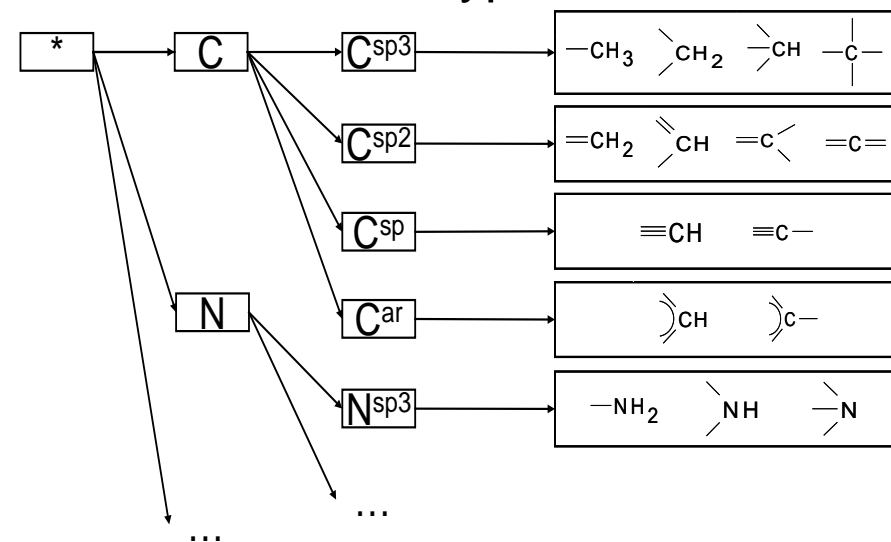
## Cycles



## Branches



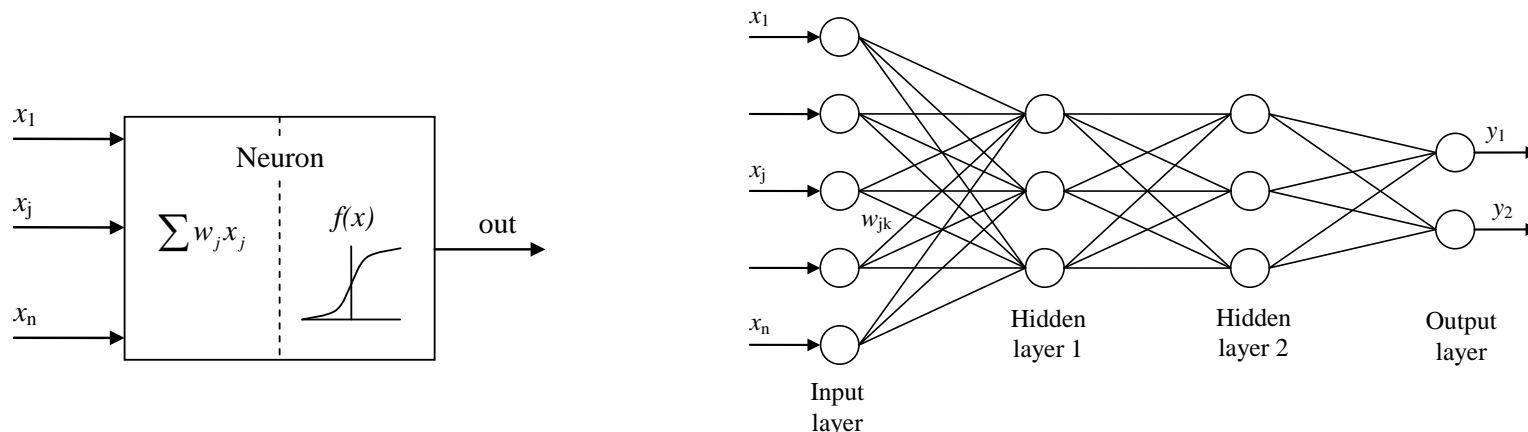
## Hierarchical atom type classification



