

# Machine learning and chemistry

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the Kulik group at MIT, [hjkgrp.mit.edu/](http://hjkgrp.mit.edu/)

under the supervision of Professor Heather J. Kulik

for the most recent version and demos: [github.com/jpjanet/ML-chem-workshop](https://github.com/jpjanet/ML-chem-workshop)  
this revision: ce901f5178d2c5ffd460dfa1b7a54197612dce49 on branch master





## Rise of the (chemical) machines

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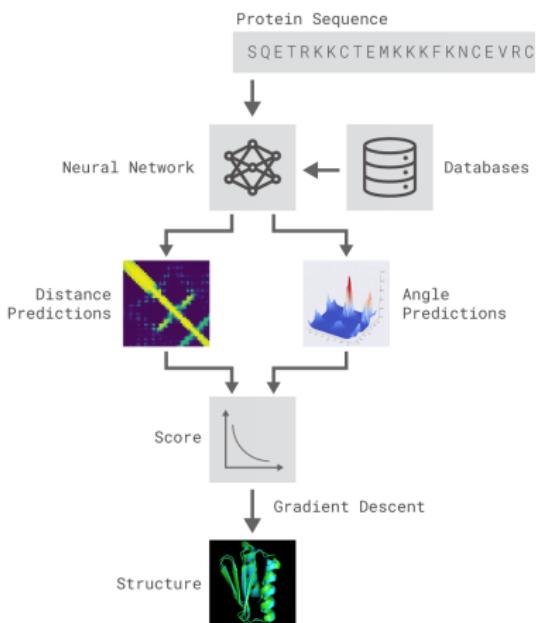
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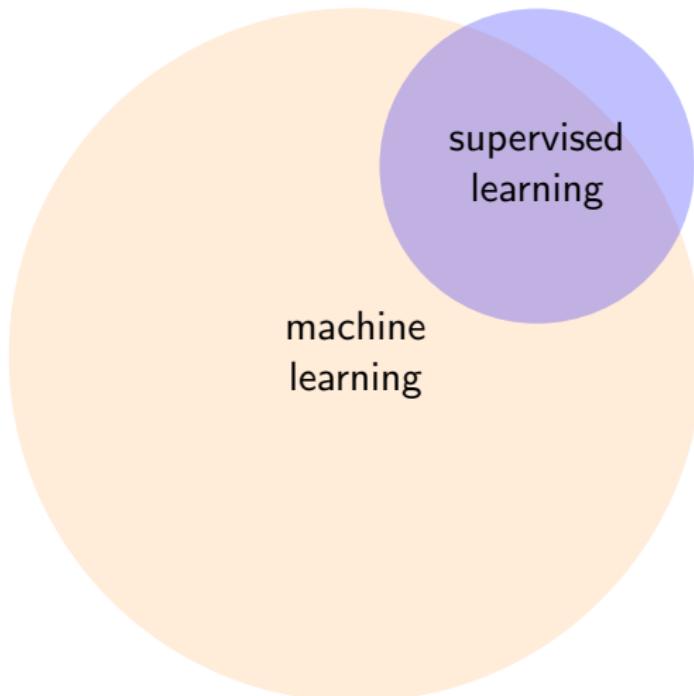
This is probably a bit strong, but all scientists generate data as a product. ML provides new, powerful ways to exploit their that information.

# Types of machine learning

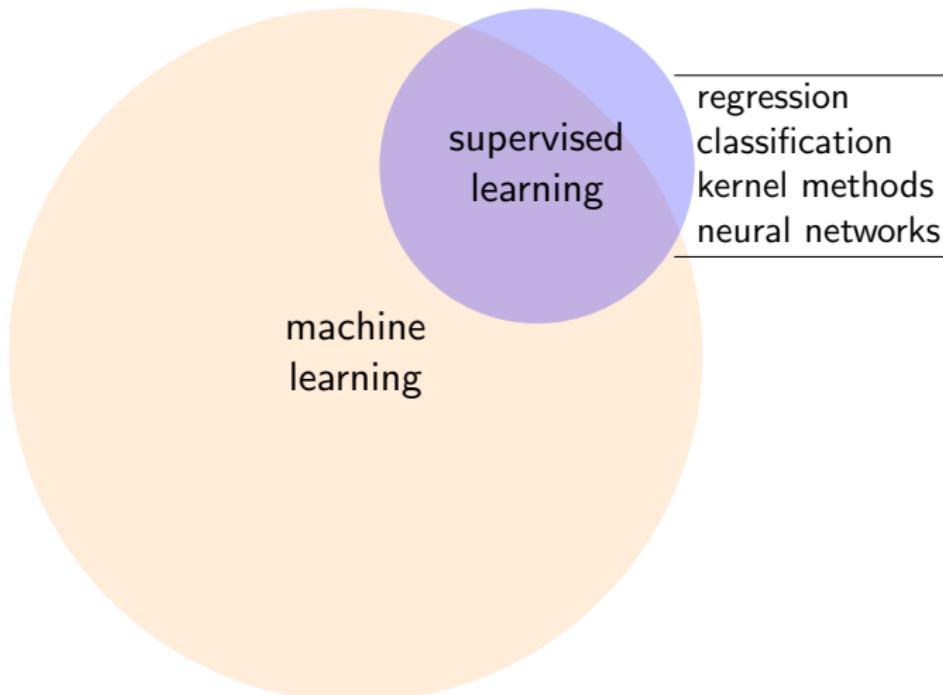
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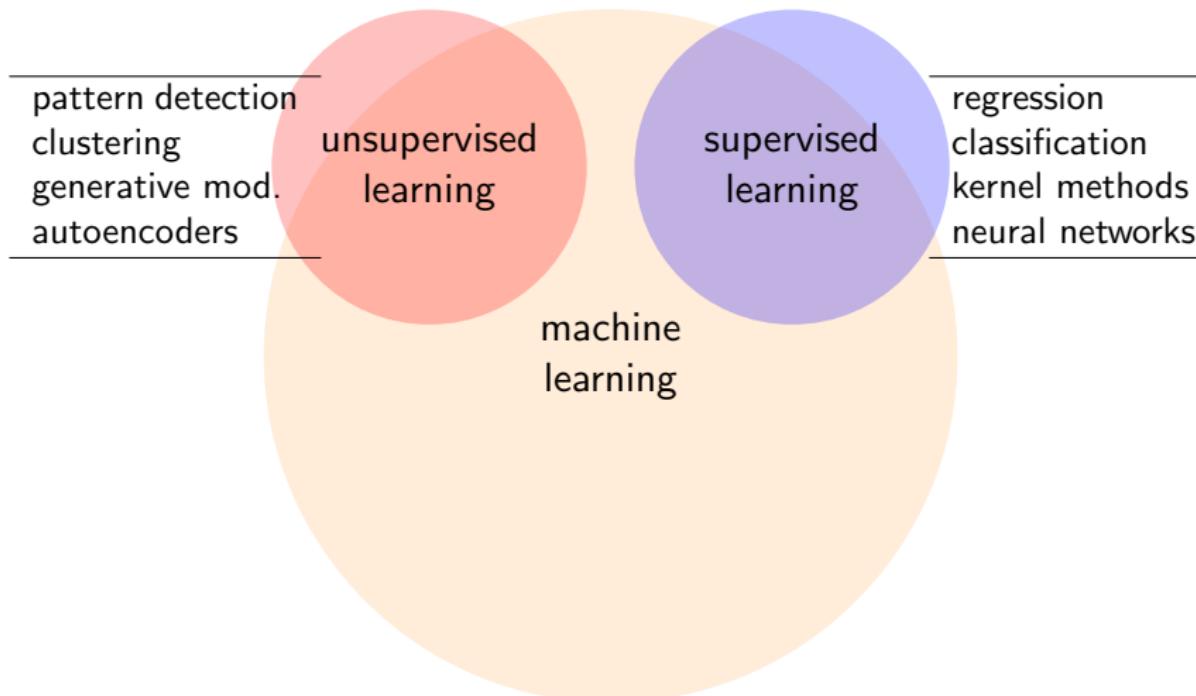
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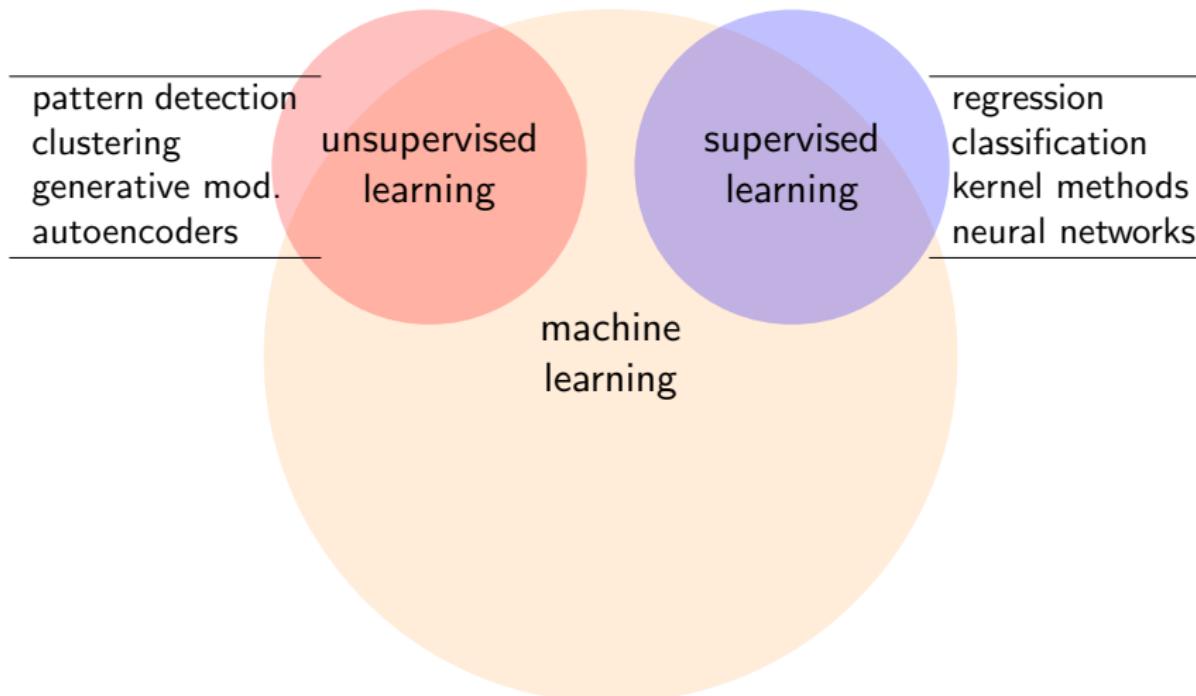
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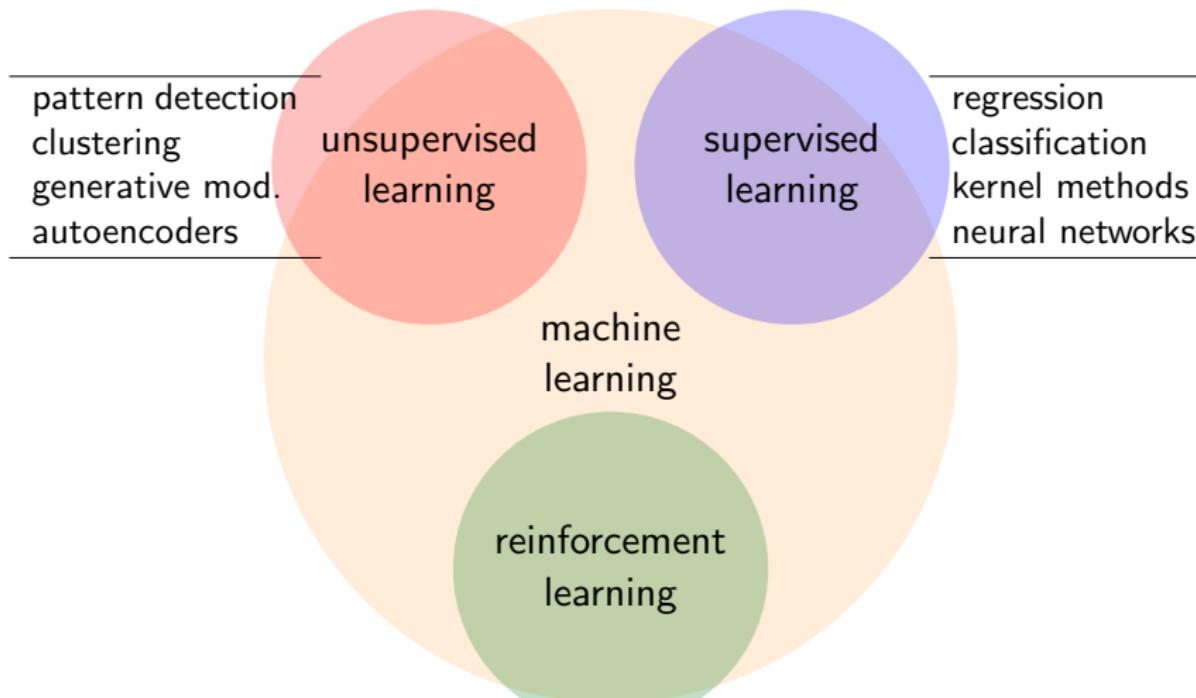
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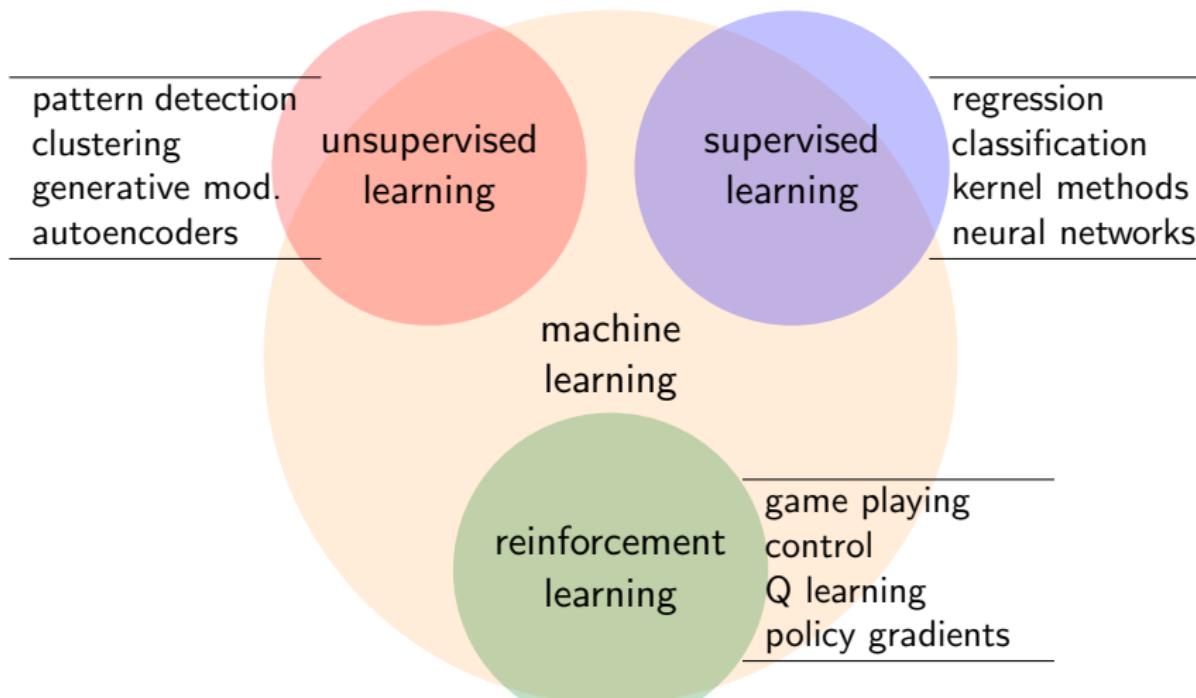
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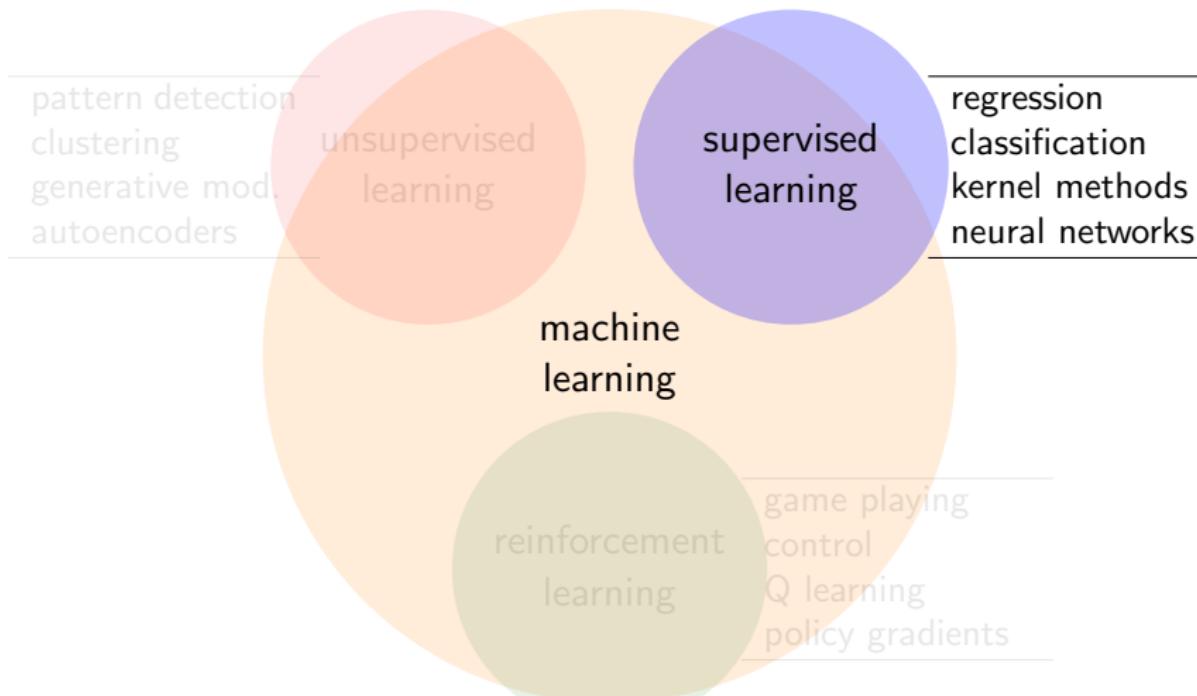
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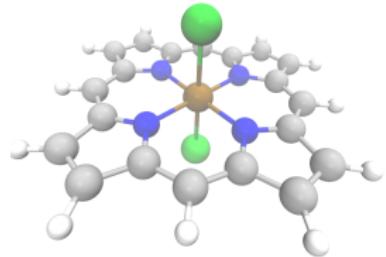
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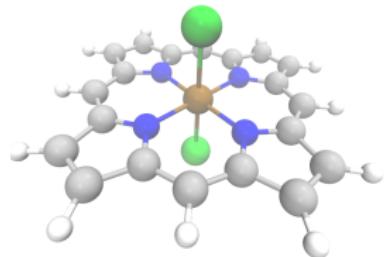
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# Why ML in chemistry?

