

# Collaborative Modeling Project for Predicting Acute Oral Toxicity

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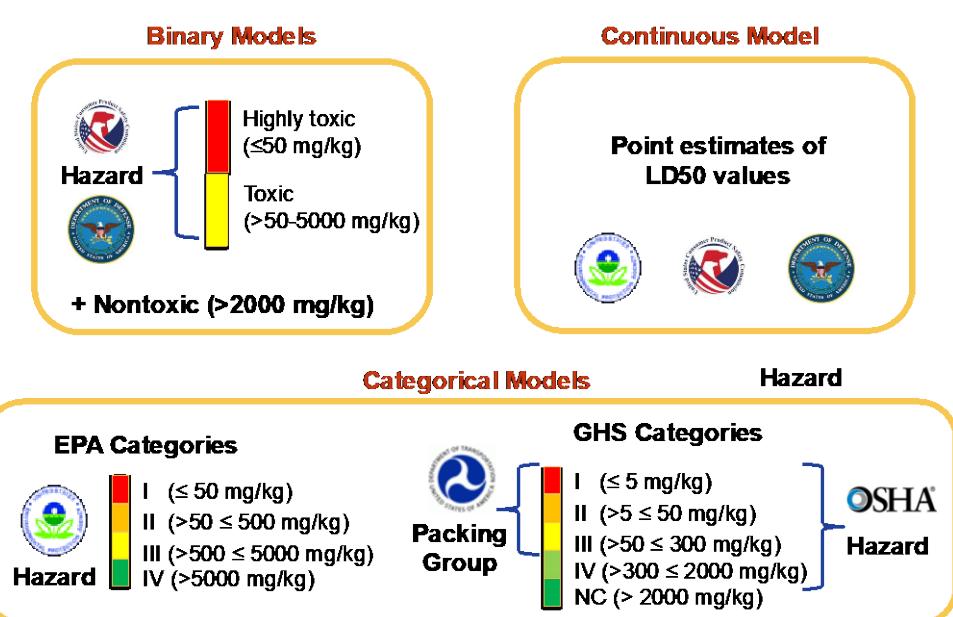
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## Abstract

With an increasing number of chemicals to assess for acute systemic toxicity potential and a lack of sufficiently predictive in vitro approaches, in silico models provide an alternative to predict acute oral toxicity and bridge data gaps. NICEATM and the ICCVAM Acute Toxicity Workgroup (ATWG) organized an international collaborative project to develop in silico models for predicting acute oral toxicity [1]. In total, 35 groups participated, submitting 139 predictive models built using a dataset of 11,992 chemicals. Models were developed for five endpoints: LD50 value, EPA hazard categories, GHS hazard categories, very toxic (LD50 < 50 mg/kg), and non-toxic (LD50 > 2000 mg/kg) [2]. Predictions within the applicability domains of the submitted models were evaluated using external validation sets, then combined into consensus predictions for each endpoint, forming the Collaborative Acute Toxicity Modeling Suite (CATMoS) [3]. The resulting consensus predictions leverage the strengths and overcome the limitations of individual modeling approaches. The consensus predictions performed at least as well as the in vivo acute oral toxicity assay in terms of accuracy and reproducibility. CATMoS consensus predictions can be generated for new chemical structures and are made available as free and open-source models via the OPERA predictive tool, which provides applicability domain assessments and accuracy estimates [4-5]. CATMoS predictions for the ~850k chemical structures in DSSTox will ultimately be publicly accessible via NTP's Integrated Chemical Environment and the EPA's CompTox Chemicals Dashboard [6-7].

## Project Data

- Endpoints: five endpoints were selected by the ICCVAM ATWG member agencies to serve as endpoints for predictive modeling within the CATMoS project.
- Collected data: 34,508 rat oral LD50 values for 16,297 chemicals total.