- Thousands of fragments
- “Holographic portrait” of a molecule
- Applicable to diverse series of compounds
- Easy prediction for new compounds
- Simple structural interpretation

# Artificial neural networks

- Generic modeling of nonlinear structure–property/activity (QSAR/QSPR) relationships



- Descriptor preselection by multiple linear regression
- Predictivity assessment using double cross-validation
- Selection of optimal network architecture and descriptor set
- Reliable prediction using ensemble of trained networks
- Estimation of individual descriptor contributions for interpretation purposes

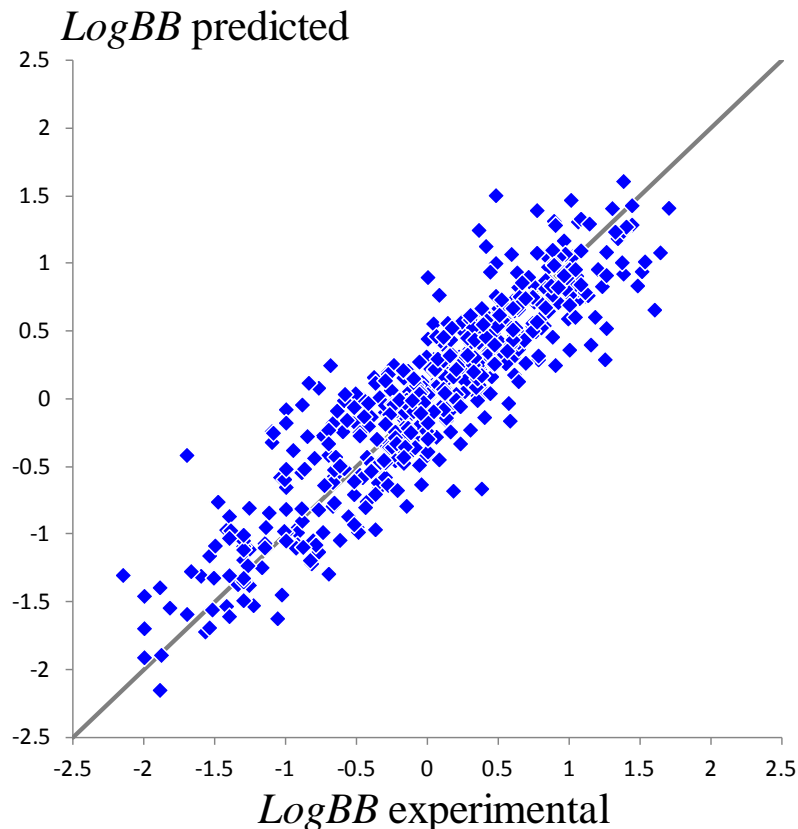
# Blood-brain barrier (BBB) permeability

Probably the most complete data set based on open quantitative published data – verified against original publications

Different transport mechanisms are not considered explicitly

Comparable or better in accuracy and/or applicability domain compared to previously published models

$$\text{LogBB} = \frac{C_{\text{brain}}}{C_{\text{blood}}}$$



$N = 529, Q^2 = 0.82, RMSE = 0.32$

**Abraham, 2006**

$N = 292, R^2 = 0.75, RMSE = 0.33$

**Garg, 2008**

$N = 132, Q^2 = 0.79, RMSE = 0.33$

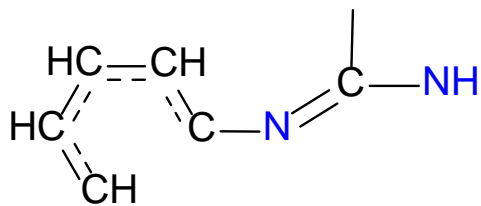
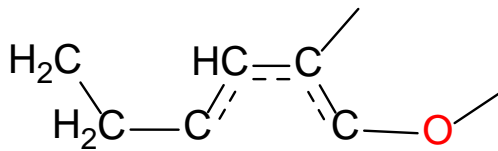
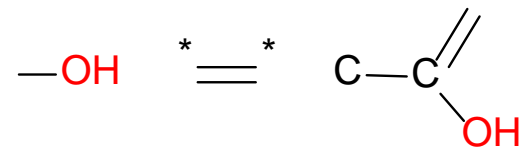
**Muehlbacher, 2011**