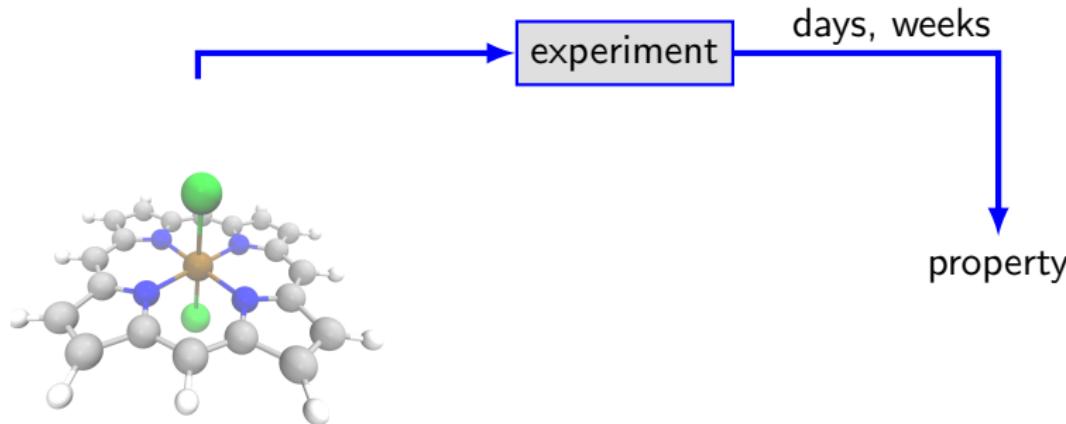


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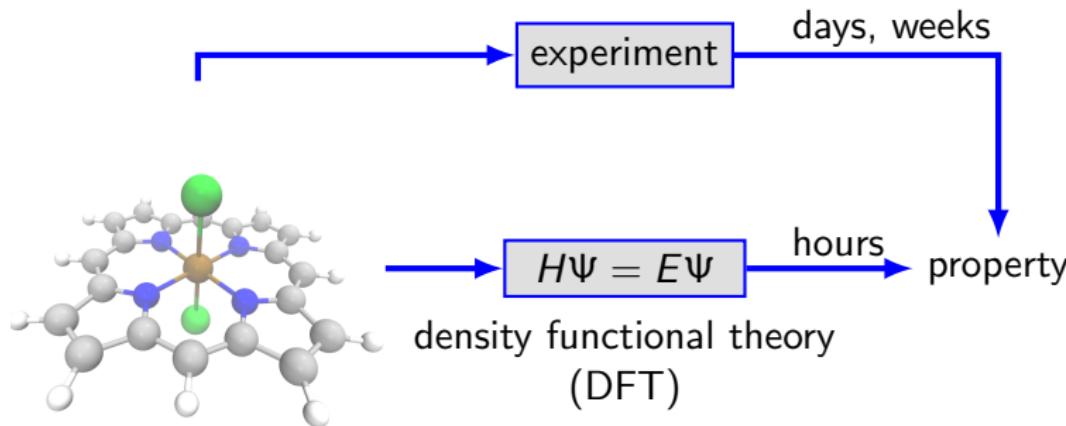


property

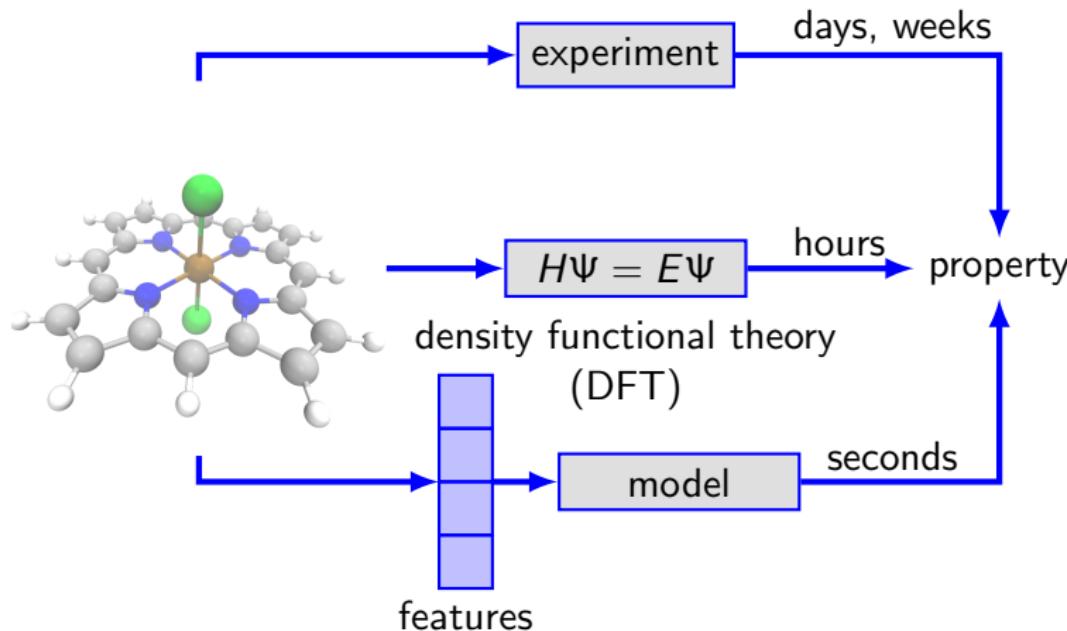
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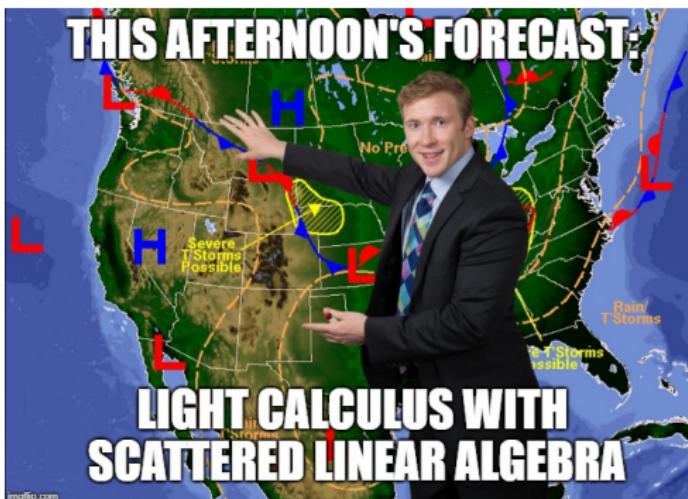
Please ask questions throughout!

# Disclaimer

Warning: this talk contains some *light* mathematics.

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Some useful notation:

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$X$	training data, as rows
$x^*$	one new molecule/systems
$y, \hat{y}$	property(energy?), predicted value
$\mathcal{L} = \ y - \hat{y}\ _2^2$	loss function
$W, w$	model parameters
$\hat{y} = f(x, W)$	our model

---

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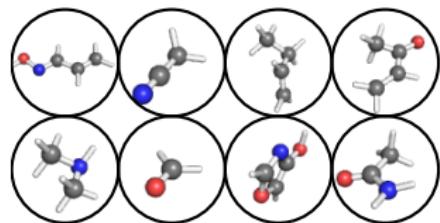
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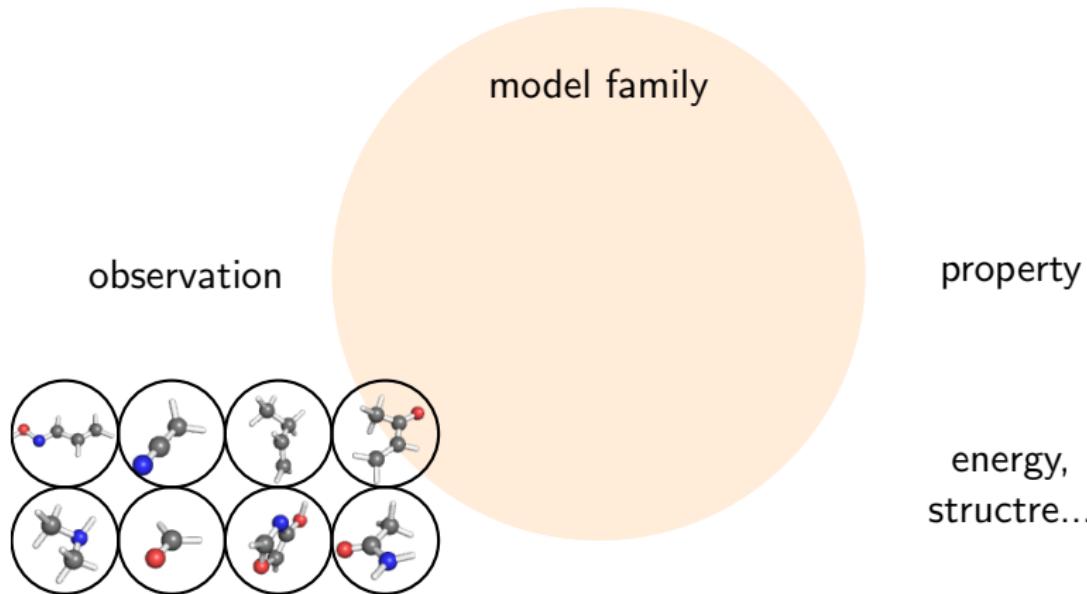
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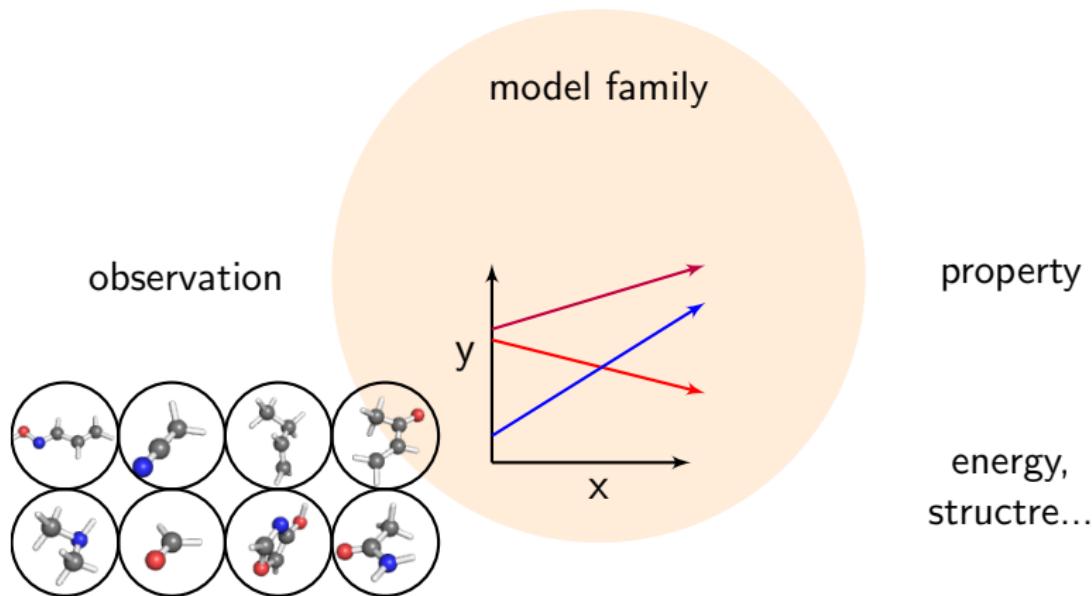


energy,  
structre...

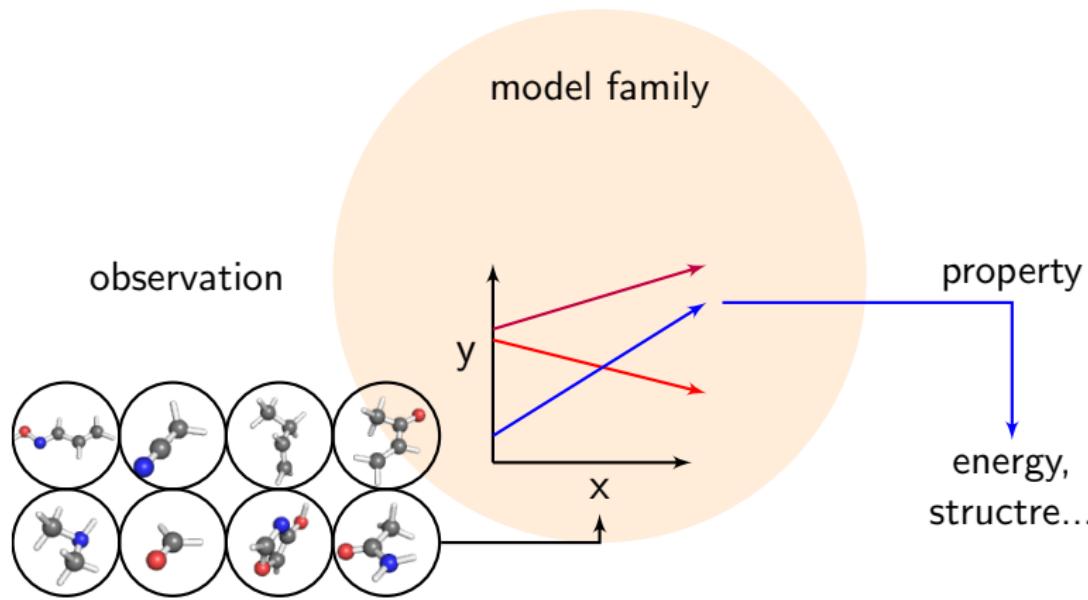
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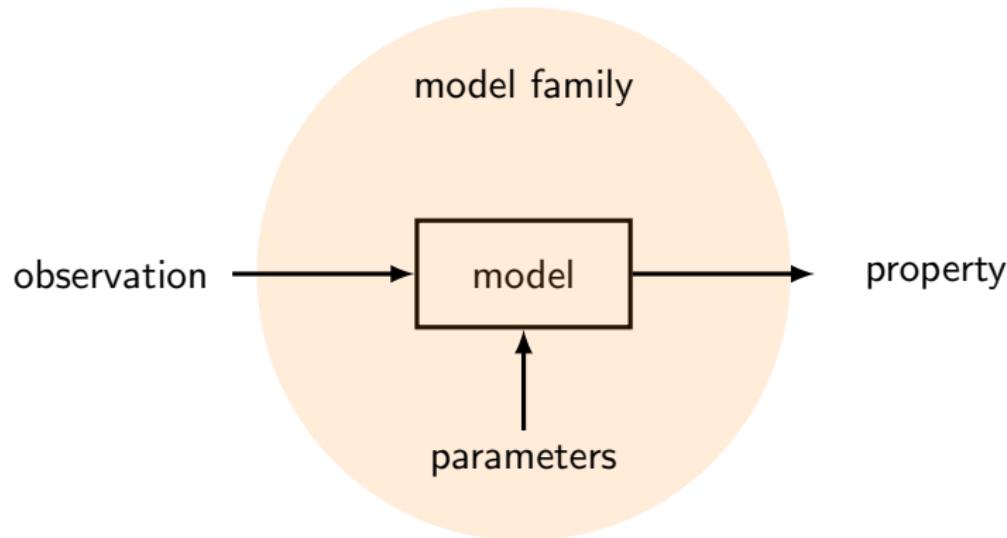
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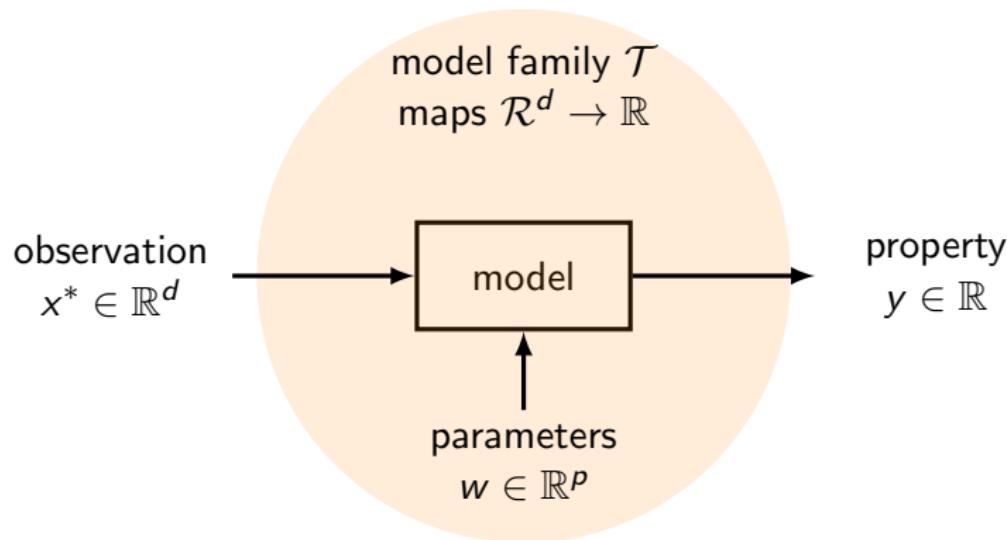
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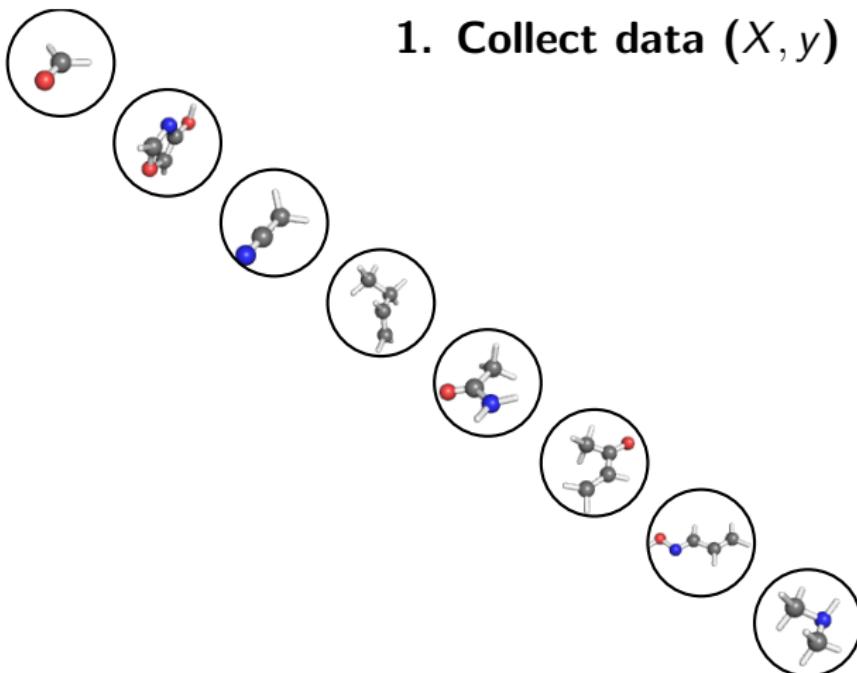


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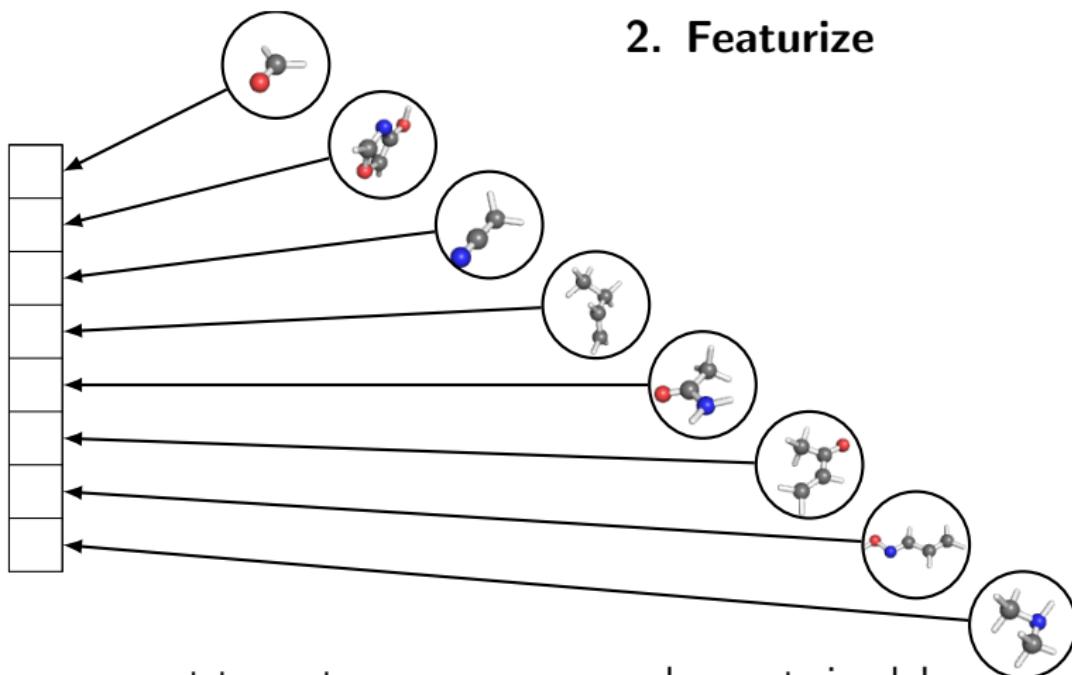
# Overview of supervised learning

## 1. Collect data ( $X, y$ )



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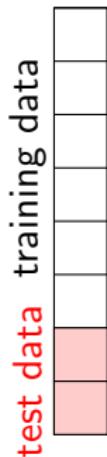
## 2. Featurize



convert to vectors, preprocess, scale – not simple!