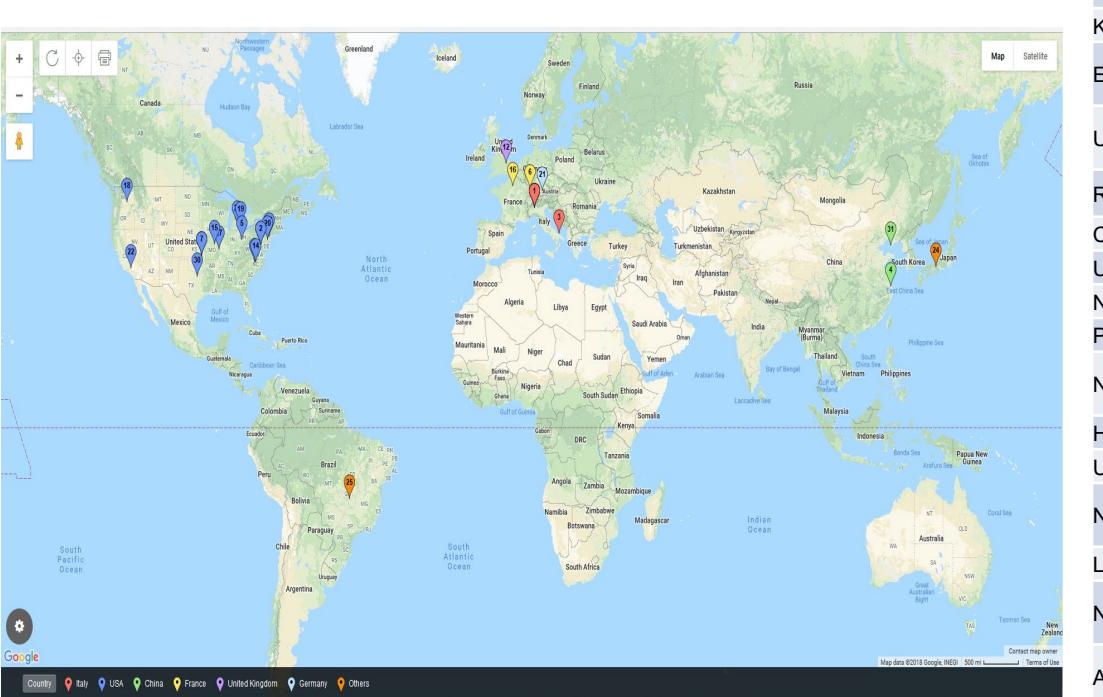


QSAR-ready standardization  
Desalting, stereochemistry stripped, tautomers and nitro groups standardized, valence corrected, structures neutralized

15,688 chemical structures  
21,200 LD50 values

## Collaborators

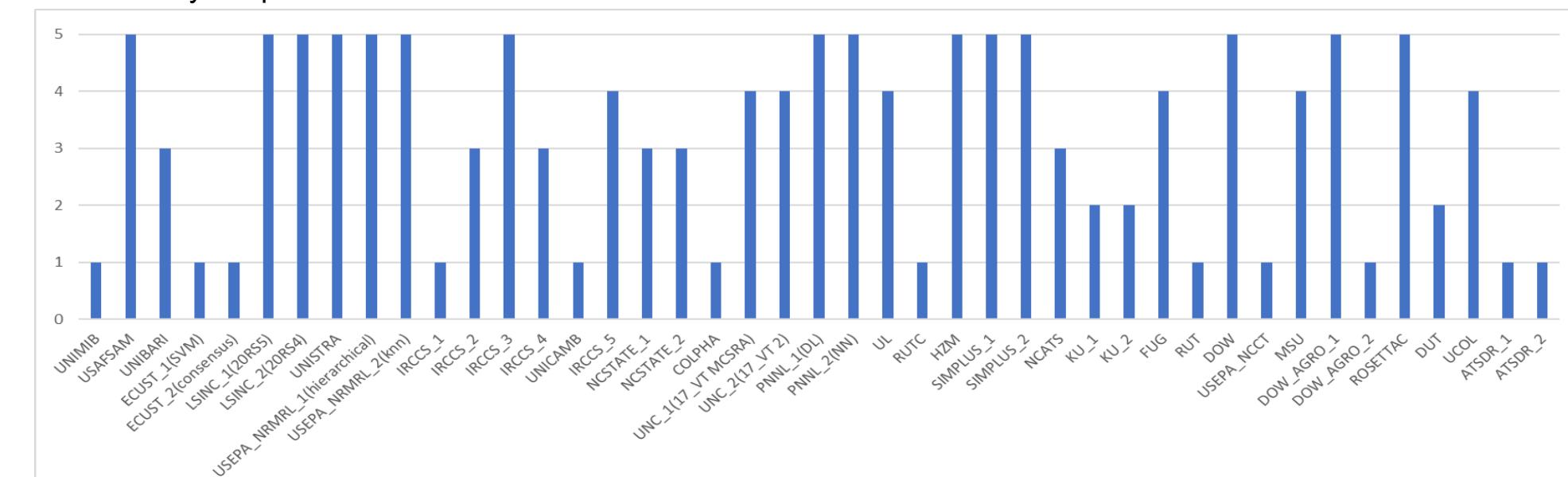
A consortium of 35 participants/groups from around the globe representing academia, industry, and government



