

Semi-supervised multi-target prediction for analysis of screening data

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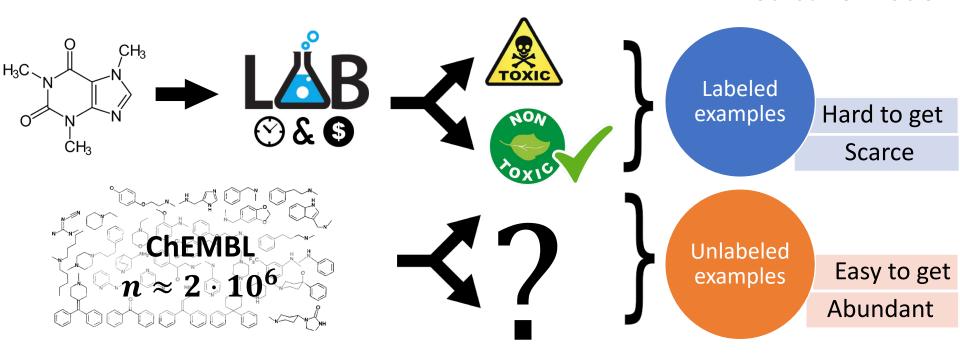
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What is semi-supervised learning?

Supervised learning: Labeled data \rightarrow Predictive model

Semi-supervised learning: Labeled + Unlabeled data → (Better) Predictive model



Why semi-supervised learning?

1200 800 Count 400 0 1000 1500 2000 2500 3000 3500 4000 4500 5000 5500 6000 500 0 Number of labeled compounds

Histogram of dataset sizes (in terms of number of labelled compounds) for 3047 biological targets extracted from the ChEMBL database shows that, for a vast majority of targets, less than 100 compounds is labeled.

QSAR datasets available at OpenML

outline

- Introduction
- (Semi-supervised) predictive clustering trees (PCTs)
- Evaluation and illustrative examples
- Conclusions

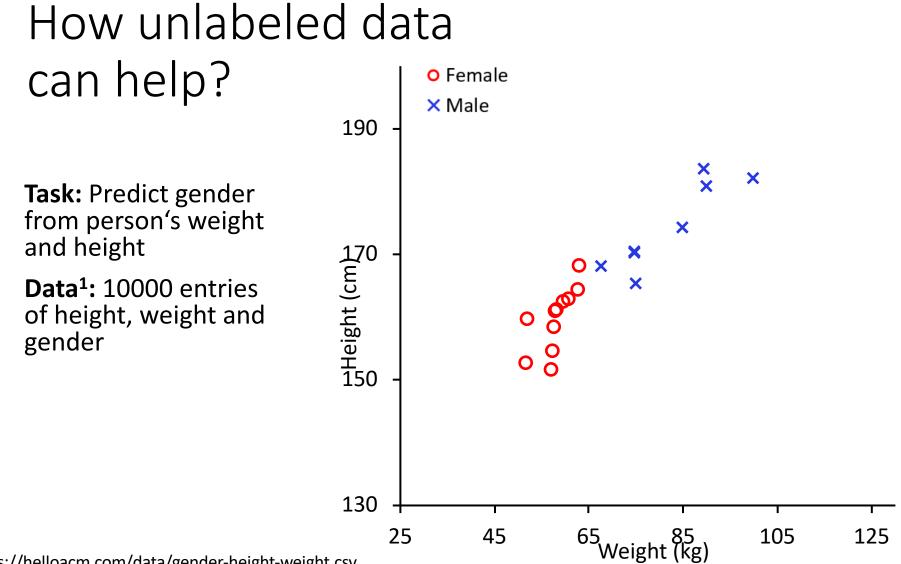
The task of semi-supervised learning

Given:

- An input (descriptive) space X
- A output (or target) space Y
- A set of labeled examples $E_l = \{(x_i, y_i) : x_i \in X, y_i \in Y, 1 \le i \le N_l\}$
- A set of **unlabeled** examples $E_u = \{x_i : x_i \in X, 1 \le i \le N_u\}$
- A quality criterion q