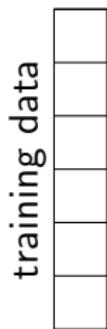
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## 3. Partition data

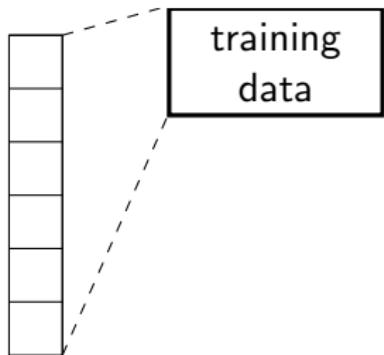


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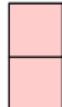
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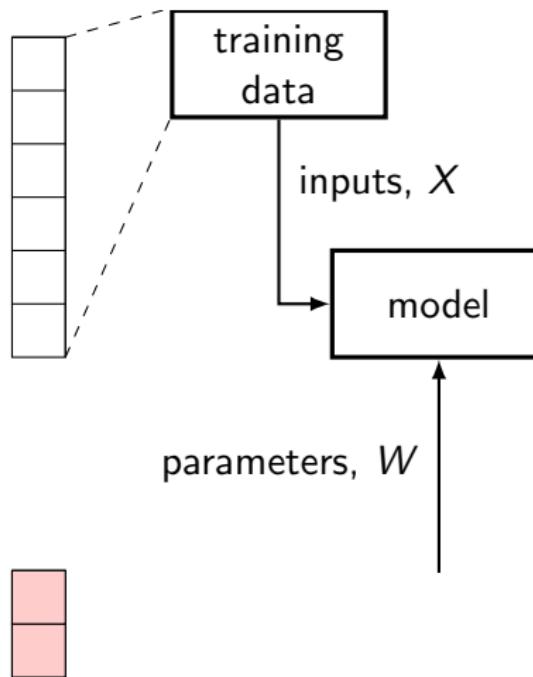
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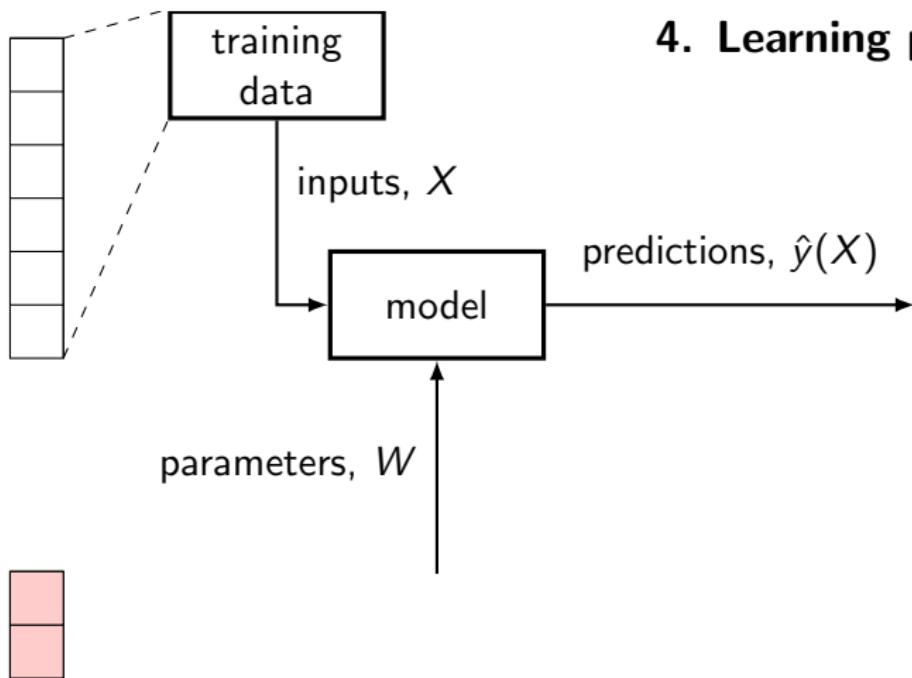


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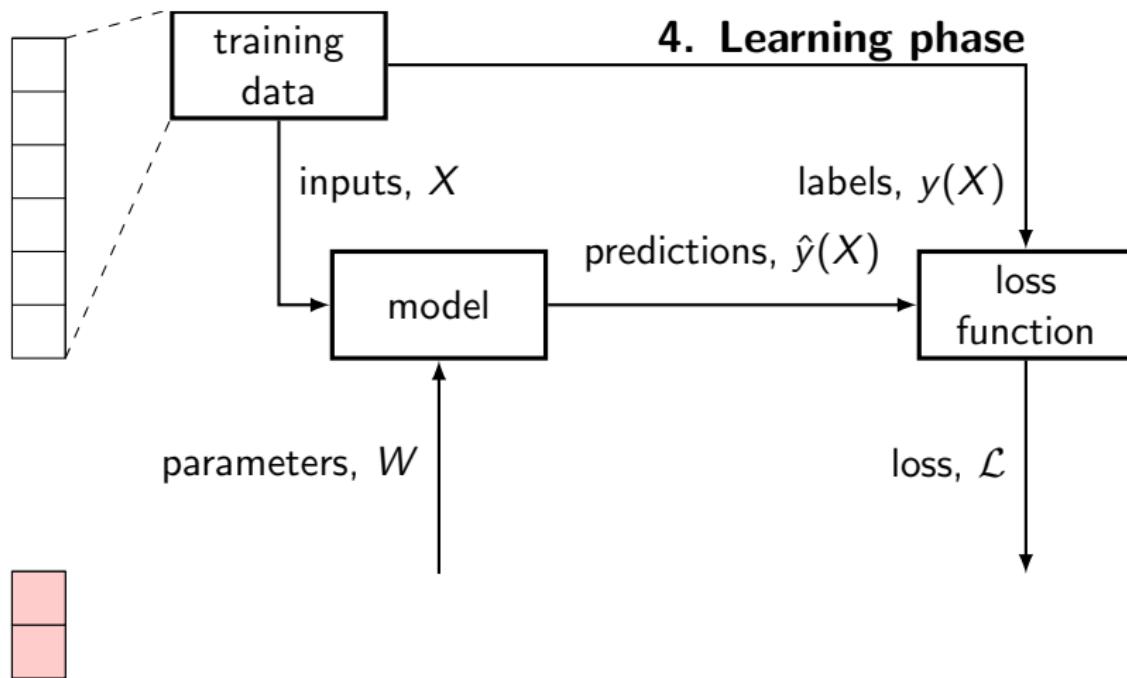
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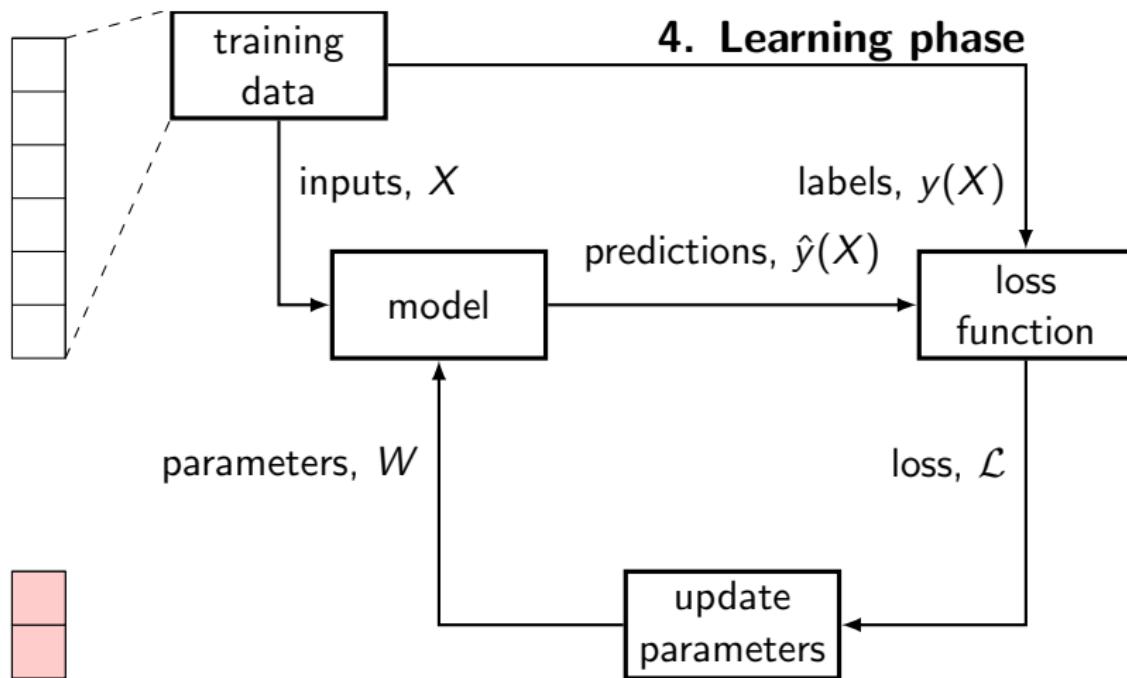


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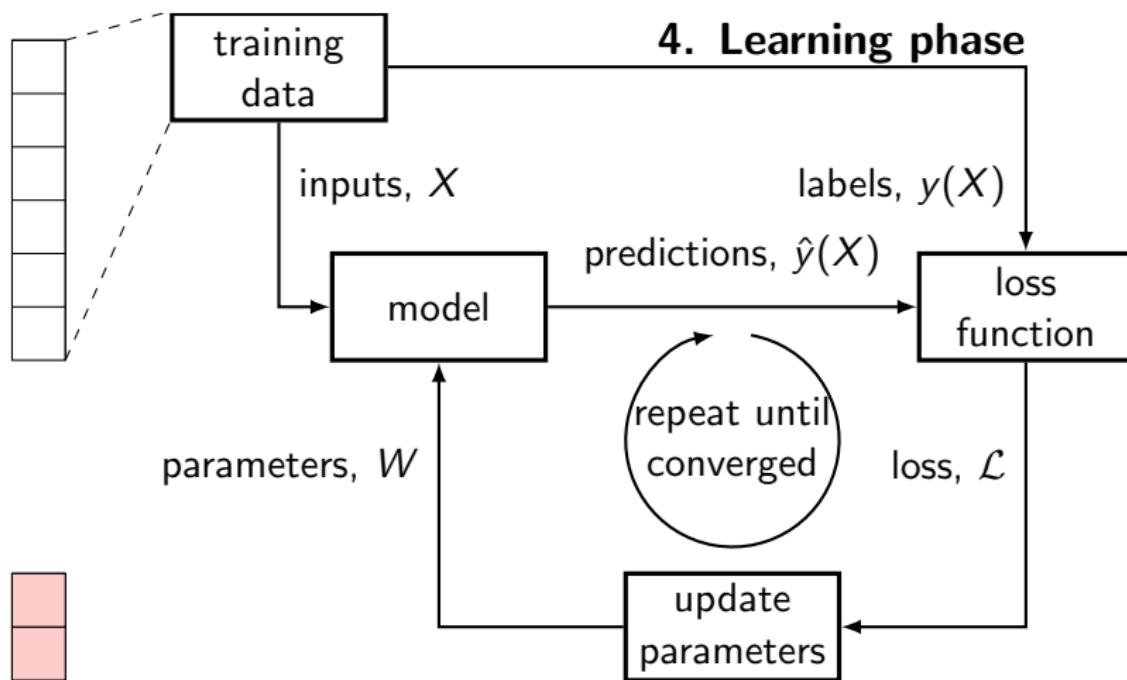
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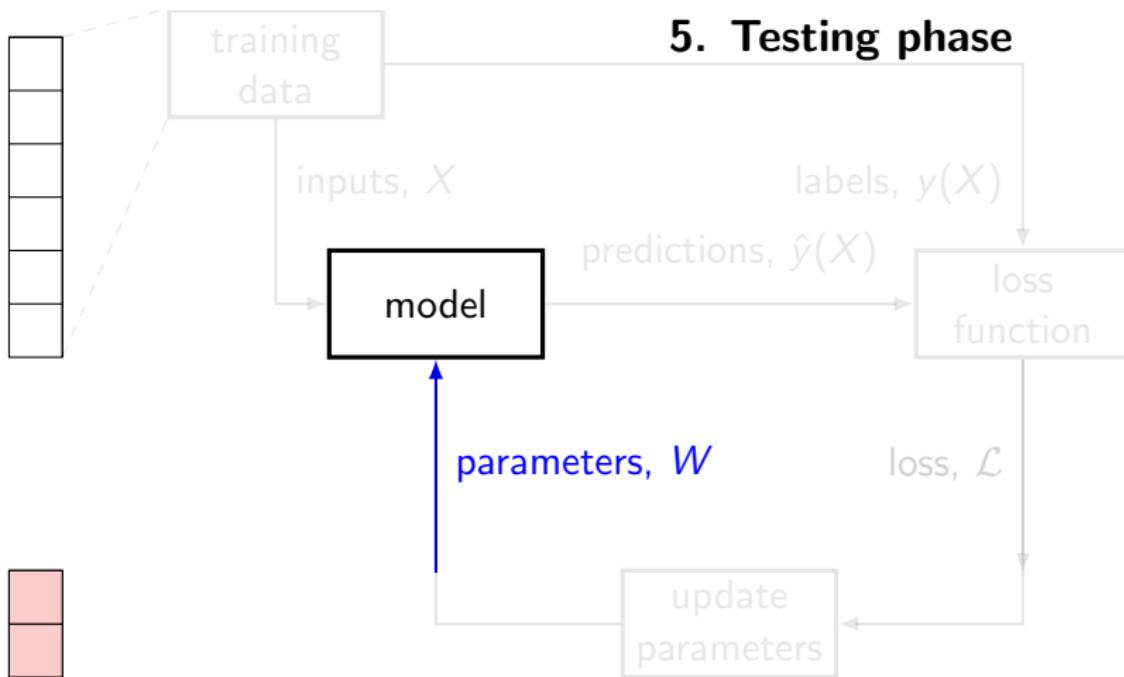
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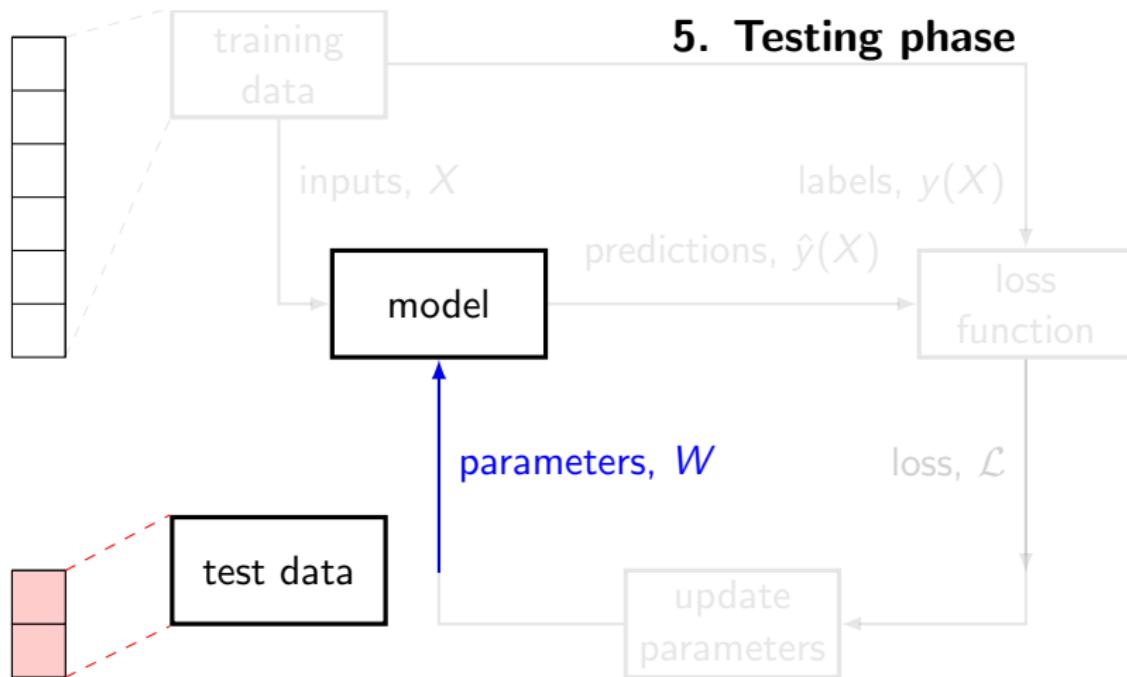
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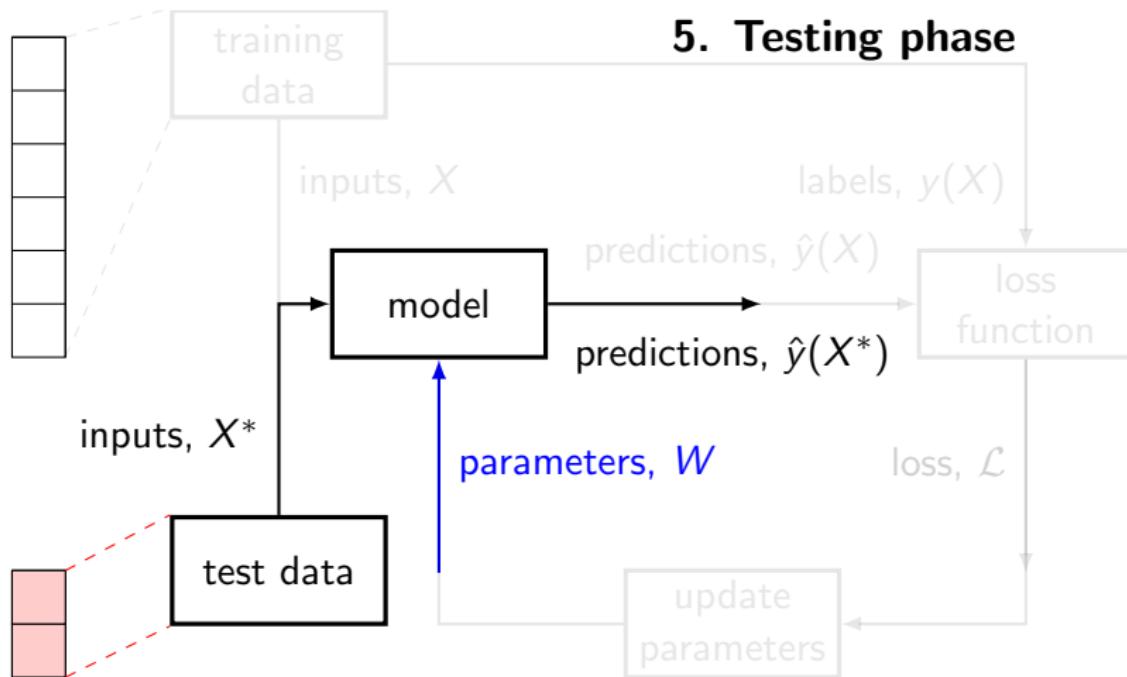
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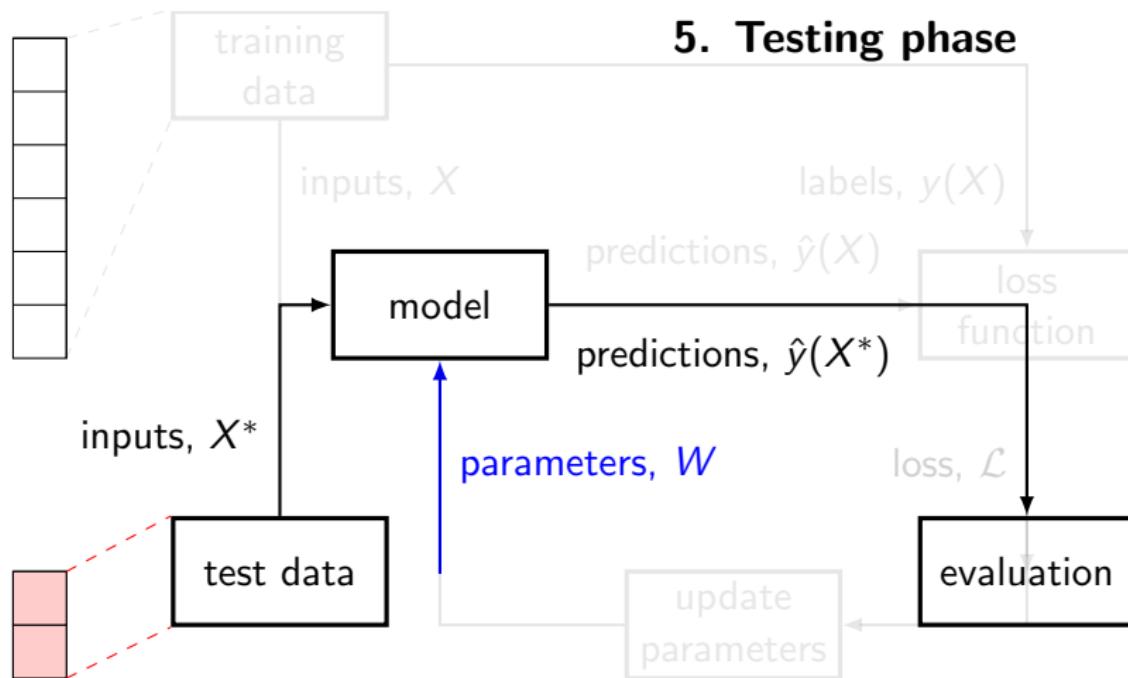
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$$f^* = \mathbb{E} [Y | X = x]$$