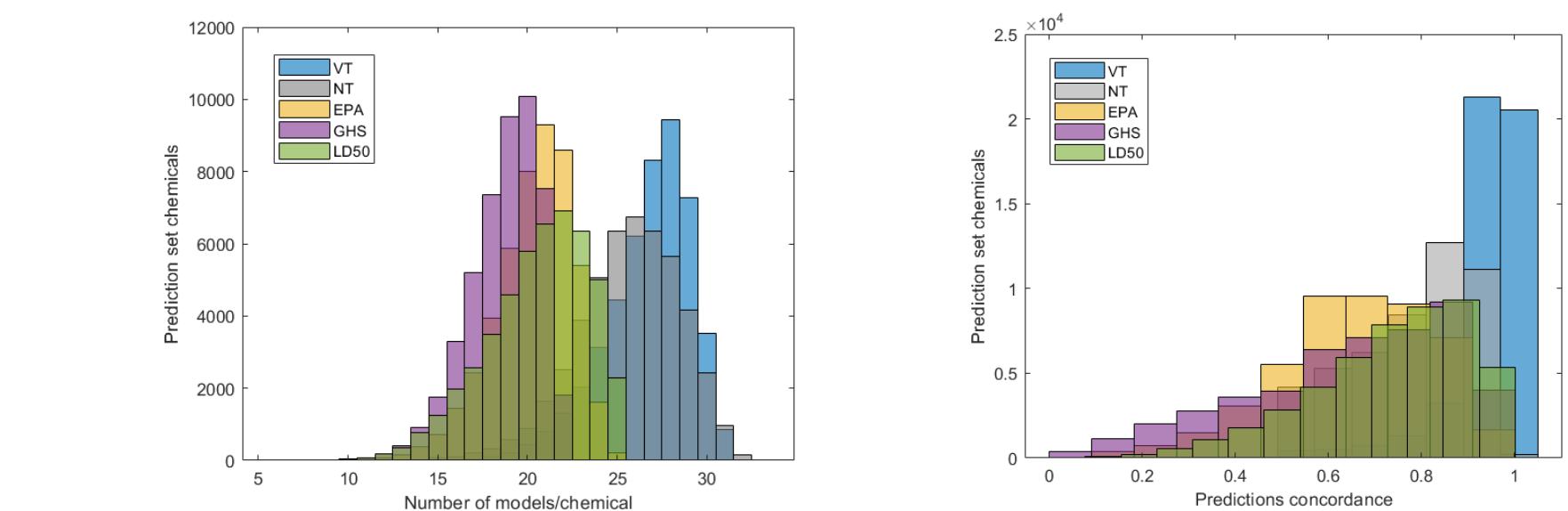
## Consensus Modeling

### Models received from participants

Participating groups submitted predictions for any one or up to all five of the acute toxicity endpoints.



### Coverage and concordance of the models



### Single model evaluation procedure

#### Qualitative evaluation:

- Documentation
- Defined endpoint
- Unambiguous algorithm
- Availability of code
- Applicability domain definition
- Availability of data used for modeling
- Mechanistic interpretation

$$S = 0.3 * (\text{Goodness of fit}) + 0.45 * (\text{Predictivity}) + 0.25 * (\text{Robustness})$$

#### Categorical models (binary and multi-class):

$$\begin{aligned} \text{Goodness of fit} &= 0.7 * (BA_{Tr}) + 0.3 * (1 - |Sn_{Tr} - Sp_{Tr}|) \\ \text{Predictivity} &= 0.7 * (BA_{Eval}) + 0.3 * (1 - |Sn_{Eval} - Sp_{Eval}|) \\ \text{Robustness} &= 1 - |BA_{Tr} - BA_{Eval}| \end{aligned}$$

$$BA = \frac{(Sn + Sp)}{2} \quad Sn = \frac{TP}{TP + FN} \quad Sp = \frac{TN}{TN + FP} \quad R^2 = 1 - \frac{\sum_{i=1}^{n_{TR}} (y_i - \hat{y}_i)^2}{\sum_{i=1}^{n_{TR}} (y_i - \bar{y})^2}$$