Find: A function $f : X \rightarrow Y$ such that f maximizies q

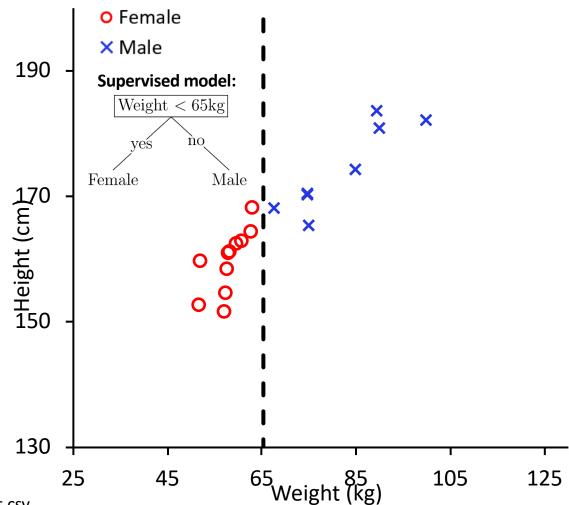
Goal: Achieve better performance than only with labeled data E_l



¹https://helloacm.com/data/gender-height-weight.csv

Task: Predict gender from person's weight and height

Data¹: 10000 entries of height, weight and gender



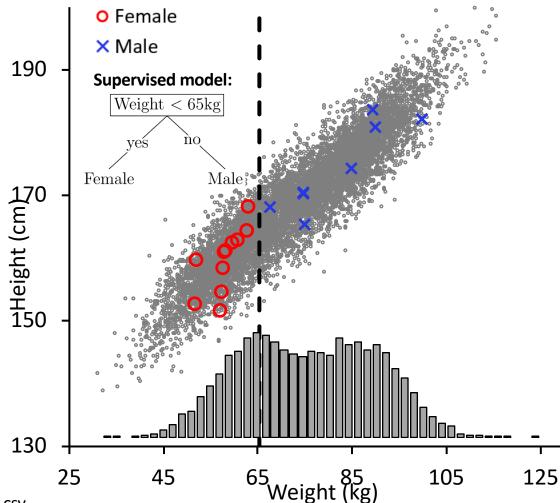
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Task: Predict gender from person's weight and height

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Assumptions about the labels with respect to the structure of unlabeled data



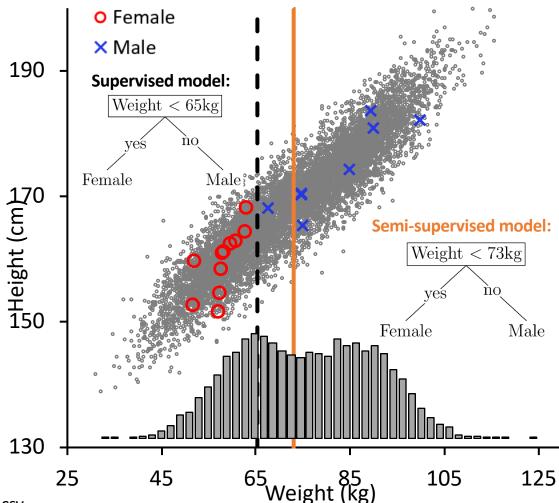


Task: Predict gender from person's weight and height

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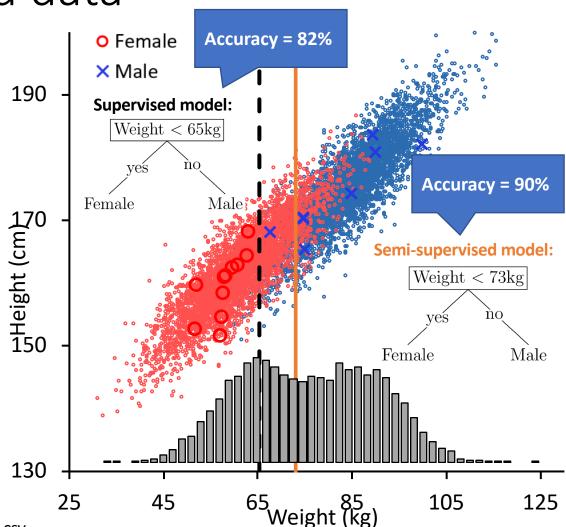


Task: Predict gender from person's weight and height

Data¹: 10000 entries of height, weight and gender

Assumptions about the labels with respect to the structure of unlabeled data





Why multi-target prediction?

Primitive outputs: $Y \subseteq \mathbb{R}$ (regression), $Y \subseteq \mathbb{N}$ (classification)

Multi-target prediction: tuple of values, potentially present hierarchical dependencies of the values

Applications:

- Gene function prediction
- Gene disease, drug/compound gene, drug side effects, …

Global or local models:

(Global) methods that take the structure into account are better!