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We want  $\mathcal{T}$  to be large/complicated enough to have low approximation error, **but no more complicated**.

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With limited data, we are often better off searching for a model in a simpler family models of that 'learn' more robustly and quickly as opposed to very complicated models with lots of parameters.

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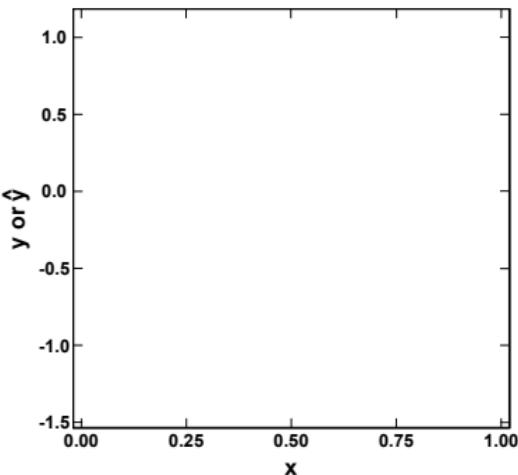
Conversely, a simple model will stop improving with more data past a certain point – where the approximation error dominates.

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Let us use **polynomials** to estimate:

$$y(x) = \sin(2\pi x)$$

Note that  $f^* \notin \mathcal{T}$ !



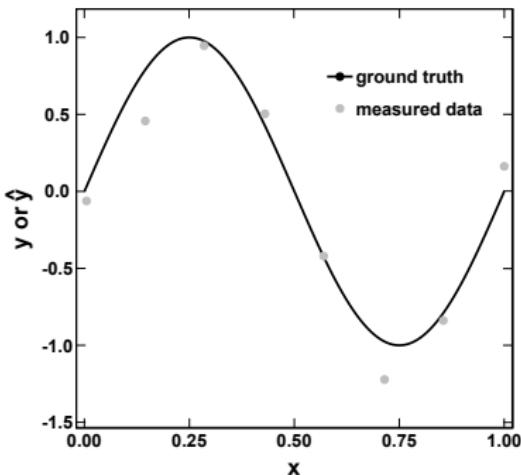
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Assume 8 measurements with noise  $\mathcal{N}(0, 0.2)$



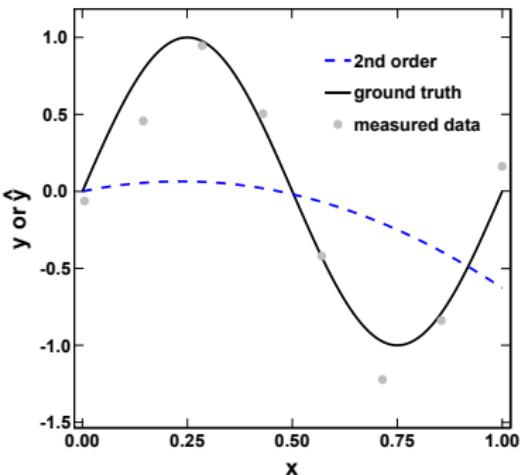
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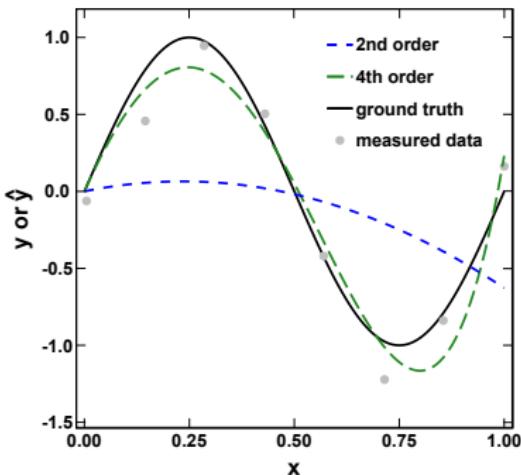
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Start with degree 2...What happens when we increase the order?

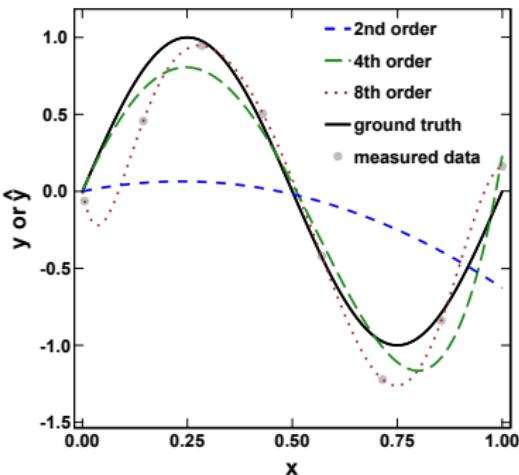


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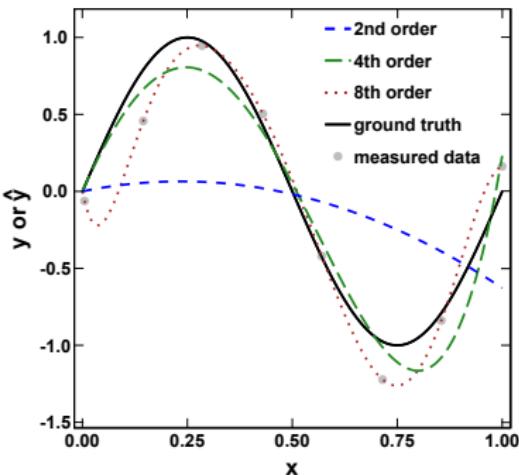
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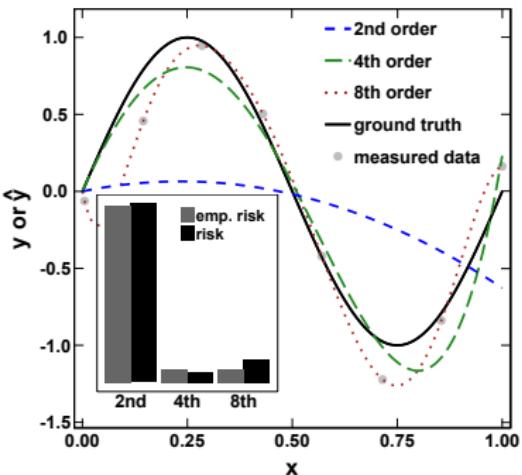
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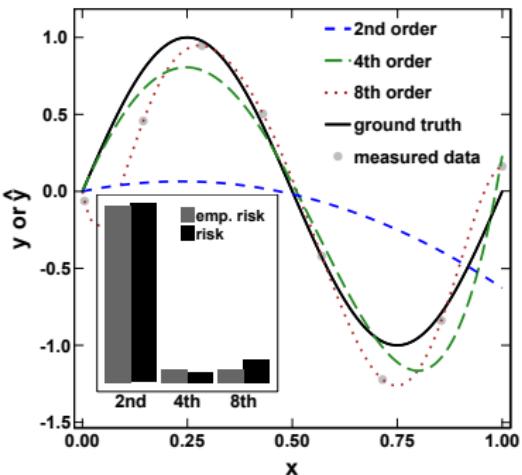


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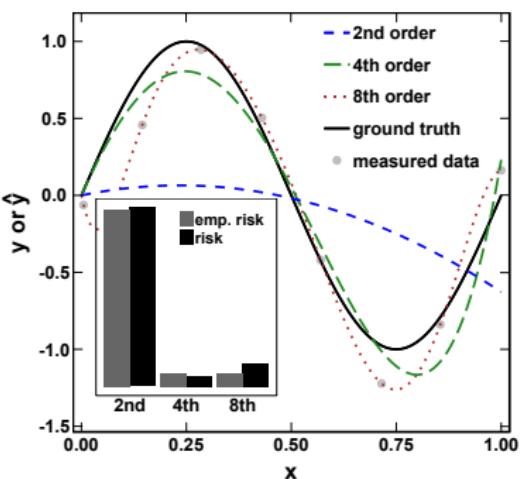
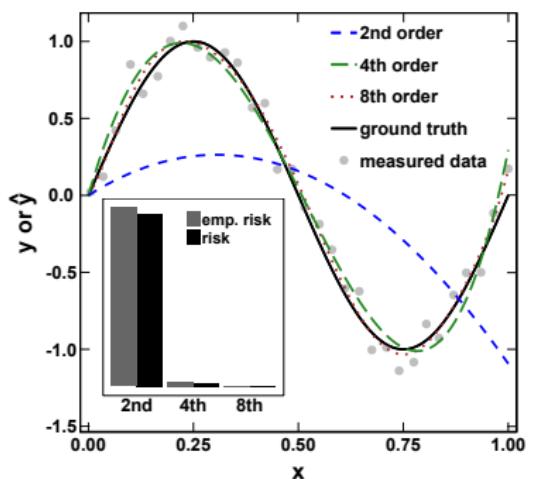
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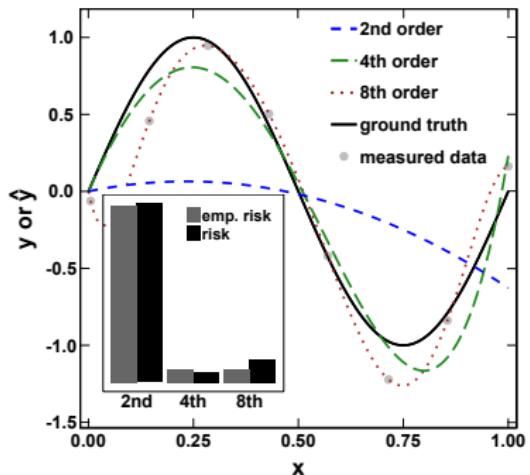
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- This makes empirical errors worse.
- This *can* improve generalization/excess risk.

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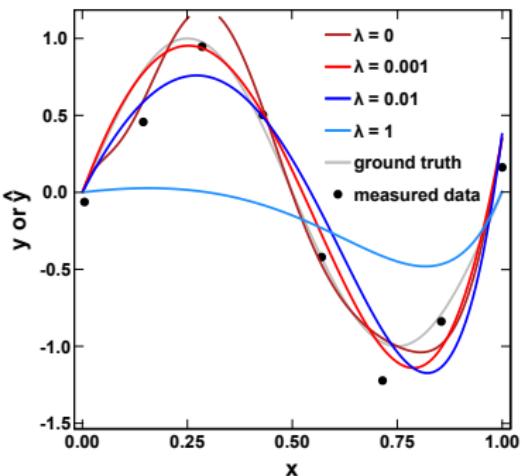
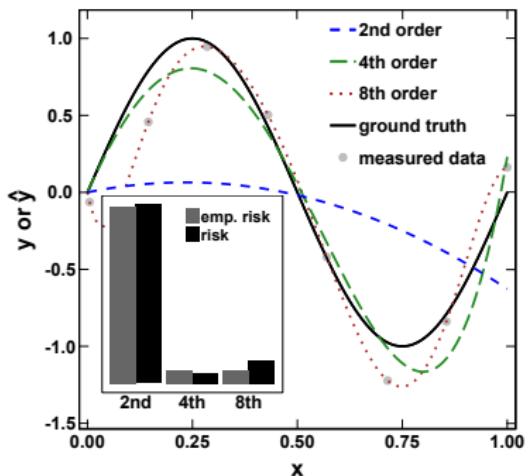
Let's return to our previous example:



Remember: larger  $\lambda$  = simpler, flatter model.

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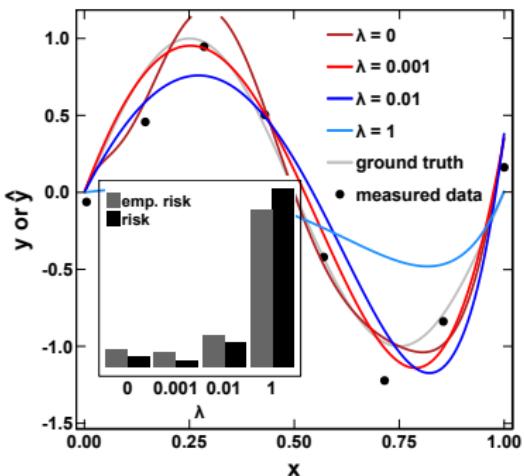
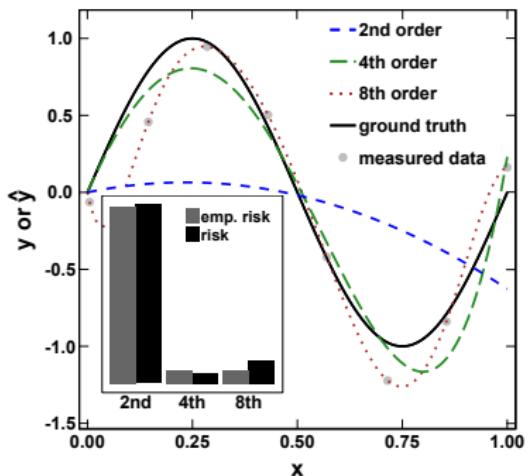
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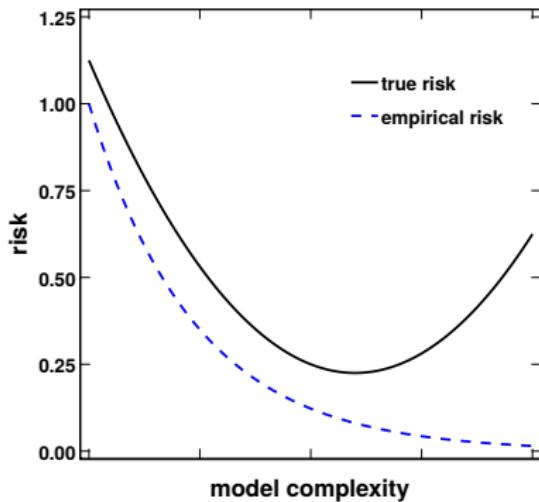
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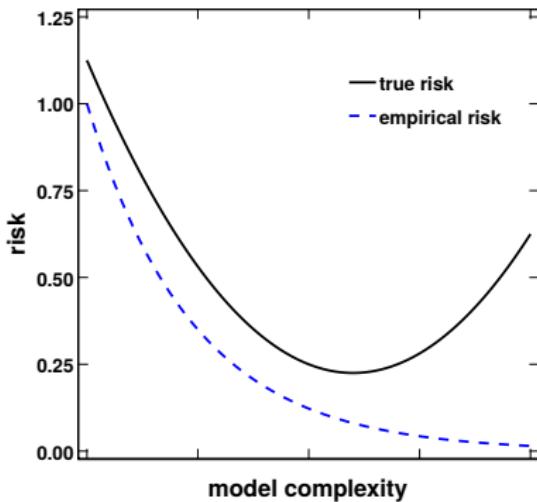


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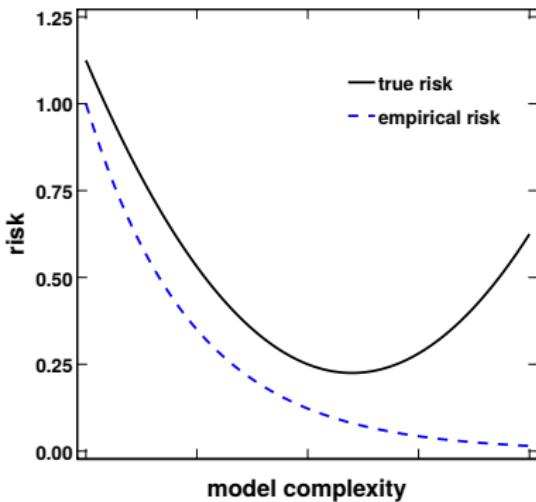