$N = 352, Q^2 = 0.55$

# Blood-brain barrier (BBB) permeability

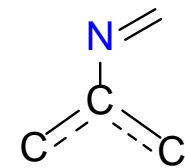
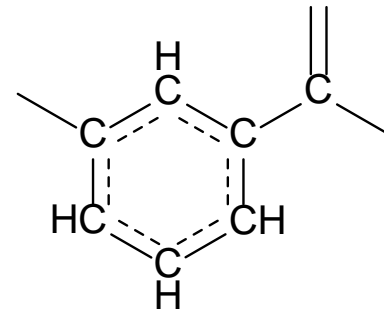
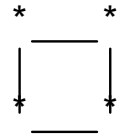
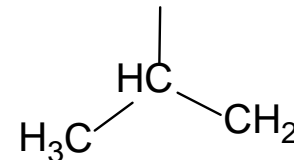
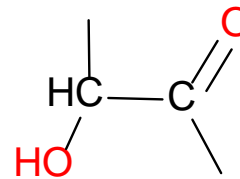
Reasonable interpretation of major fragment contributions

Decrease LogBB



Polar groups

Increase LogBB



Hydrophobic groups, active transport of substituted monocarboxylic acids

# Blood-brain barrier (BBB) permeability

Good validation results on independent test set (\*)

*Estimated qualitative data: BBB+ / BBB-*

LogBB predictions converted to qualitative scale  
using the cut-off value  $\text{LogBB} = -1$

**Correctly recognized more than 90% of BBB+ compounds**

Lower prediction quality for BBB- (partly due to often approximate indirect estimates in the test set)

	Prediction: full set		Prediction: no overlap	
	BBB+	BBB-	BBB+	BBB-
Actual BBB+	<i>TP = 1464</i>	<i>FN = 105</i>	<i>TP = 1255</i>	<i>FN = 100</i>
Actual BBB-	<i>FP = 281</i>	<i>TN = 203</i>	<i>FP = 259</i>	<i>TN = 192</i>
Total	2053		1806	
Overall accuracy	81%		80%	
Sensitivity	93%		93%	
Specificity	42%		43%	

(\*) Martins I.F., Teixeira A.L., Pinheiro L., Falcao A.O., *J. Chem. Inf. Mod.*, 2012, 52 (6), 1686-1697.