SSL for classification tasks

		Target space			
Example 1	1	TRUE	0.49	0.69	Yes
Example 2	2	FALSE	0.08	0.07	?
Example 3	1	FALSE	0.08	0.07	?
Example 4	2	TRUE	0.49	0.69	Yes
Example 5	3	TRUE	0.49	0.69	No
Example 6	4	FALSE	0.08	0.07	?

SSL for regression tasks

		Target space			
Example 1	1	TRUE	0.49	0.69	0.84
Example 2	2	FALSE	0.08	0.07	?
Example 3	1	FALSE	0.08	0.07	0.11
Example 4	2	TRUE	0.49	0.69	?
Example 5	3	TRUE	0.49	0.69	?
Example 6	4	FALSE	0.08	0.07	0.78
•••					

SSL for multi-label classification

	Descriptive space			Т	arget space	е	
Example 1	1	TRUE	0.49	0.69	?	?	?
Example 2	2	FALSE	0.08	0.07	0	1	1
Example 3	1	FALSE	0.08	0.07	?	?	?
Example 4	2	TRUE	0.49	0.69	1	0	1
Example 5	3	TRUE	0.49	0.69	?	?	?
Example 6	4	FALSE	0.08	0.07	1	0	0
	•••				•••	•••	

SSL for multi-target regression

	Descriptive space				Ta	arget space	ce
Example 1	1	TRUE	0.49	0.69	?	?	?
Example 2	2	FALSE	0.08	0.07	0.56	0.99	7.59
Example 3	1	FALSE	0.08	0.07	?	?	?
Example 4	2	TRUE	0.49	0.69	0.08	0.77	8.86
Example 5	3	TRUE	0.49	0.69	?	?	?
Example 6	4	FALSE	0.08	0.07	0.43	2.10	8.09
•••	•••			•••	•••	•••	

Existing SSL methods for SOP

I. Methods for a specific SOP task:

- MLC: Graph based (Chen 2008; Zha 2009; Wang 2011; Kong 2013; Wang 2014, 2016), *k*NNs (d Lucena 2015), Co-training (Xu 2014), Binary relevance (Švec 2014), Boosting (Zhao 2015), SVMs (Wu 2013)
- HMLC: Spectral graph transducer (Ceci 2008), Self-training (Santos 2014)
- MTR: Gaussian processes for computer vision (Navaratnam 2007)

II. Methods for several SOP tasks:

- MLC + HMLC: SVMs (Altun 2006; Brefeld 2007; Li 2014), Co-training (Brefeld 2006), Conditional Random Fields (Wang 2009; Subramanya 2010; Dhillon 2011), *k*NNs (Jiang 2016; Du 2017), Hybrid discriminative-generative (Suzuki 2007), Graph based (Hu 2010)
- MLC + MTR: Kernelized Bayesian matrix factorization (Gönen 2014)
- HMLC + MTR: Input Output Kernel Regression (Brouard 2016)
- MLC + HMLC + MTR: This talk

Limitations of the existing methods

1) Can handle only specific type(s) of structured output(s)

Mostly nominal types

2) High Computational complexity

Conditional Random Fields, SVMs, Graph and kernel based methods

3) Difficult to use for non-experts

• The user needs to define task-specific kernels

4) None of the existing methods produce interpretable models

• Important in knowledge discovery aspect of predictive modeling

5) Limited application and evaluation

- Evaluated only on specific domains and/or very few datasets
- Advantages as compared to supervised methods are not clear

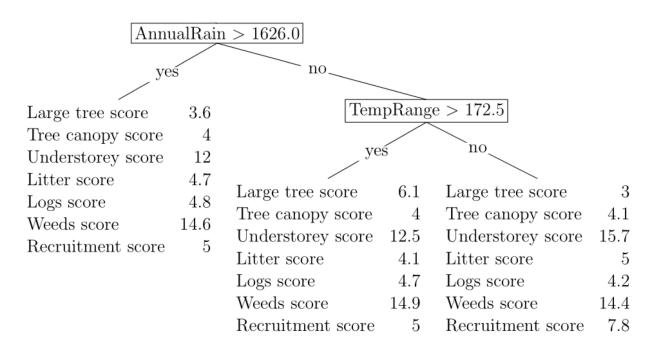
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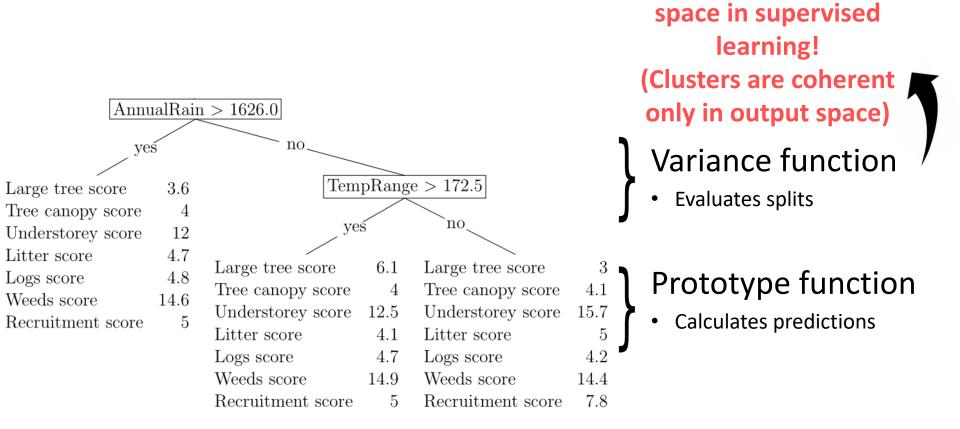
Predictive clustering trees