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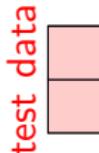
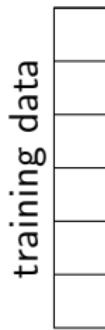
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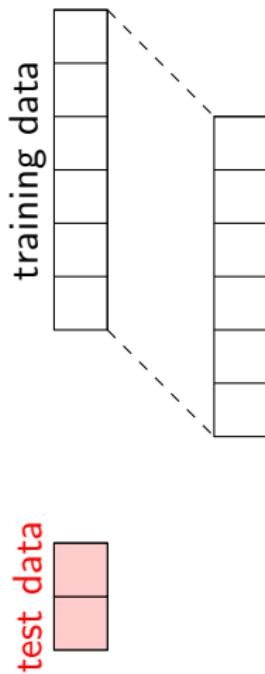


None of this helps us understand how complicated our model should be. Unfortunately, **errors on our training data cannot tell us the answer**

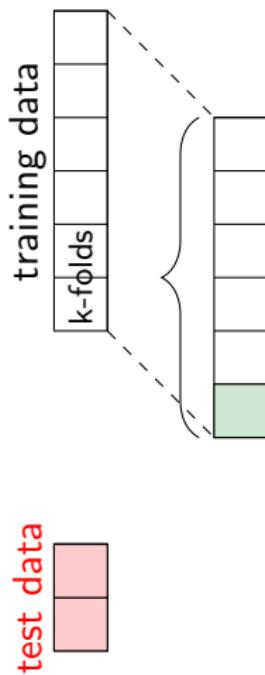
# (Cross)-validation



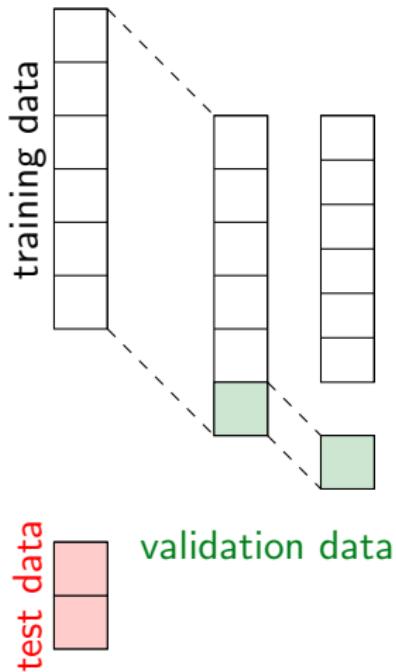
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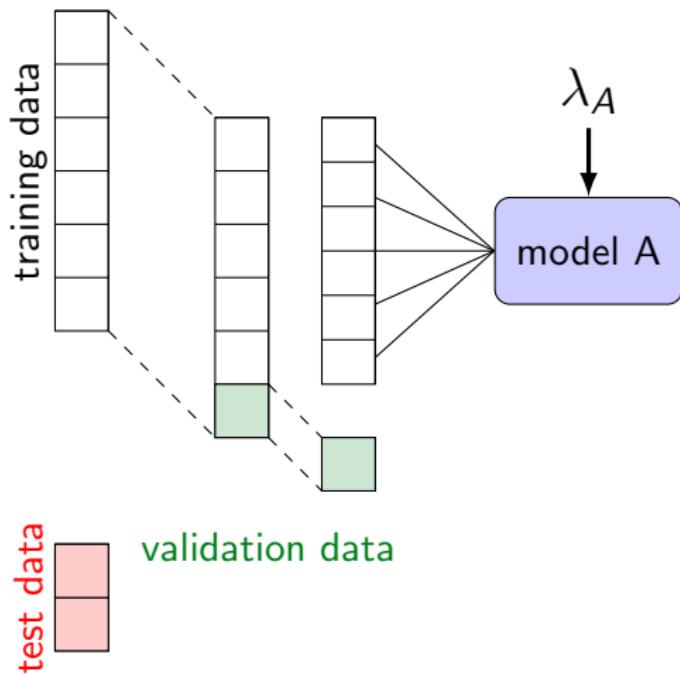
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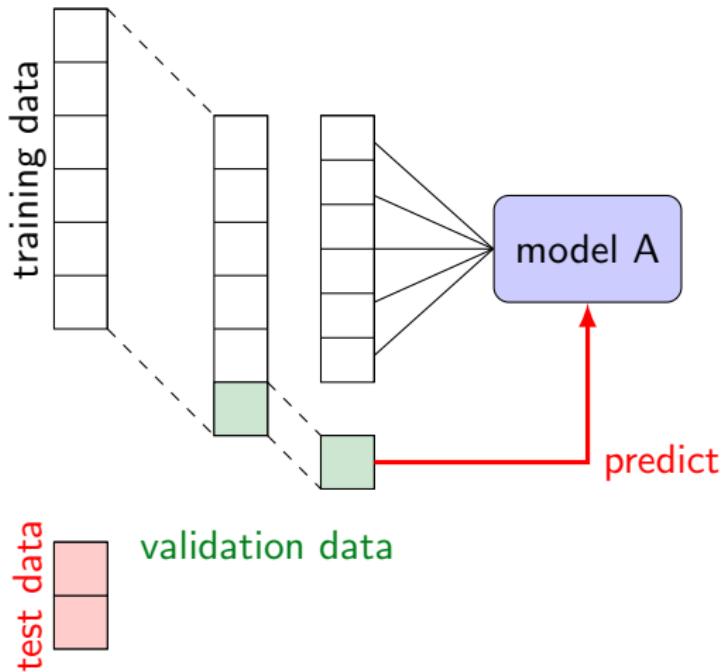
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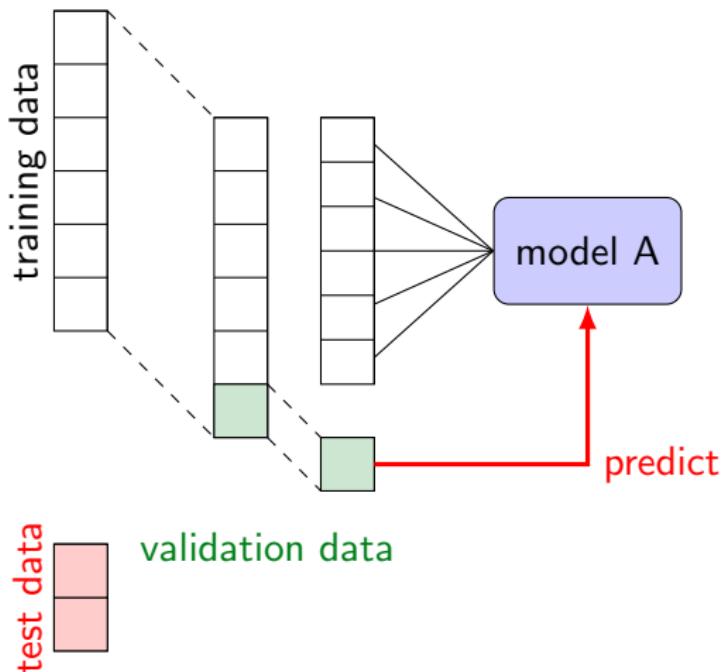
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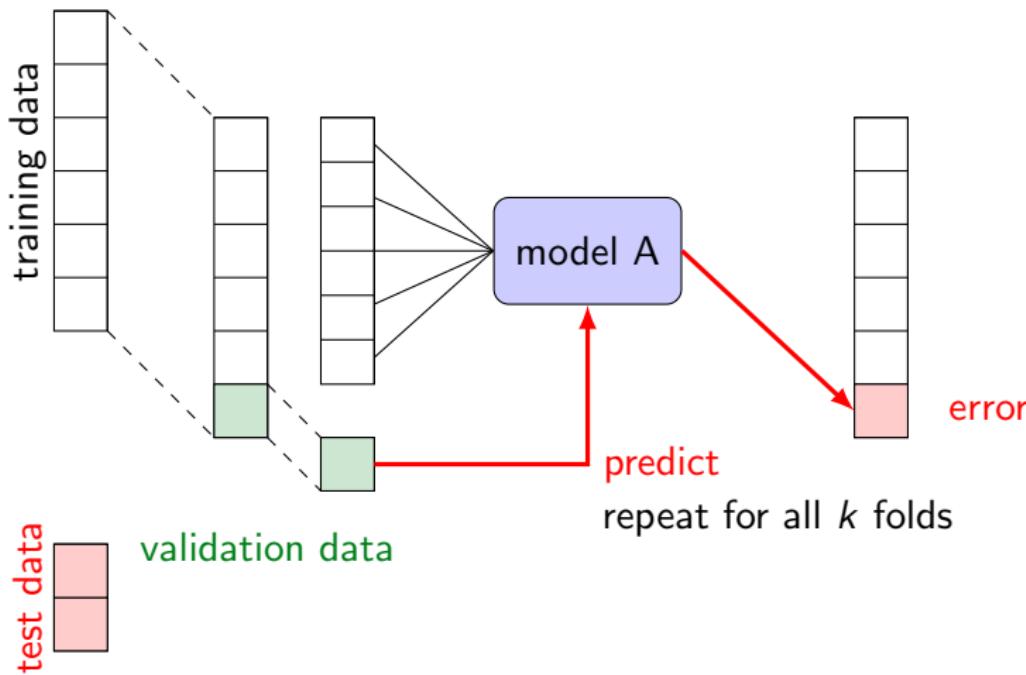
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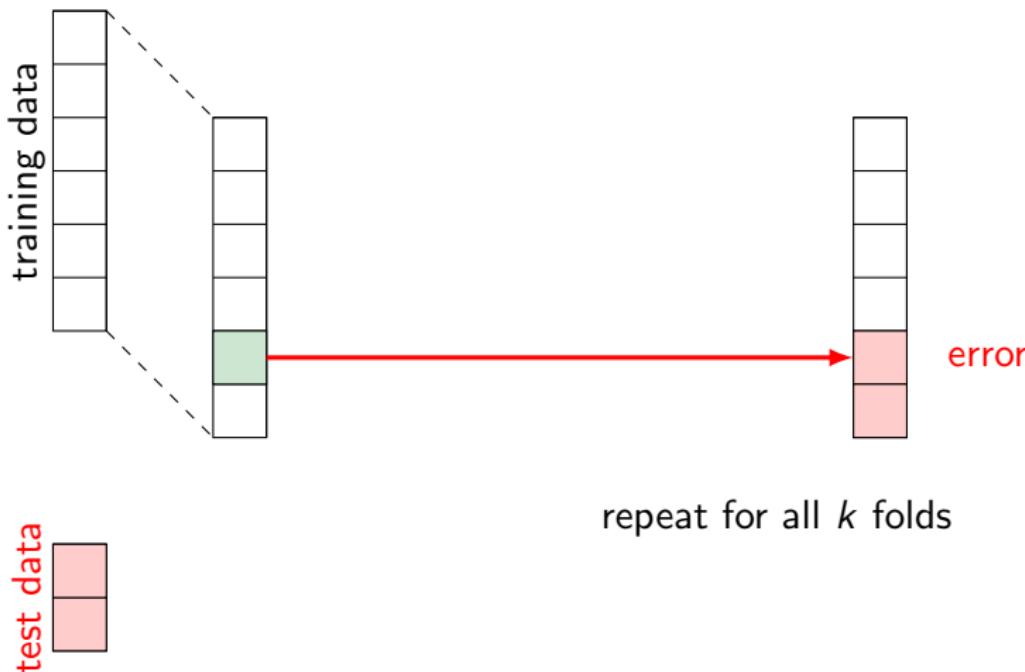
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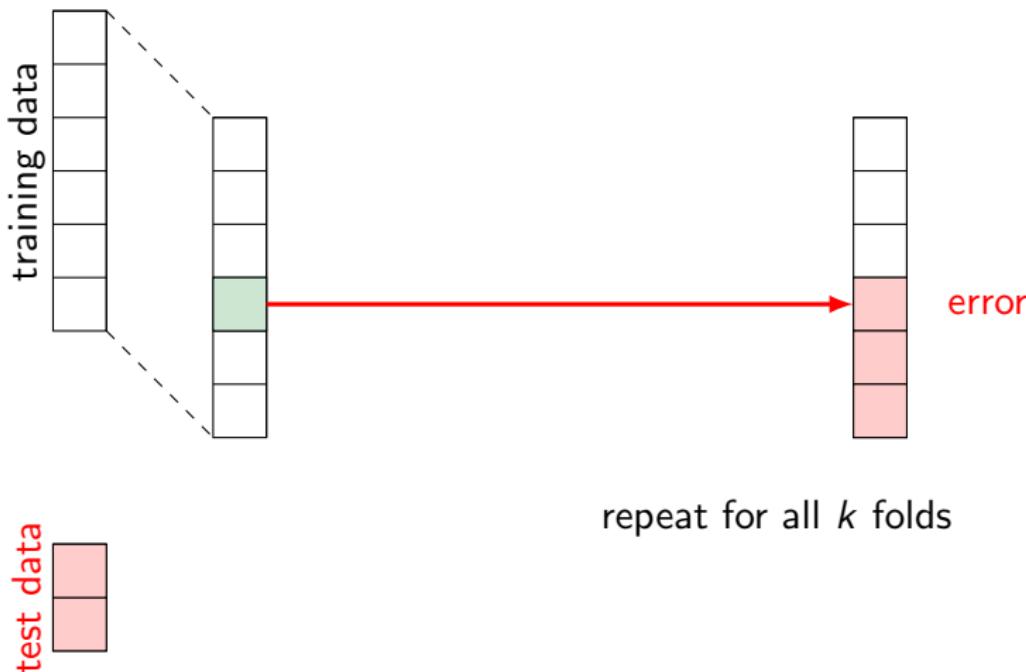
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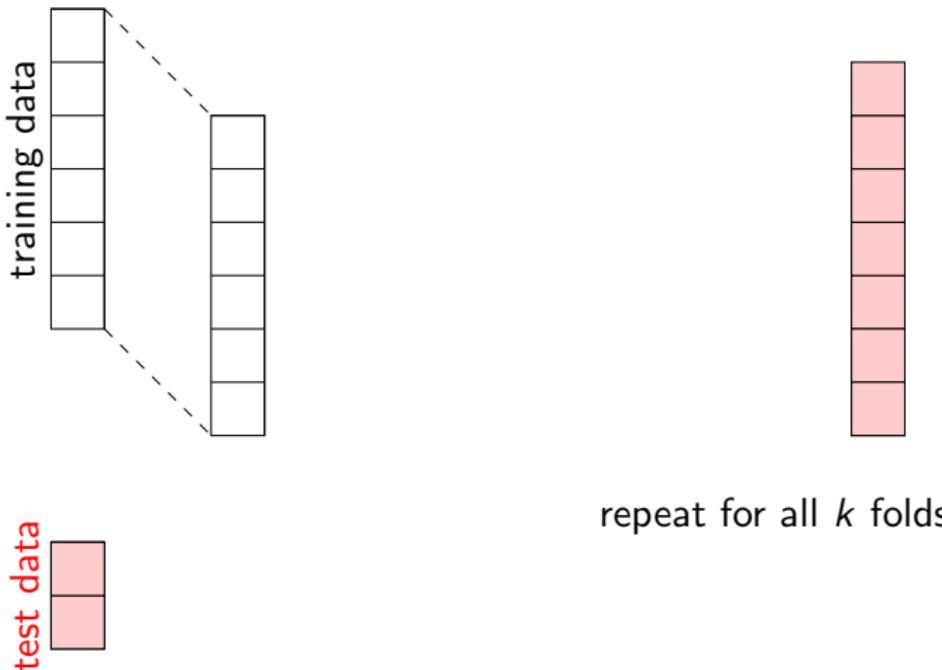
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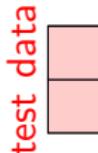
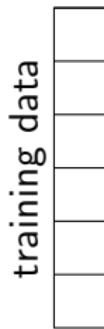
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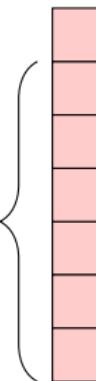
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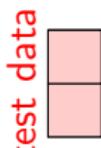
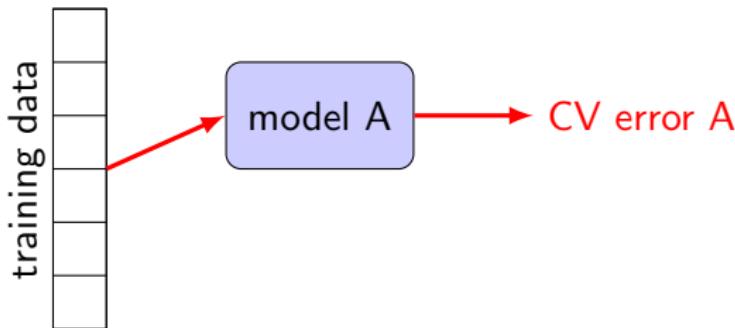
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average error =  
CV error

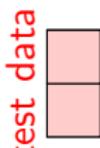
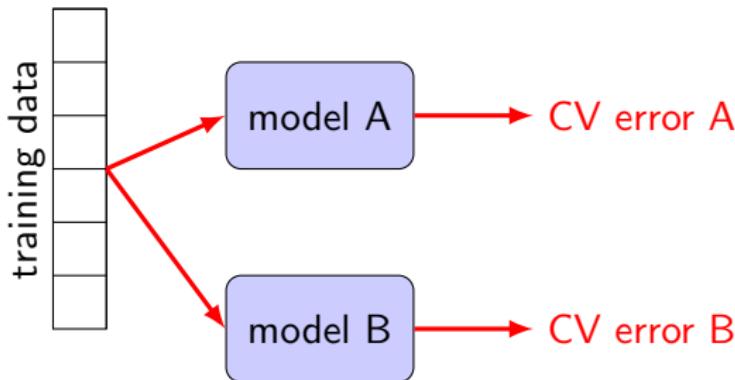


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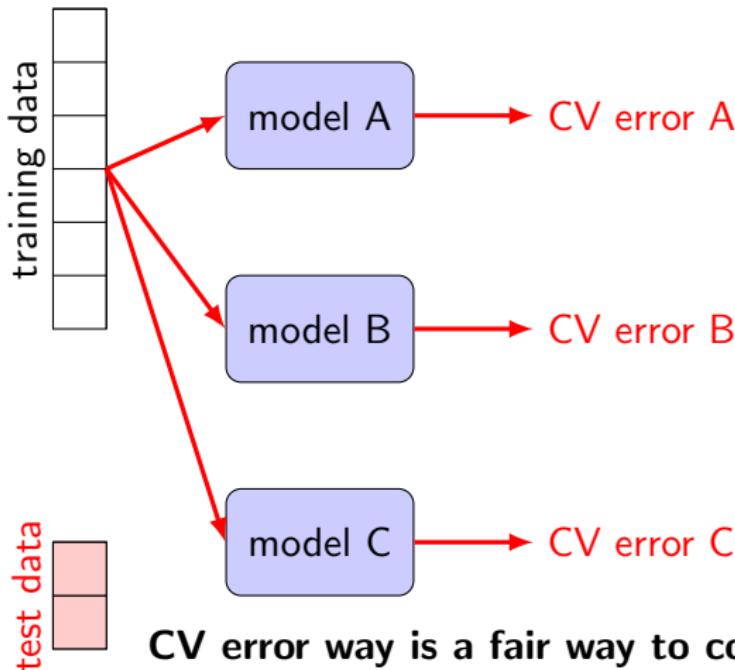
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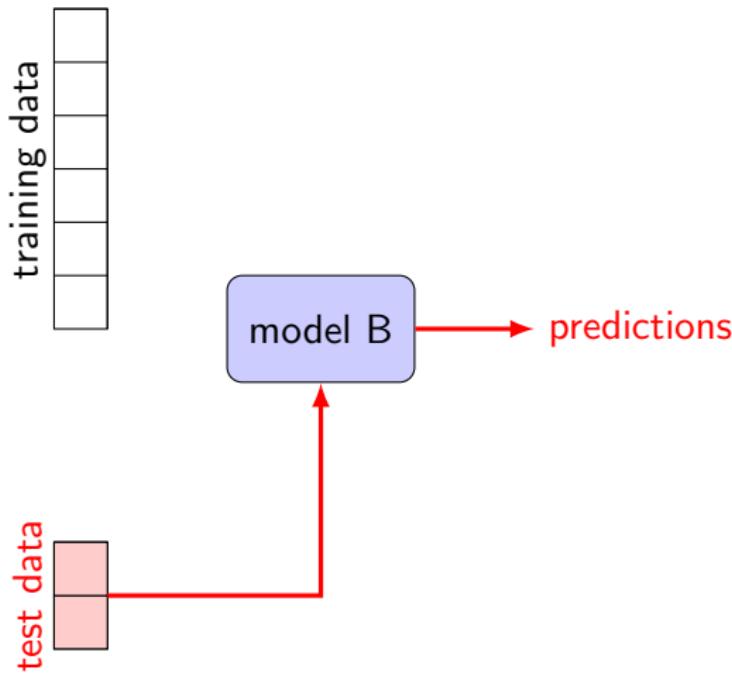


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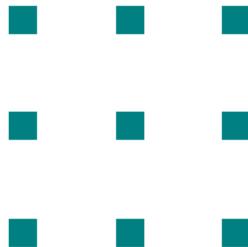
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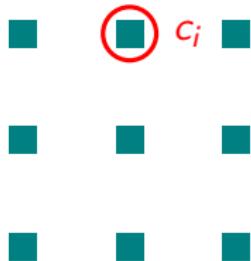
Deep neural networks (might) need better theories.