# Human intestinal absorption (HIA)

Probably the most complete data set based on open data

Less uniform distribution of data

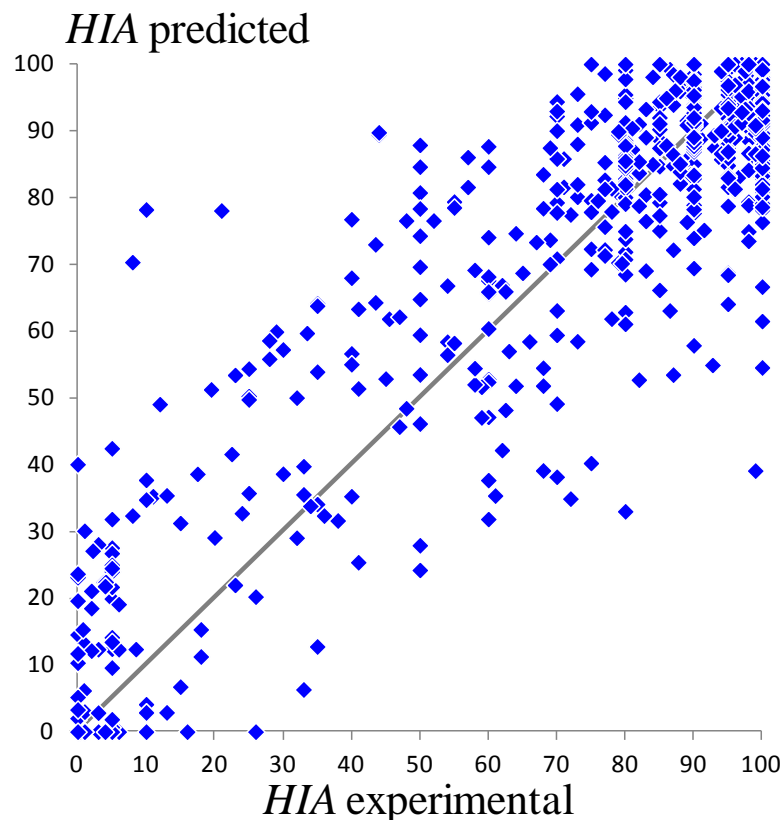
(for 60% of compounds HIA > 80%)

Different transport mechanisms are not considered explicitly

Comparable or better in accuracy and/or applicability

domain compared to previously published models

$$HIA = \frac{D_{blood}}{D_{dose}}$$



$N = 708, Q^2 = 0.80, RMSE = 13.8$

**Hou, 2007**

$N = 435, R^2 = 0.76, RMSE = 12.7$

**Yan, 2008**

$N = 552, R^2 = 0.79, RMSE = 16.4$

**Moda, 2011**

$N = 638, Q^2 = 0.67, RMSE = 11.2$

# hERG-mediated cardiotoxicity risk

hERG potassium channel is among the most important antitargets in drug development

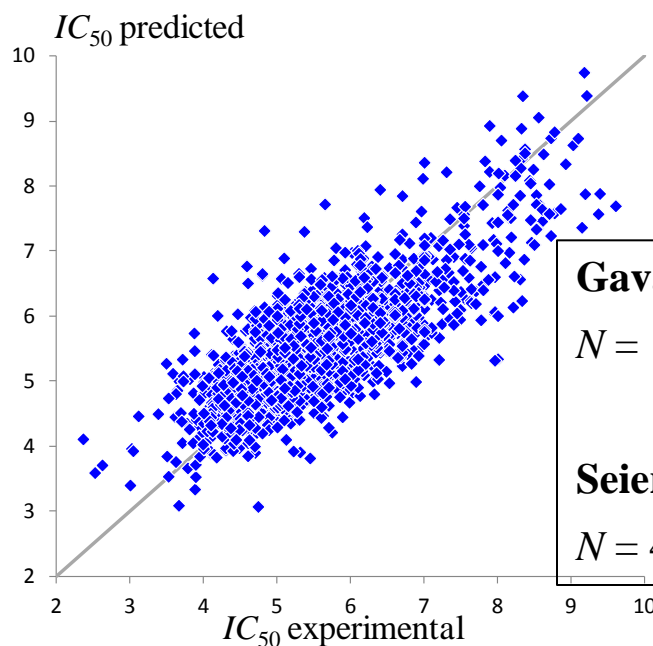
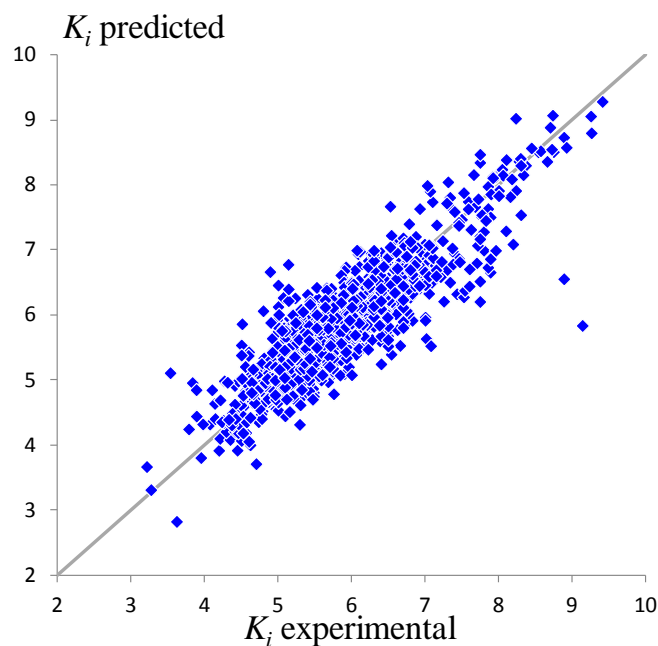
Probably the most complete data set based on open data