- Generalization of decision trees towards various tasks, including MTR, MLC and HMLC
- Computationally efficient
- Easy to use Interpretable models

Easily extendable towards SSL for SOP!







Considers only output

PCTs instantiations

- Multi-target regression
 - Prototype: Average
 - Variance: $Var(E) = \sum_{i=1}^{T} Var(Y_i)$
- Multi-target classification/Multi-label classification
 - Prototype: Probability distribution and Majority vote
 - Variance: $Var(E) = \sum_{i=1}^{T} Gini(E, Y_i) \text{ or } Var(E) = \sum_{i=1}^{T} Entropy(E, Y_i)$
- Hierarchical multi-label classification
 - Prototype: Average with a threshold for class membership
 - Hierarchy type: tree or DAG

Variance:

$$Var(E) = \frac{1}{|E|} \cdot \sum_{E_i \in E} d(L_i, \overline{L})^2,$$

$$d(L_1, L_2) = \sqrt{\sum_{i=1}^{|L|} \omega(c_i) \cdot (L_{1,i} - L_{2,i})^2}, \ \omega(c_i) = \omega_0 \cdot \omega(par(c_i))$$

Semi-supervised PCTs

Variance function: Variance of output space + Variance of input space

 $Var_f(E, Y, X) = w \cdot Var_f(E, Y) + (1 - w) \cdot Var_f(E, X)$

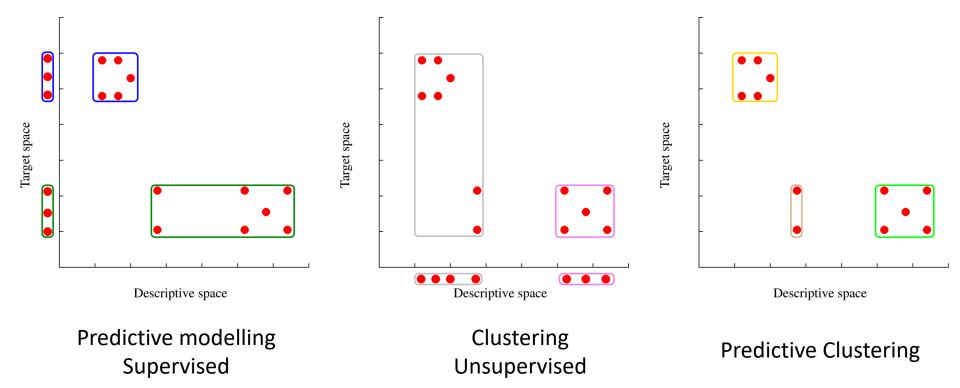
 $w \in [0, 1]$ = controls the amount of supervision:

w = 00 < w < 1w = 1UnsupervisedSemi-supervisedSupervised

- Var_f(E, Y) and Var_f(E, X) extended to handle unlabeled data
- Resolved mixing different variances: numeric/nominal/hierarchical