# Purpose



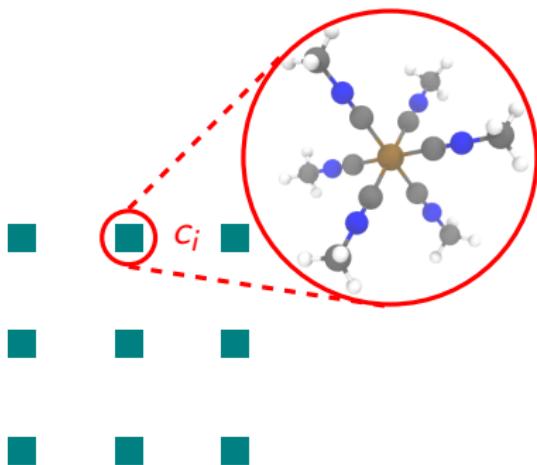
Chemical Space  $C_f$

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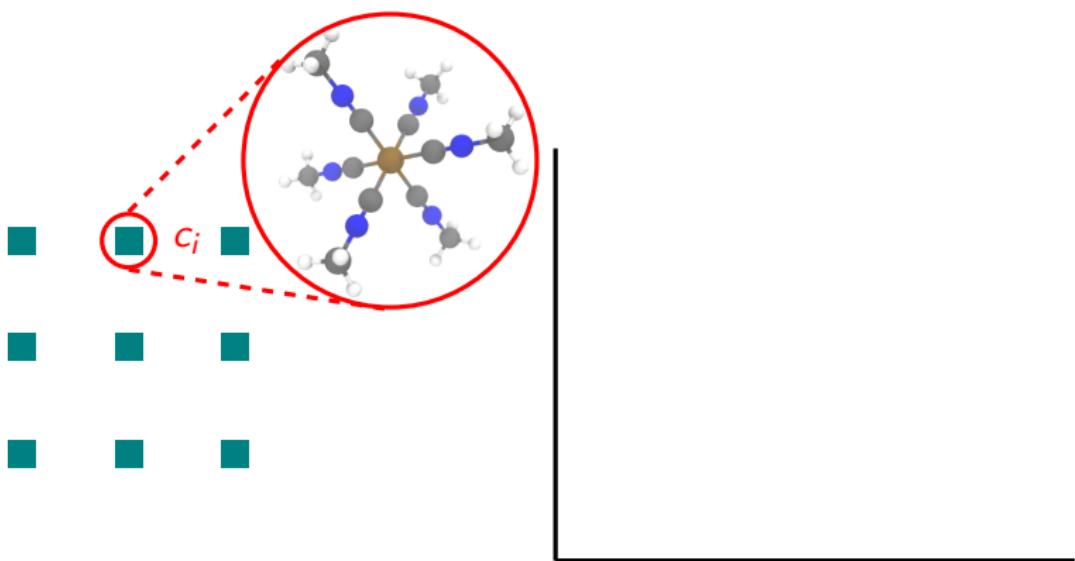
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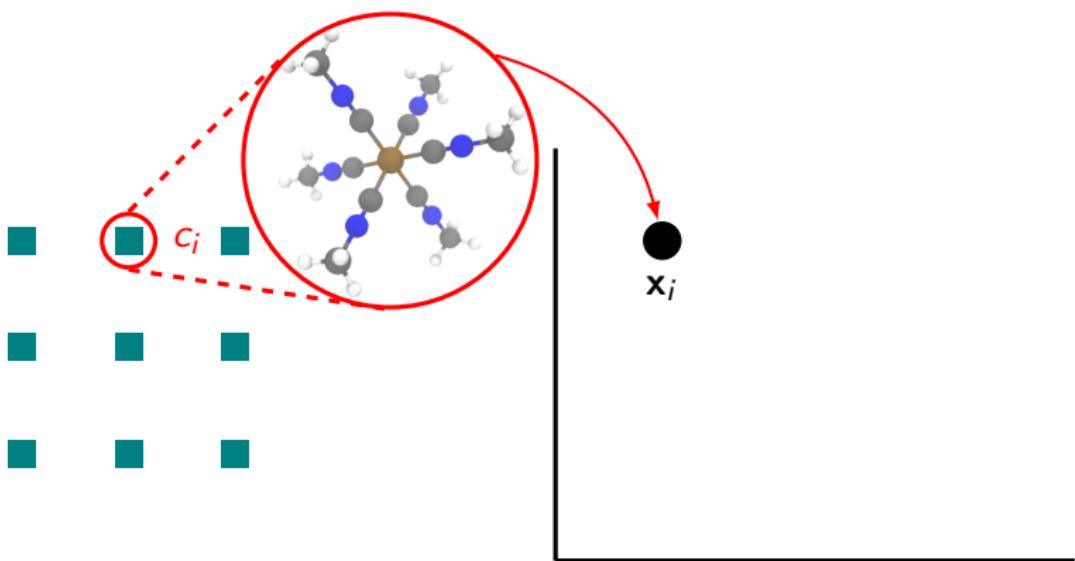
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Chemical Space  $C_f$

Descriptor Space  $\mathcal{X} \subset \mathbb{R}^d$

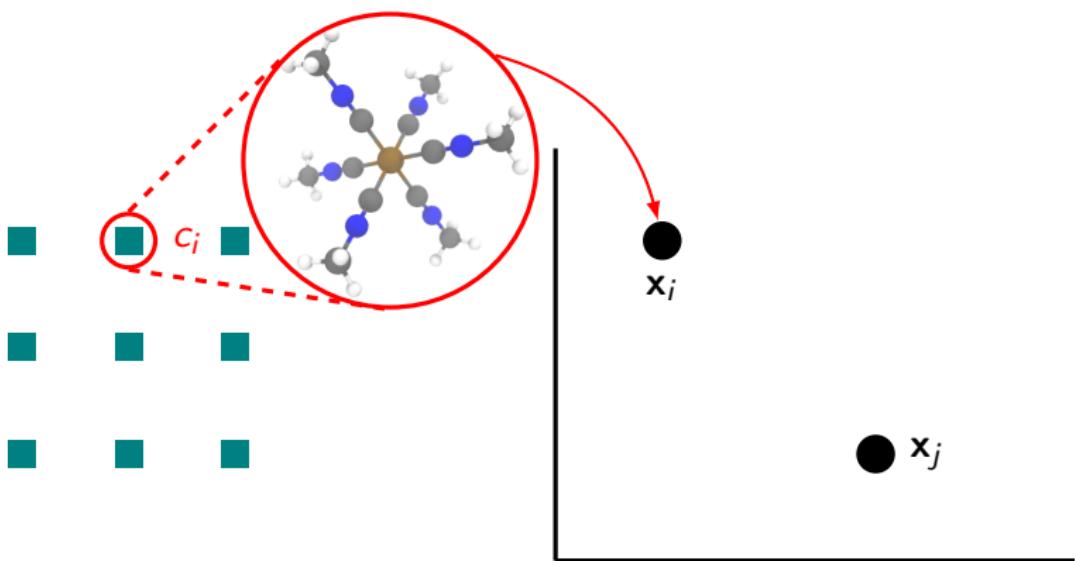
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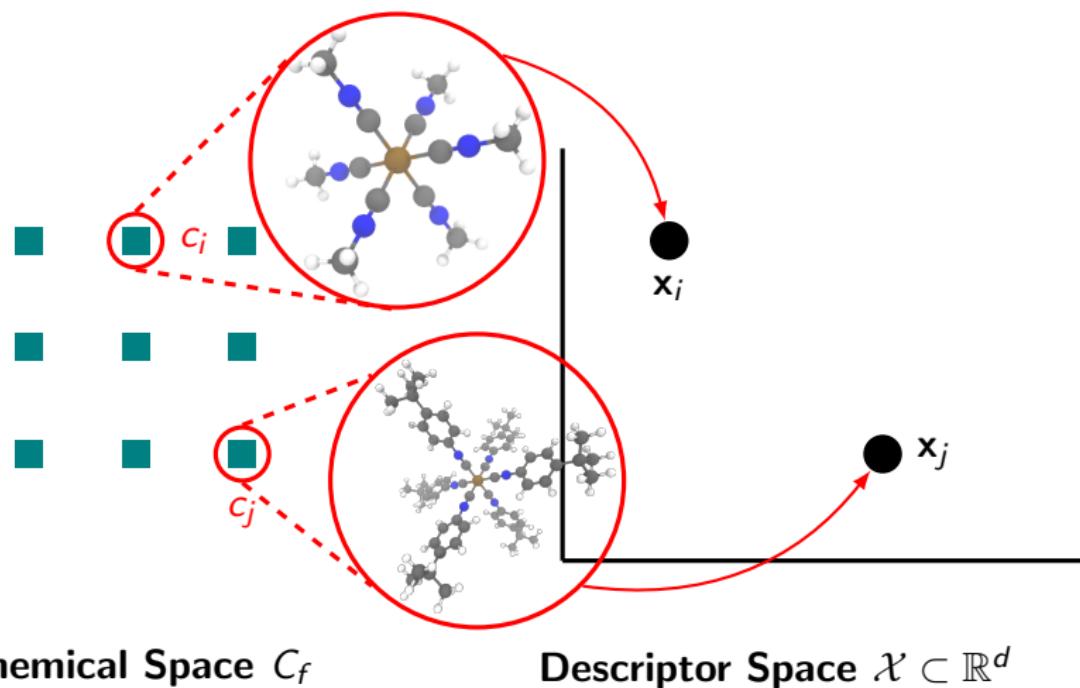
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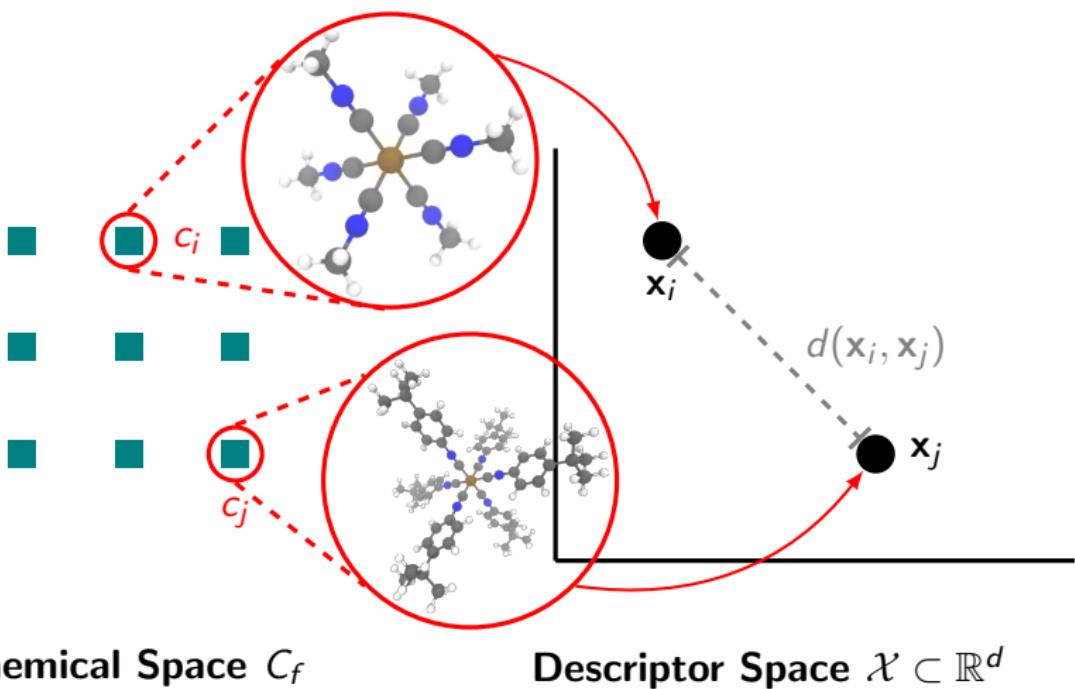
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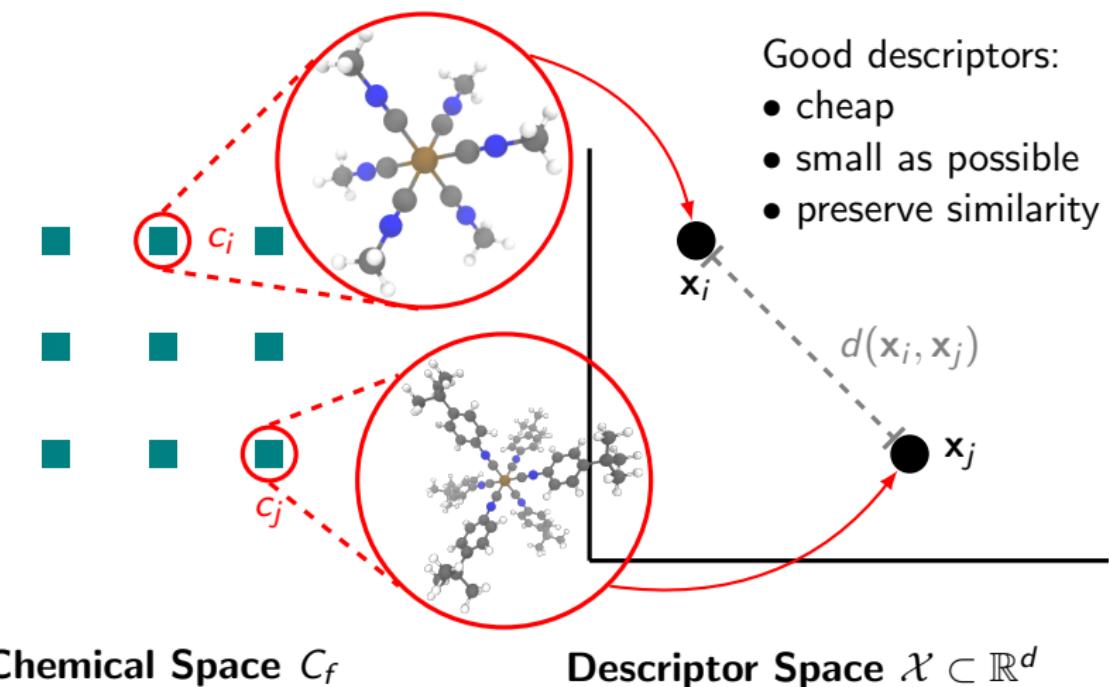
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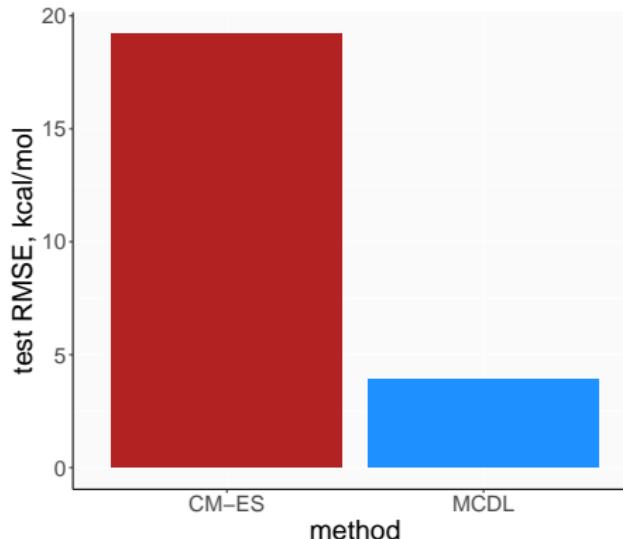


## Why similarity is important

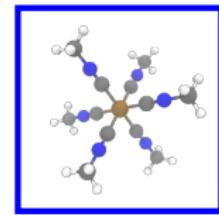
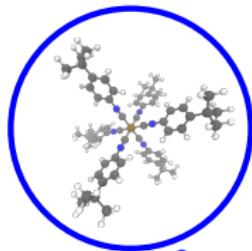
Different representations can have very different performance, particularly if they do not preserve notions of chemical similarity correctly:

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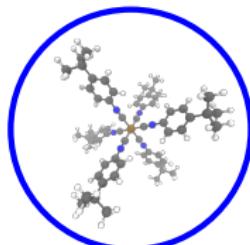
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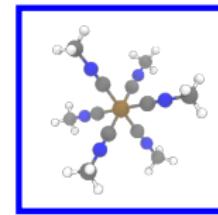


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$\text{Fe}[\text{pisc}]_6^{3+}$