#### Quantitative evaluation:

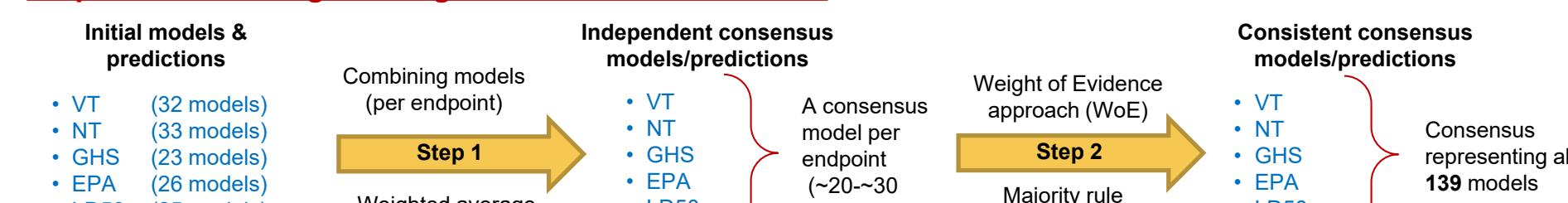
- Goodness of fit: training (Tr) statistics
- Predictivity: statistics on the evaluation set (Eval)
- Robustness: balance between (Goodness of fit) & (Predictivity)

#### Continuous models:

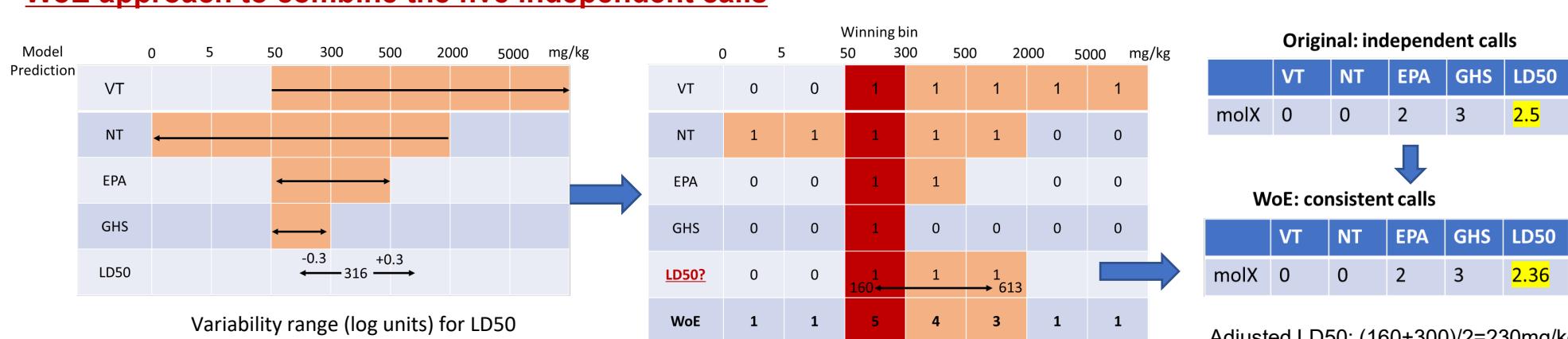
$$\begin{aligned} \text{Goodness of fit} &= R^2_{Tr} \\ \text{Predictivity} &= R^2_{Eval} \\ \text{Robustness} &= 1 - |R^2_{Tr} - R^2_{Eval}| \end{aligned}$$

$\hat{y}_i$  and  $y_i$  are the estimated and observed responses

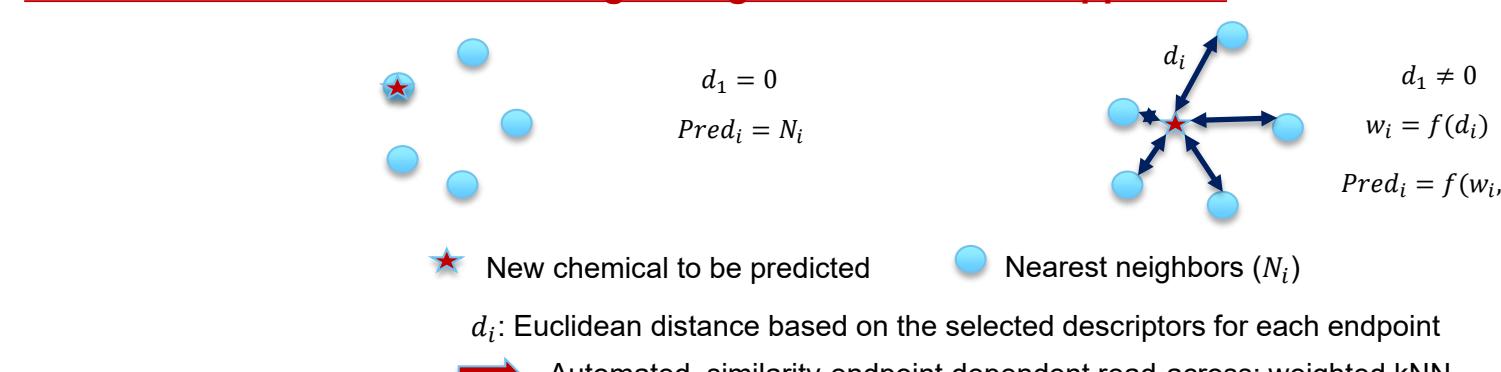
### Steps for combining the single models into consensus