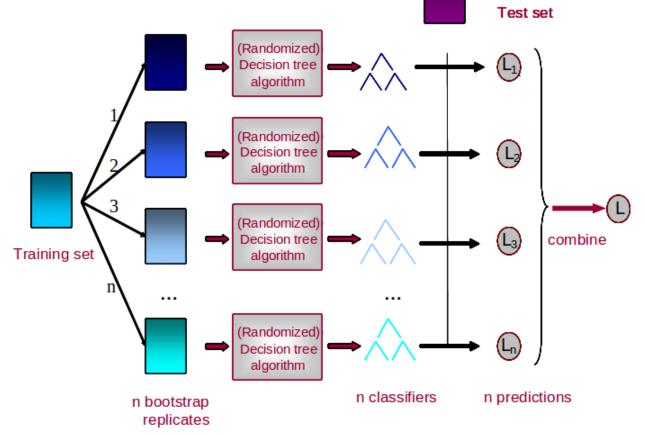
Predictive clustering

Clusters are coherent in both input and output spaces



Ensembles of semi-supervised PCTs

Once we have developed SSL PCTs, it is fairly easy to learn ensembles



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Experimental evaluation

1) Predictive performance

- Can we improve over supervised PCTs?
- Influence of the amount of labeled data?

2) Influence of the *w* parameter

• How it affects the performance?

3) Influence of the unlabeled data

- is it necessary to improve?
- 4) Interpretability and model sizes
- 5) Predictive performance for tasks with primitive outputs

Experimental setup

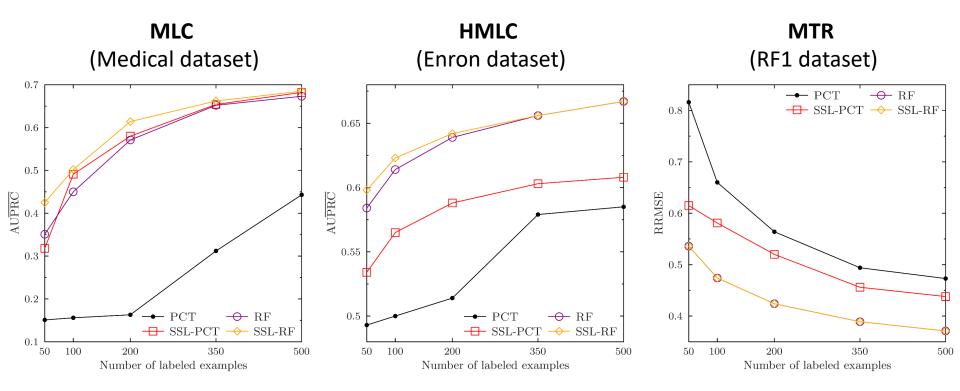
Comparison: Supervised PCTs (PCT) and Random Forests (RF)

Datasets: ecology, economy, biology, astronomy, text, audio, images... 12 datasets each task

- Multi-target prediction: MTR, MLC and HMLC
- Primitive output: binary, multi-class classification and regression
- Labeled data: 50, 100, 200, 350, 500 labeled examples
- Selected at random, the rest is unlabeled
- 10 random repetitions •
- **Evaluation:** Unlabeled data = Test set

w **parameter:** optimized via internal 3-fold cross validation

Predictive performance (examples)



Statistical analysis

p-values of Wilcoxon paired signed rank test (lpha=0.05)*

	Mothods		Number of labeled examples						
	Methods			100	200	350	500		
Multi-target regression									
РСТ	VS.	SSL-PCT	0.093	0.022	0.028	0.022	0.009		
RF	VS.	SSL-RF	0.959	0.445	0.445	0.333	0.445		
		Mul	ti-label cla	ssificatio	n				
PCT	VS.	SSL-PCT	0.013	0.008	0.008	0.093	0.053		
RF	VS.	SSL-RF	0.241	0.415	0.262	0.308	0.575		
	Hierarchical multi-label classification								
РСТ	VS.	SSL-PCT	0.834	0.093	0.028	0.028	0.028		
RF	VS.	SSL-RF	0.345	0.345	0.249	0.345	0.345		

*In all tests, semi-supervised algorithms have better sum of ranks

Influence of the *w* parameter

Unlabeled data can hurt the performance

• No semi-supervised method is universally good

180 experiments	Wins	Ties	Loses
SSL-PCT vs. PCT	67%	25%	8%

 Average relative improvement over PCTs is 43% (degradation 8%)

w provides safety mechanism!

w needs to be optimized for every dataset/amount of labeled data

Influence of the unlabeled data

PCT^{*D*+*T*} : supervised variant of SSL-PCTs

- Considers both input and output space
- It is not supplied with unlabeled data

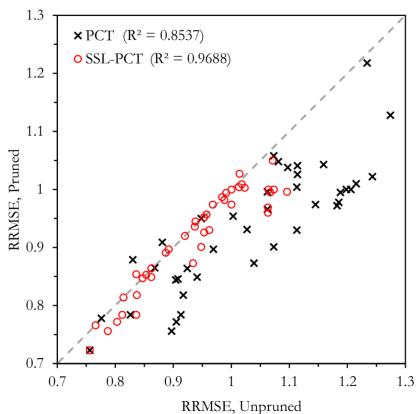
180 experiments	Wins	Ties	Loses
SSL-PCT vs. PCT^{D+T}	41%	46%	13%
SSL-PCT vs. PCT	67%	25%	8%

Average relative improvement of PCT^{*D*+*T*} over PCTs is 5% Unlabeled data are the principal component of SSL-PCTs!