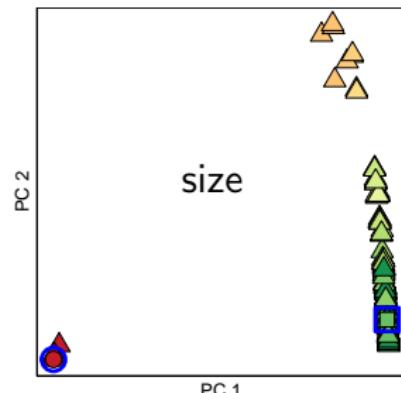
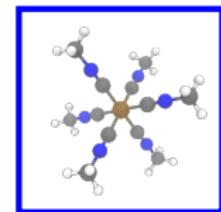
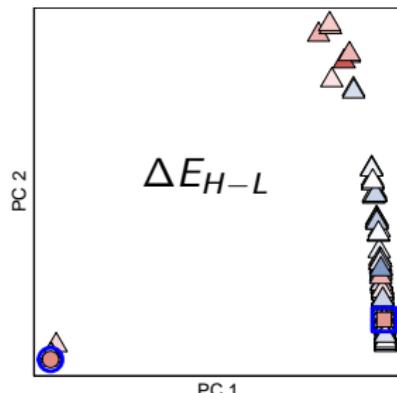
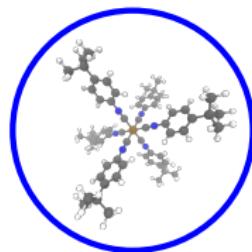
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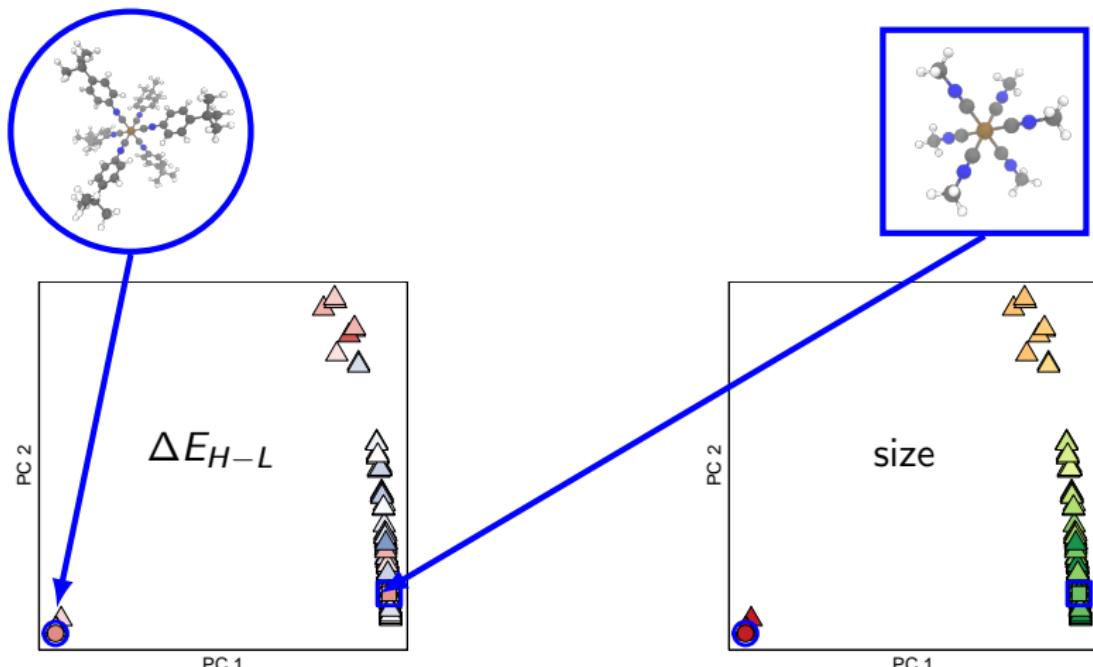
$\text{Fe}[\text{misc}]_6^{3+}$

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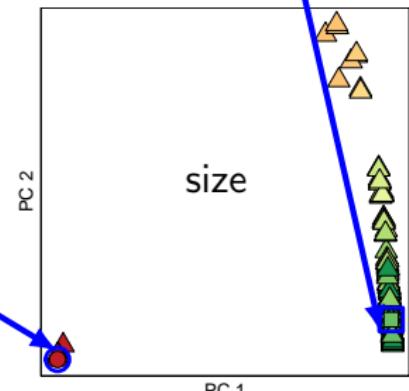
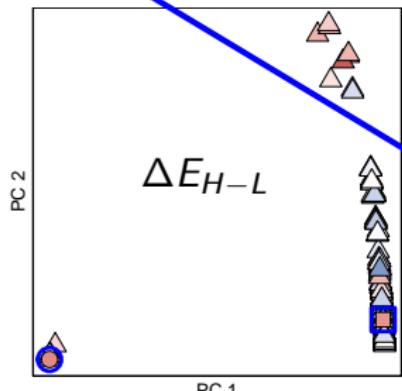
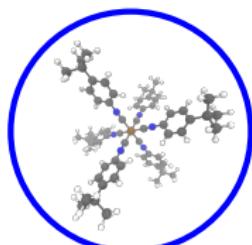
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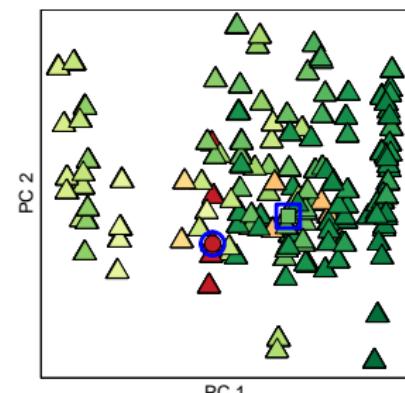
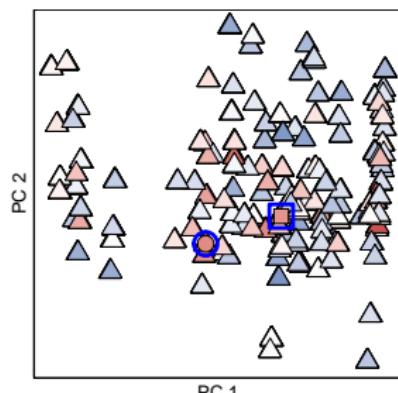
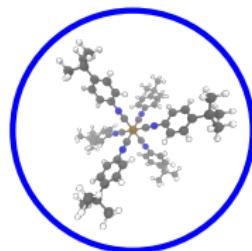
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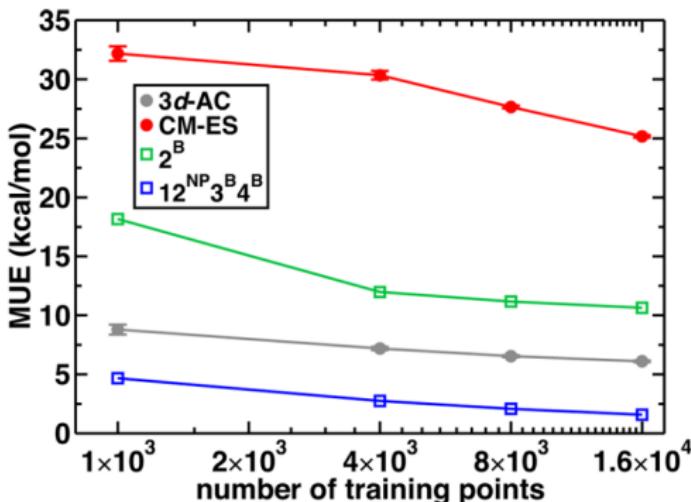


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complexity



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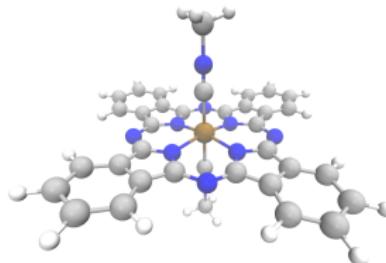


## 3D structure

- fine-grained structural information in 3D
- mimic input to a quantum chemistry code
- expensive to compute, rich information

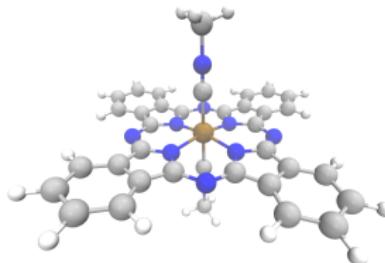
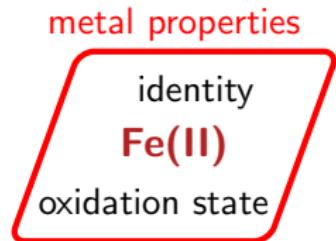
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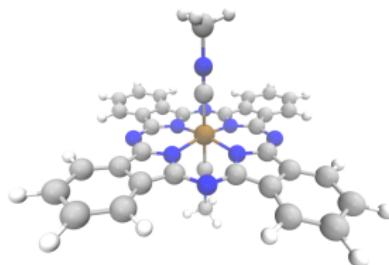
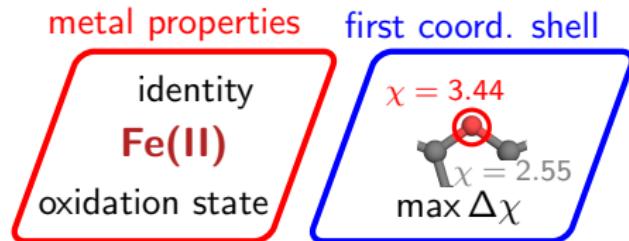
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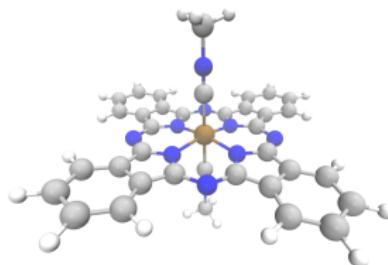
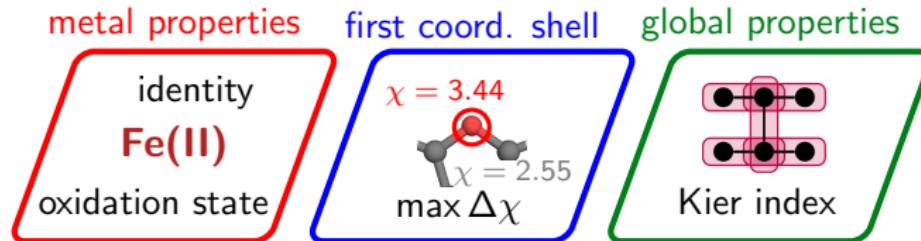
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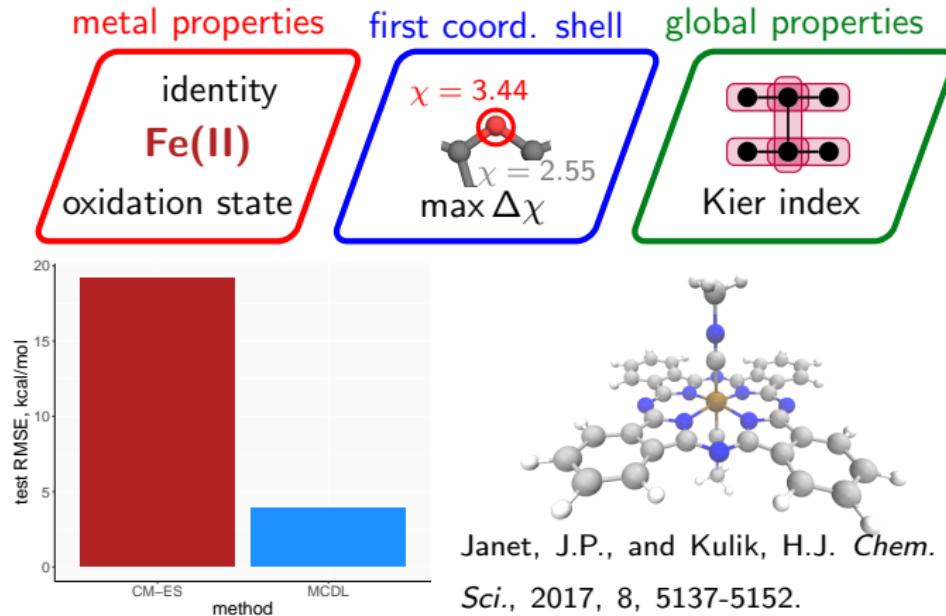
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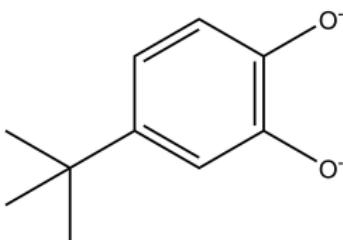


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In cheminformatics (esp. drug design literature) fingerprints are binary vectors used to determine molecular similarity. For example, FP2 fingerprint is a 1024 bit fingerprint:

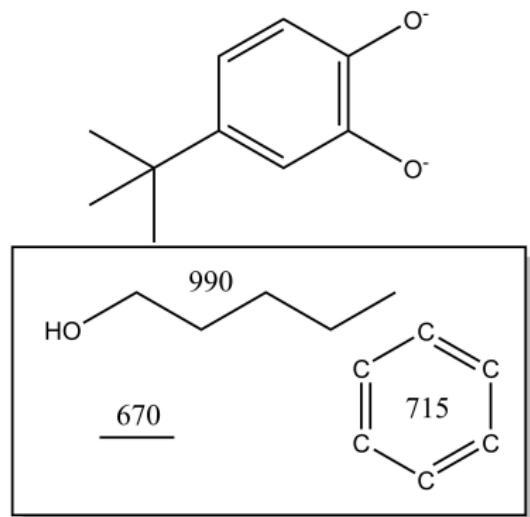
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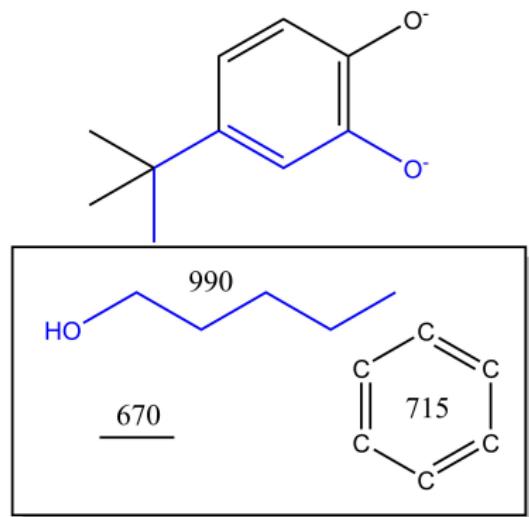
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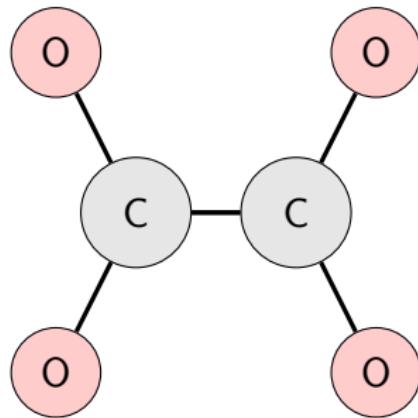
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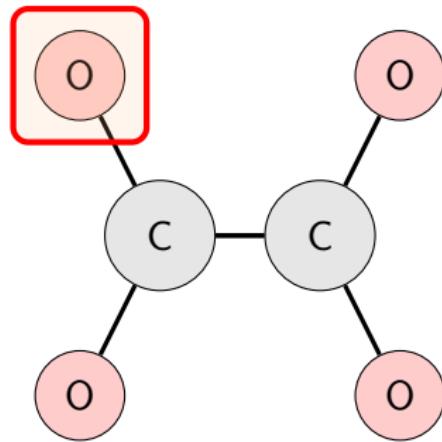
Based on autocorrelations<sup>1</sup>



<sup>1</sup>Broto, P., Moreau, G. and Vandycke, C. *Eur. J. Med. Chem.*, 19(1):71-78, 1984.

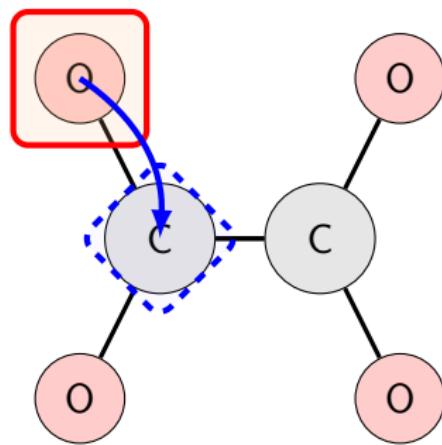
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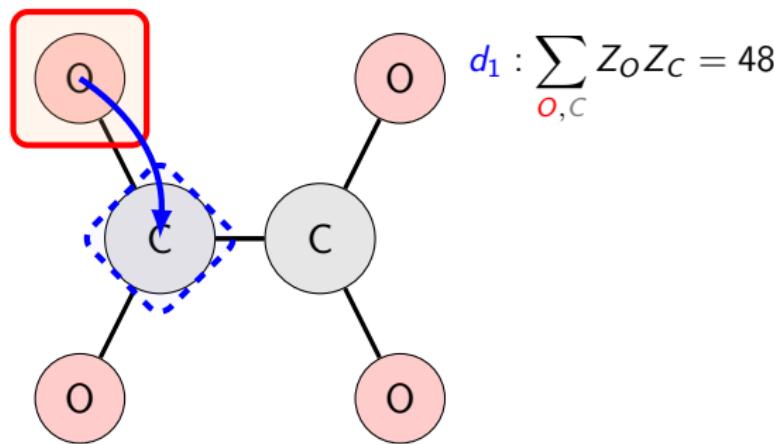
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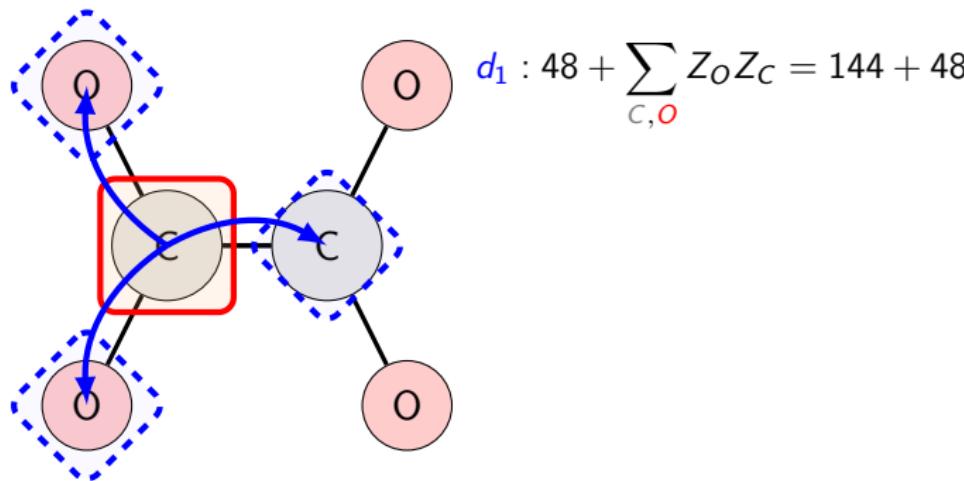
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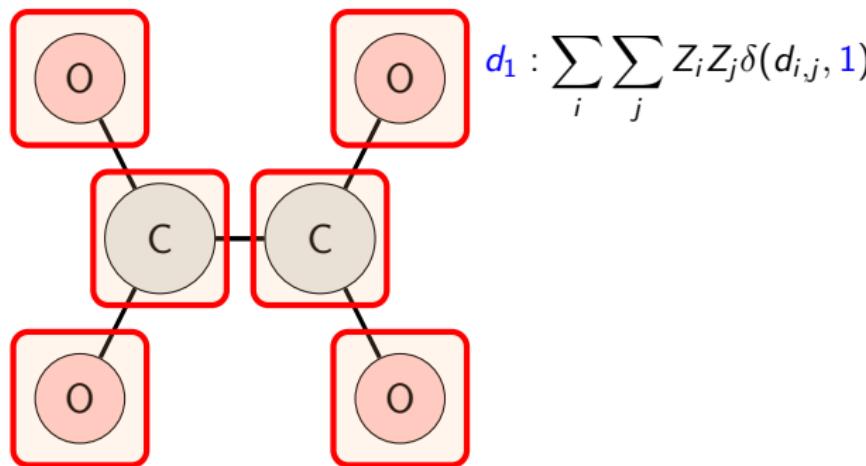
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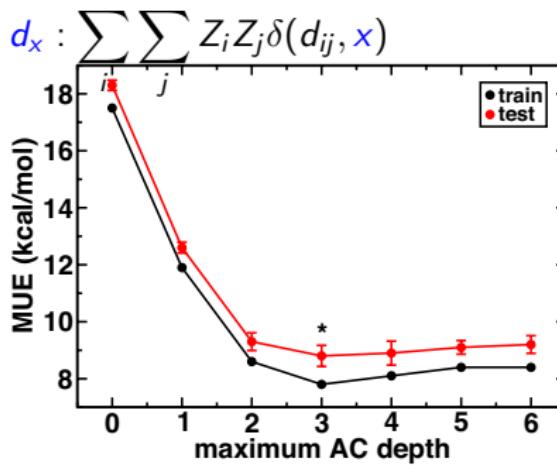
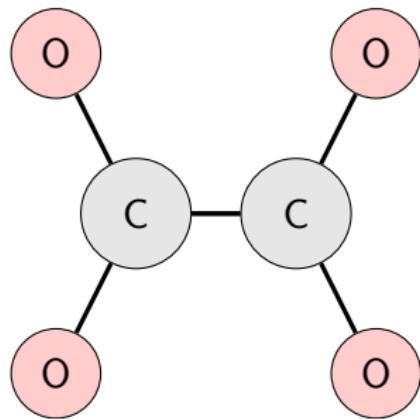
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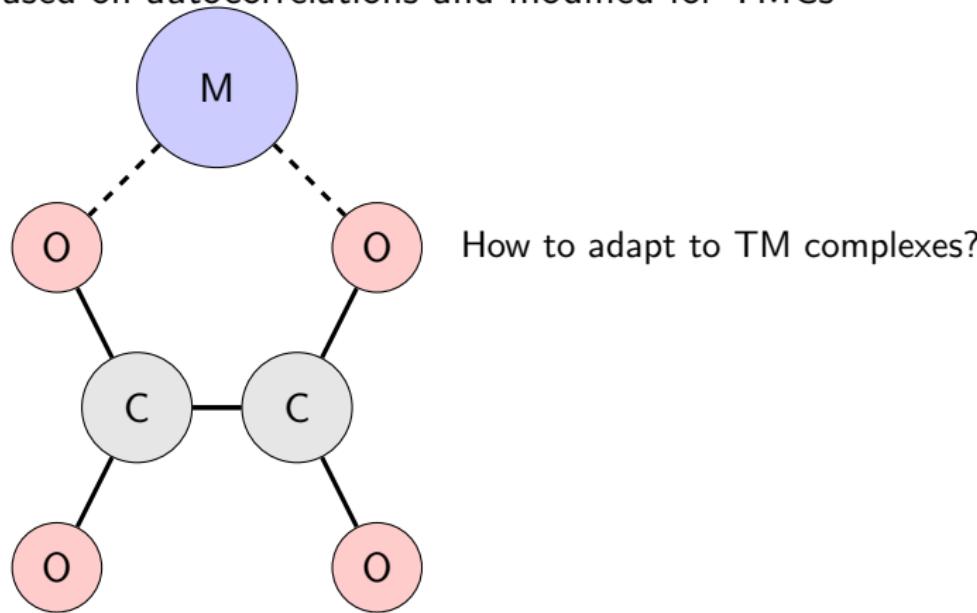
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<sup>4</sup>Janet, J.P., and Kulik, H.J. *J. Phys. Chem. A*, 2017, 121, 46, 8939-8954.