Affinity ( $K_i$ ) or functional ( $IC_{50}$ ) assays

Comparable or better in accuracy and/or applicability domain compared to previously published models

$pK_i$ :  $N = 1000$ ,  
 $Q^2 = 0.77$ ,  $RMSE = 0.45$

$pIC_{50}$ :  $N = 2886$ ,  
 $Q^2 = 0.60$ ,  $RMSE = 0.55$



**Gavaghan, 2007 ( $pIC_{50}$ )**

$N = 1312$ ,  $Q^2 = 0.48$ ,  $RMSE = 0.49$

**Seierstad, Agrafiotis, 2006 ( $pIC_{50}$ )**

$N = 439$ ,  $Q^2 = 0.67$ ,  $RMSE = 0.02$

# Integrated Web platform for ADMET properties prediction

- Structure entry
- Descriptor calculation
- Property prediction
- Result visualization and preliminary analysis
- <http://qsar.chem.msu.ru/admet/>

# Integrated Web platform for ADMET properties prediction

<http://qsar.chem.msu.ru/admet/>

ADMET Prediction Service

This is an integrated online service for ADMET properties prediction developed at the [Laboratory of Medicinal Chemistry](#) of Department of Chemistry, Lomonosov Moscow State University.

**Welcome to the online ADMET prediction service**

Please draw a structure (click the "i" icon for drawing help) and then press the Calculate button.

If you have any questions, problems, or suggestions, please do not hesitate to email us

[Dr. Eugene V. Radchenko](#)  
[Dr. Vladimir A. Palyulin](#)