Interpretability and model sizes

- SSL-PCTs produce readily interpretable models
- The only such SSL method for MTP
- SSL-PCTs can even enhance interpretability of PCTs
 - smaller model size
- SSL-PCTs less affected by pruning
 - overfit less than PCTs





SSL-PCTs for primitive outputs

p-values of Wilcoxon paired signed rank test (lpha=0.05)*

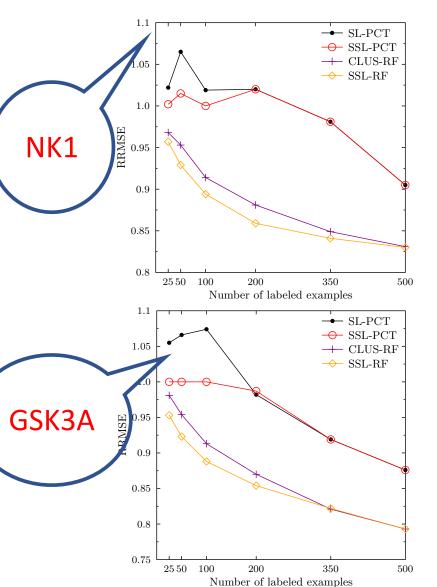
	Methods		Number of labeled examples					
	Methot	12	25	50	100	200	350	500
			Binary c	lassificat	tion			
РСТ	VS.	SSL-PCT	0.009	0.388	0.066	0.005	0.019	0.019
RF	VS.	SSL-RF	0.529	0.192	0.002	0.099	0.093	0.012
		Μ	ulti-class	s classifi	cation			
PCT	VS.	SSL-PCT	0.248	0.084	0.014	0.007	0.192	0.081
RF	VS.	SSL-RF	0.563	0.011	0.011	0.003	0.004	0.02
	Regression							
РСТ	VS.	SSL-PCT	0.011	0.01	0.004	0.367	0.48	0.583
RF	VS.	SSL-RF	0.008	0.065	0.008	0.023	0.034	0.126

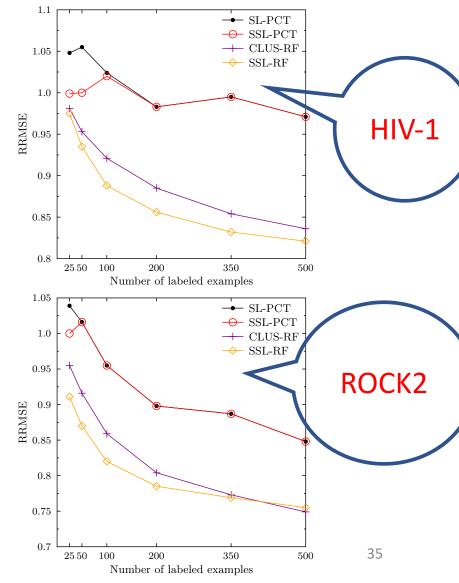
*In all tests, semi-supervised algorithms have better sum of ranks