### WoE approach to combine the five independent calls



### Extended consensus model using a weighted read-across approach

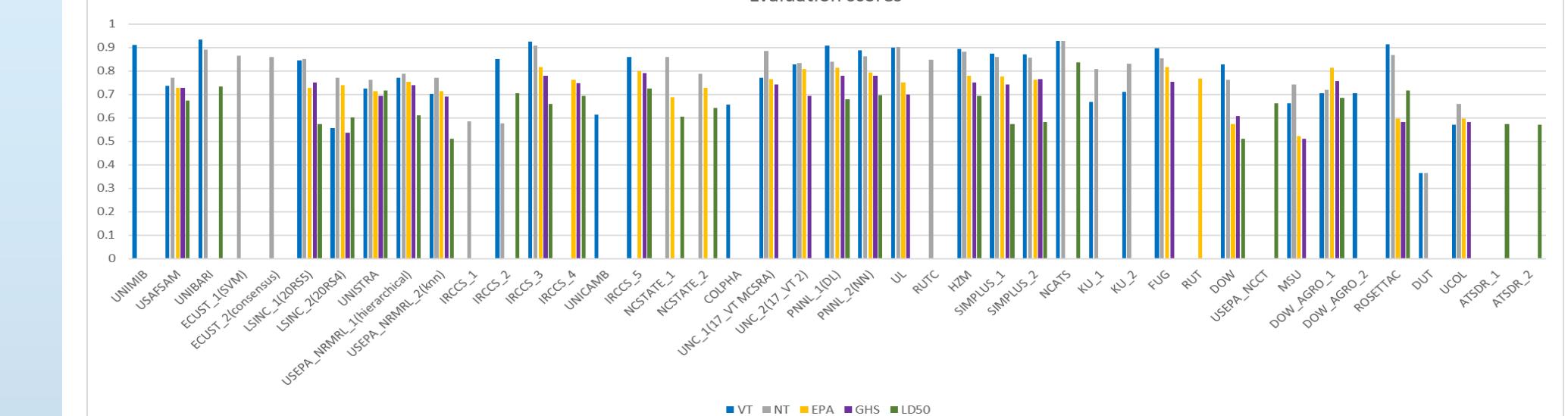


$d_i$ : Euclidean distance based on the selected descriptors for each endpoint  
→ Automated, similarity-endpoint dependent read-across: weighted kNN

## Models Performance Evaluation

### Single models evaluation

Resulting scores (per model) from the evaluation procedure.



### Consensus models evaluation

	LD50		EPA		GHS	
	Training	Evaluation	Training	Evaluation	Training	Evaluation
R <sup>2</sup>	0.85	0.65				
RMSE	0.30	0.49				
	EPA Training		EPA Evaluation		GHS Training	
BA	Cat 1		Cat 1		Cat 1	
Sn	0.87	0.83	0.91	0.63	0.70	0.56
Sp	0.99	0.95	0.75	0.98	0.97	0.89
	Cat 2		Cat 2		Cat 2	
BA	Cat 3		Cat 3		Cat 3	
Sn	0.73	0.75	0.84	0.80	0.88	0.50
Sp	0.99	0.99	0.92	0.89	0.96	0.97
	Cat 4		Cat 4		Cat 4	
BA	Cat 5		Cat 5		Cat 5	
Sn	0.73	0.75	0.88	0.80	0.88	0.53
Sp	0.99	0.99	0.92	0.89	0.96	0.74

## CATMoS in Practice

### Example predictions



### Consensus output

MoleculeID	CATMoS_VT_pred	CATMoS_NT_pred	CATMoS_EPA_pred	CATMoS_GHS_pred	CATMoS_LD50_pred	AD_CATMoS	AD_index_CATMoS	Conf_index_CATMoS
123-91-1	0	1	3	5	3.4053	1	1	0.9500
67-97-0	1	0	0	1	2.12845	1	1	0.8684

### CATMoS implementation in OPERA

#### OPERA suite of models:

- Free, open-source and open-data
- Command line and GUI
- Single chemical and batch mode
- Windows OS and Linux
- Embeddable wrapper libraries (java, C/C++, Python)

## References

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