**Prediction Results**

**Blood-brain barrier permeability (LogBB)**

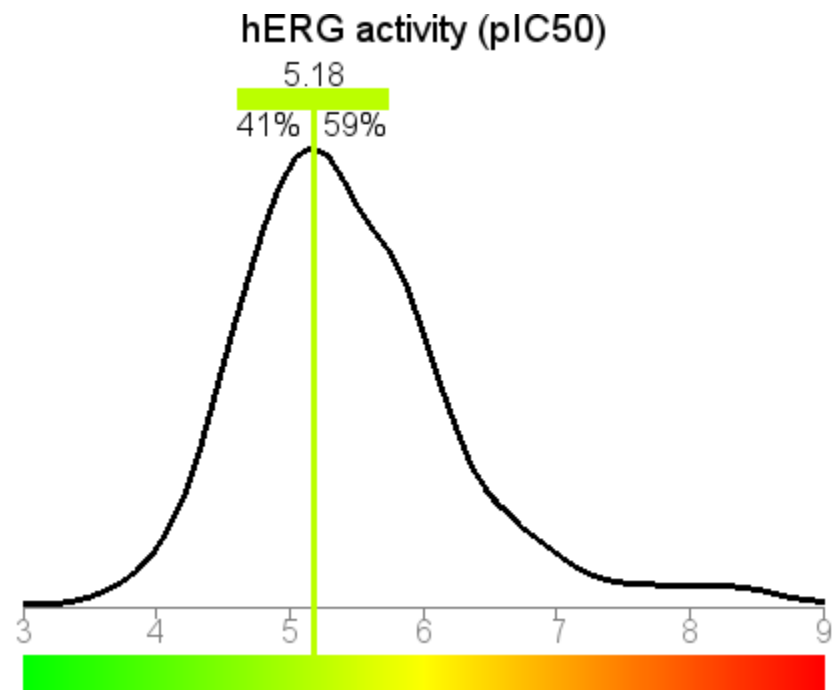
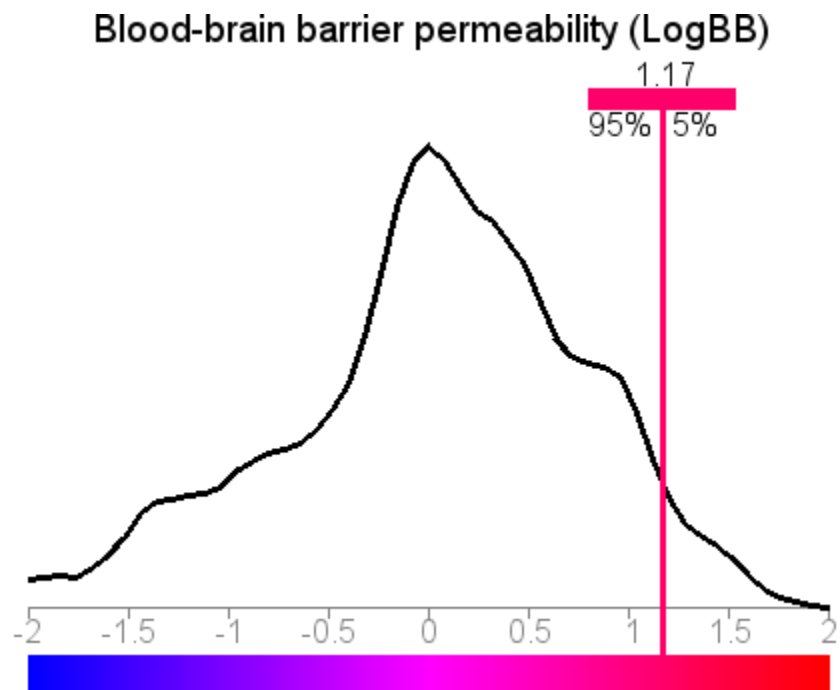
-1.48  
3% 97%

**Human intestinal absorption (HIA%)**

85.37  
49% 51%

# Integrated Web platform for ADMET properties prediction

- Parameter name
- Predicted value
- Color scale (good/bad or low/high) and compound position
- Parameter distribution for known (training set) compounds
- Fraction of compounds below/above predicted value



# Integrated Web platform for ADMET properties prediction

- Blood-brain barrier (BBB) permeability
- Human intestinal absorption (HIA)
- hERG-mediated cardiotoxicity risk
  
- Lipophilicity (LogP)
- Plasma protein binding (HSA)
- Aromatic hydrocarbon receptor (AhR) binding
- Mutagenicity
- Acute toxicity
- Cytotoxicity
- .....
- **Enhanced result analysis**

# Conclusions

- General QSAR/QSPR methodology is suitable for the construction of **predictive models** relating the structures of drug compounds to their **pharmacokinetic properties and toxicity** (ADMET parameters)
- An integrated **Web-based prediction system** developed by us supports convenient prediction of a number of **important ADMET parameters**
- The service is **freely accessible** and may be used for the research in various areas of **medicinal chemistry and pharmacology**

# Acknowledgements

**Yu.A. Rulev**

**I. Tetko**

**P. Ertl**

**A.Ya. Safanyaev**

**A. Abdelaziz**

- Russian Foundation for Basic Research
- Ministry of Education and Science of Russian Federation



*Thank you  
for your attention!*