Illustrative study on QSAR datasets

Dataset	Domain	N	D/C
Neurokinin 1 receptor	QSAR	2446	1024/0
(NK1)		2110	1021/0
Glycogen synthase kinase-3 alpha	QSAR	1211	1024/0
(GSK3A)			10-1/0
Rho-associated protein kinase 2	QSAR	1521	1024/0
(ROCK2)	- -		/ _
Human immunodeficiency virus type 1 protease	QSAR	4442	1024/0
(HIV-1)	V -		
		F	CFP
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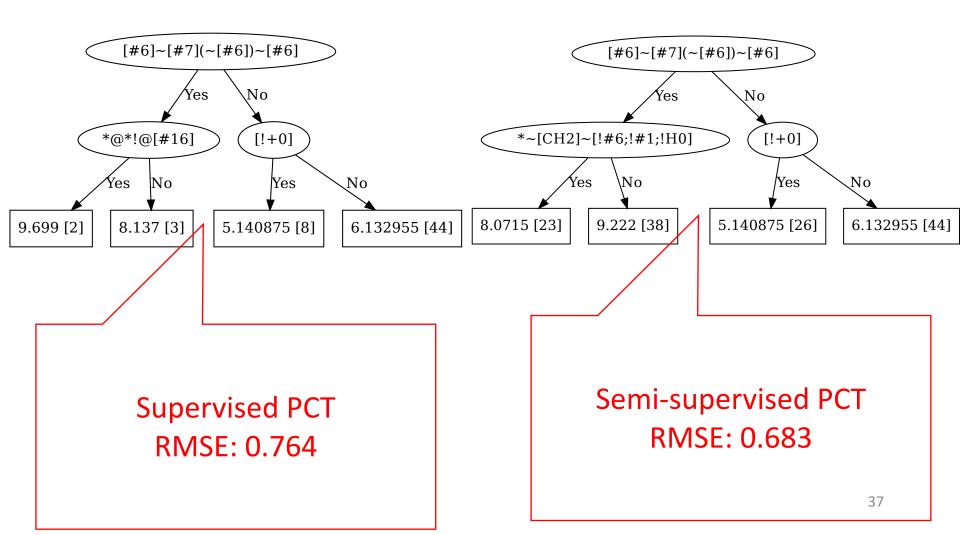
Performance results

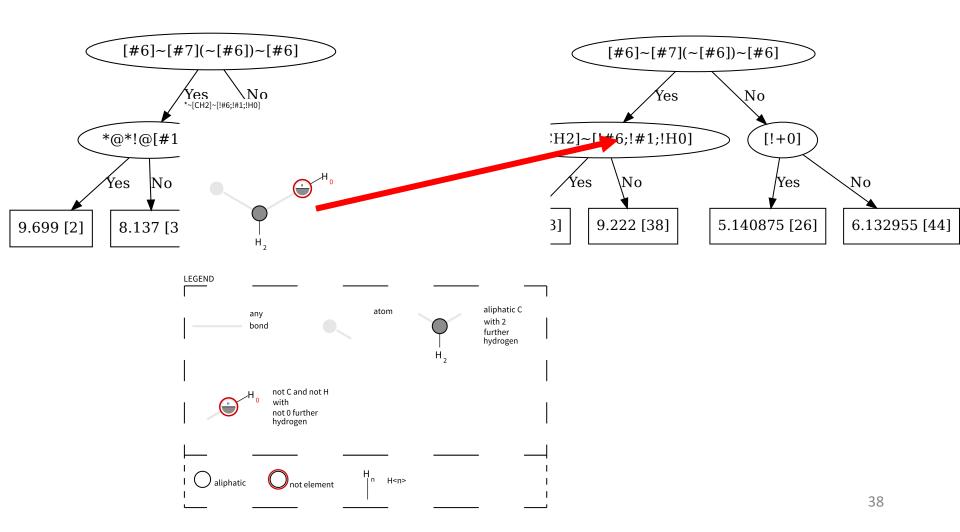


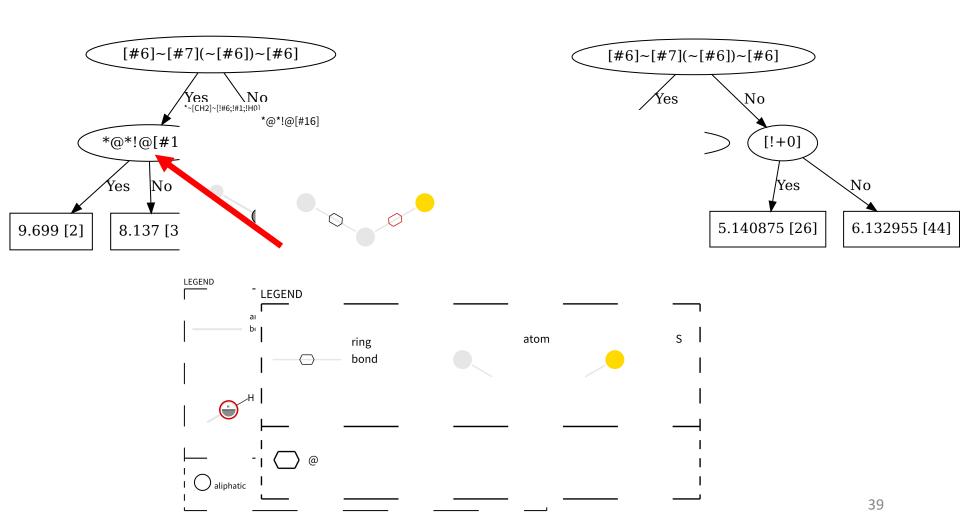


Interpretability potential

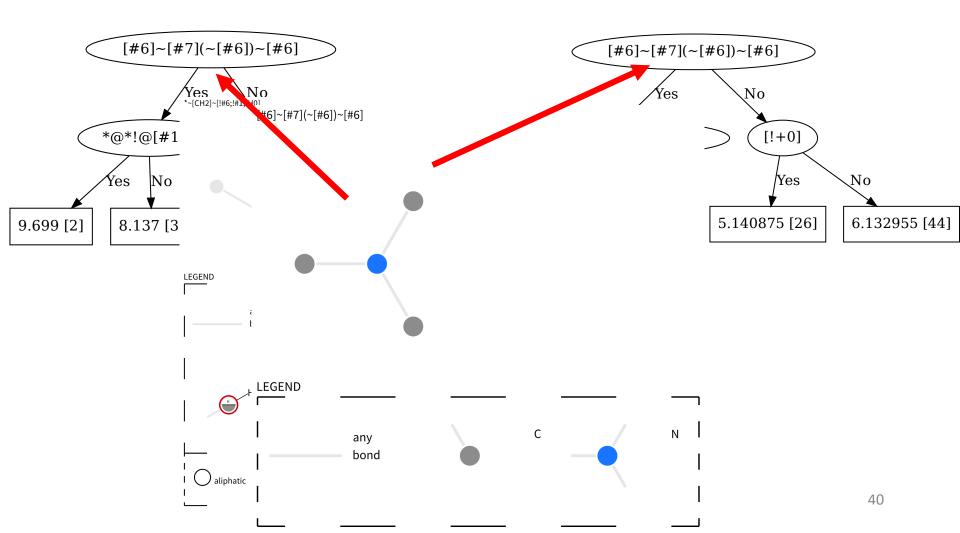
- Focus on farnesyltransferase (FTase)
- 57 compounds that inhibit FTase in *Saccharomyces* cerevisiae S288c
- Extracted 74 other compounds with unknown inhibitory property (and Tanimoto similarity > 0.8)
- MACCS structural keys fingerprints calculated with the RDKit library
- The fingerprints are binary vectors of length 166, where each bit corresponds to a specific SMARTS pattern

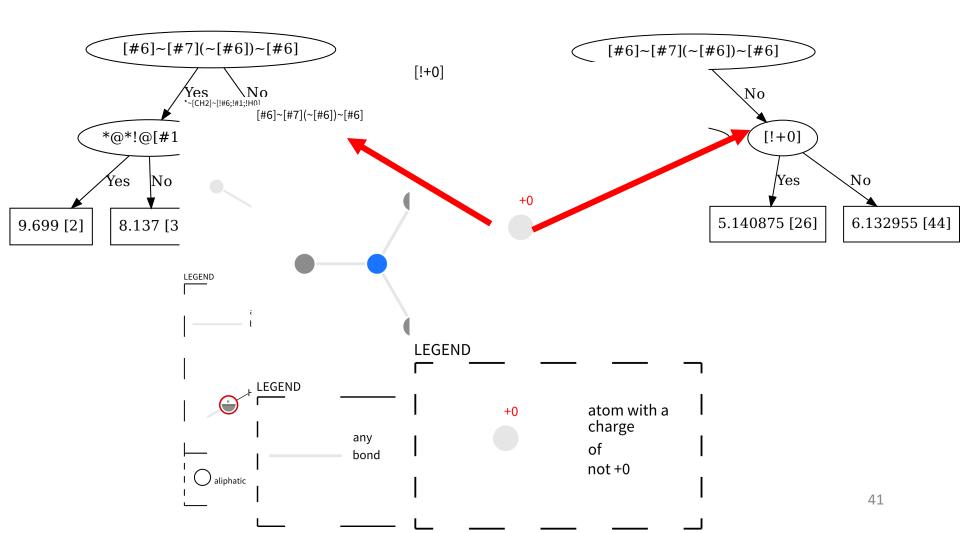












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Conclusions

- Versatile in terms of MTP tasks (and also primitive outputs)
- Improve predictive performance of supervised PCTs and overfit less
- Highly useful in practice ("safety mechanism", easy to use)
- Performance improvement does not entirely translates to the ensemble setting
- Interpretable models (even can enhance interpretability)

Questions?