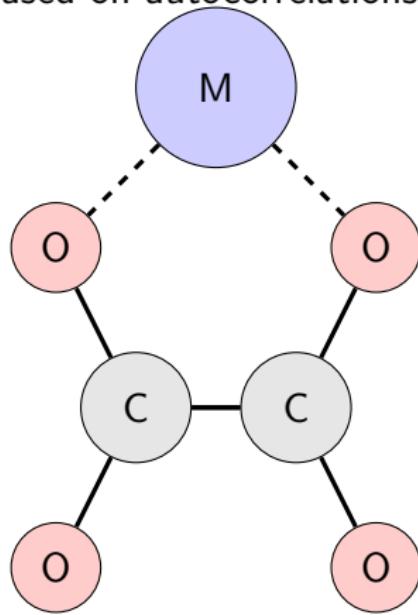
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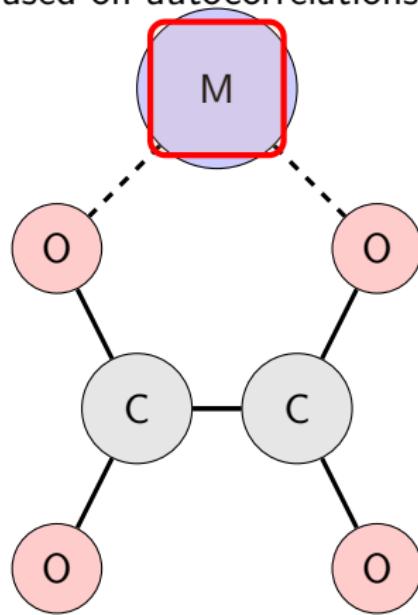
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How to adapt to TM complexes?  
restrict the scope to focus on  
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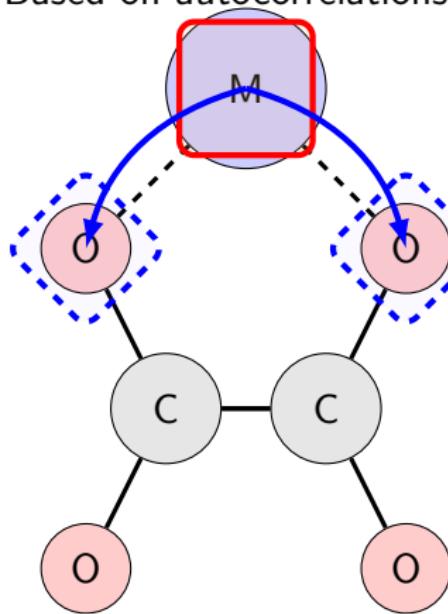
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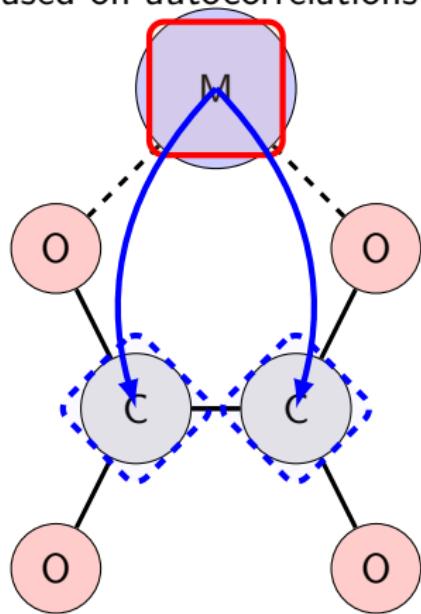


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$$d_1 : \sum_{M,O} Z_M Z_O$$

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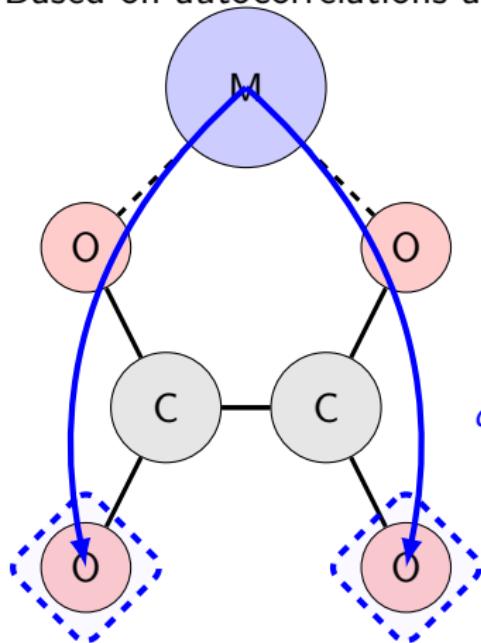
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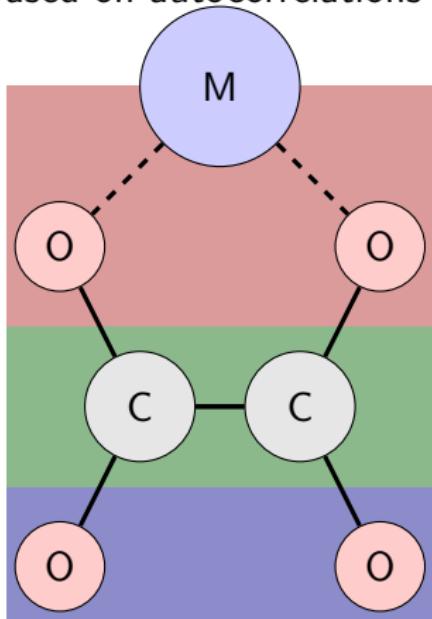


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$$d_3 : \sum_{M,O} Z_M Z_O$$

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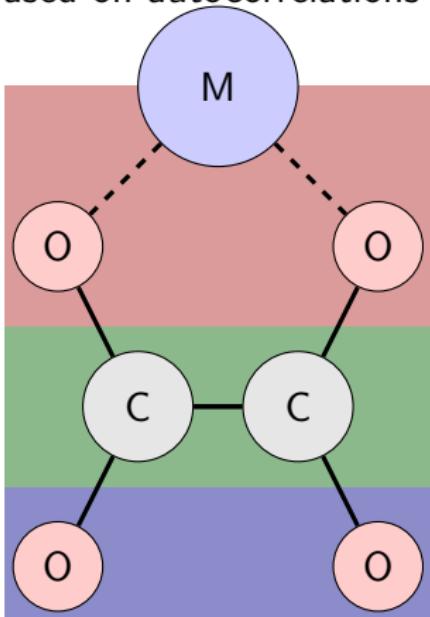


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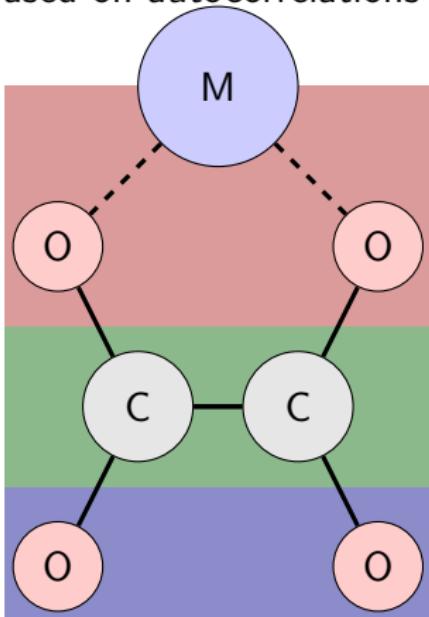
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$$(Z_i - Z_j)$$

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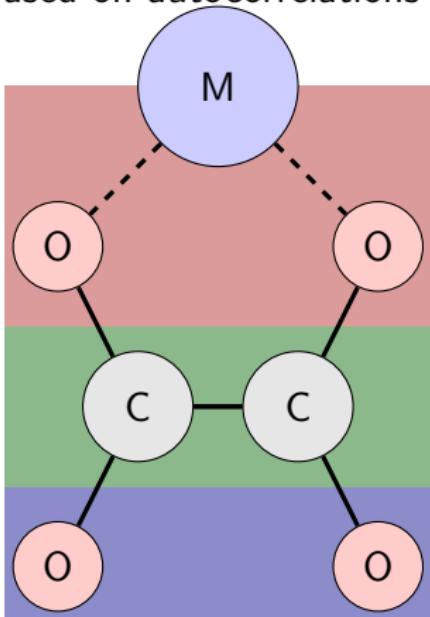
$$d_3 : \sum_{M,O} Z_M Z_O (Z_i - Z_j)$$

properties:  $T, \chi, Z, I, S$

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$$d_3 : \sum_{M,O} Z_M Z_O (Z_i - Z_j)$$

~ 160 features in total

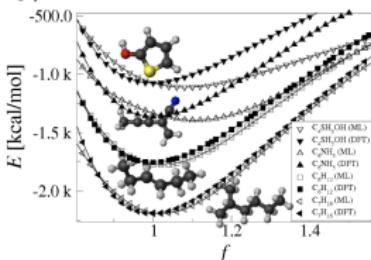
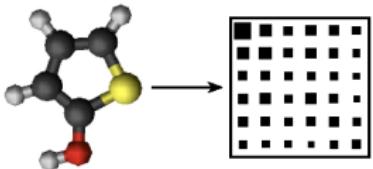
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# Coulomb matrices

One family of 3D descriptors attempt to copy information used in quantum chemistry codes, e.g. Coulomb Matrices:

Montavon, G. et al.. Learning Invariant Representations of Molecules for Atomization Energy Prediction, NIPS 25, 2012

$$M_{I,J} = \begin{cases} 0.5Z_I^{2.4} & \text{for } I = J \\ \frac{Z_I Z_J}{|R_I - R_J|} & \text{for } I \neq J \end{cases}$$

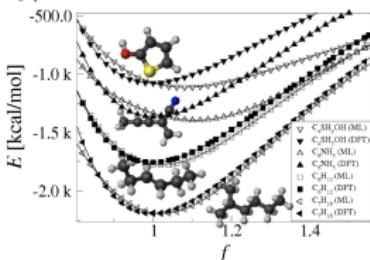
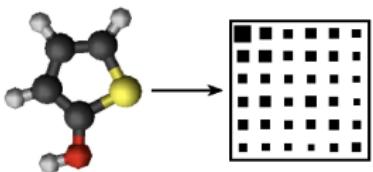


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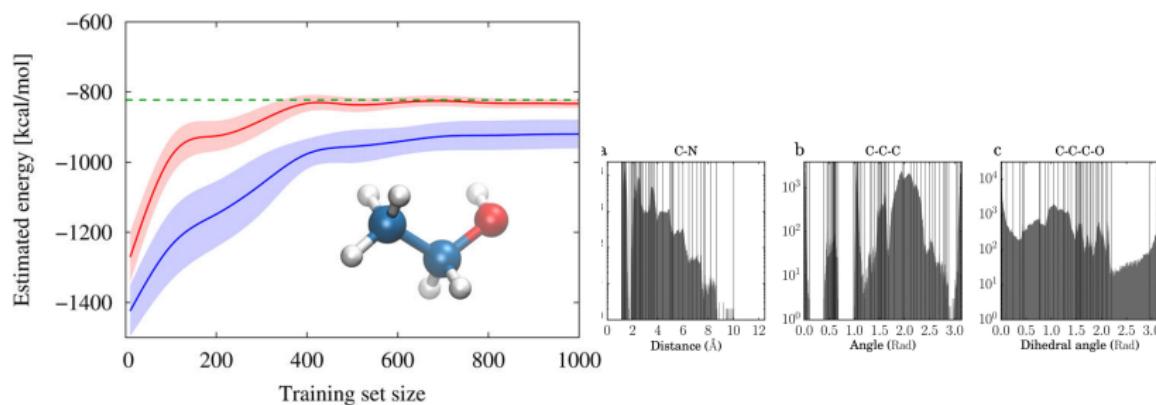


rotational and translational invariance

## HDAD and beyond-CM

Subsequent work adds descriptors derived from geometric parameters, i.e. bonds, angles, and dihedral angles:

Faber, F. et al.. Prediction Errors of Molecular Machine Learning Models Lower than Hybrid DFT Error, *J. Chem. Theory Comput.* 2017, 13, 11, 5255-5264



# System and atom level features

## molecule-level

- one vector for each system of interest
- commonly used in QSAR/QSPR, related to how we think about molecules
- easy to compare whole molecules
- some properties are really 'global', like logP

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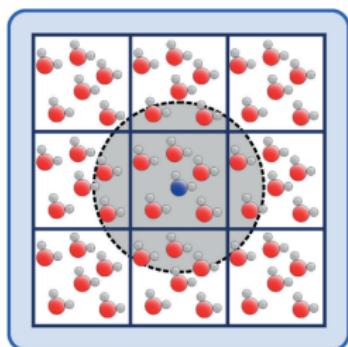
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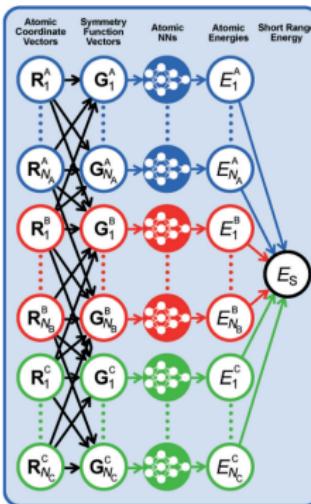
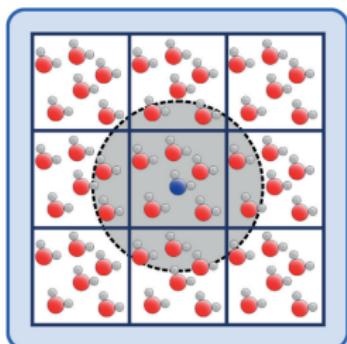
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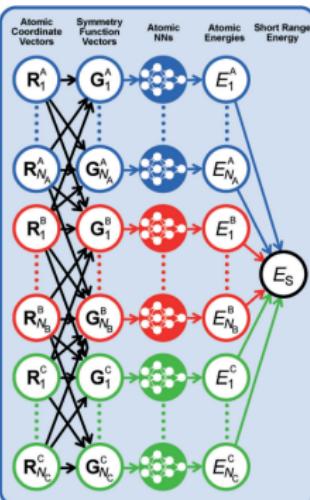
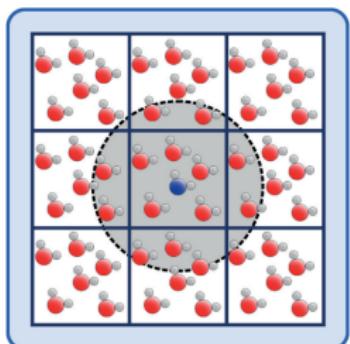
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J. Behler and M. Parrinello, Generalized Neural-Network Representation of High-Dimensional Potential-Energy Surfaces, *Phys. Rev. Lett.*, 98, 146401, 2007

# Learning representations

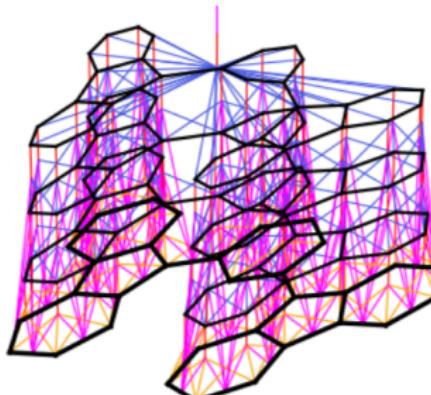
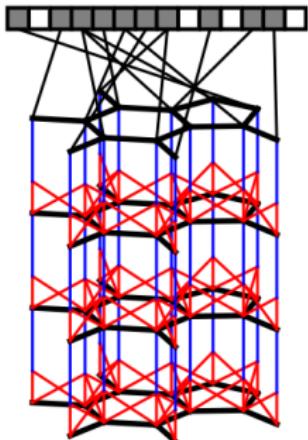
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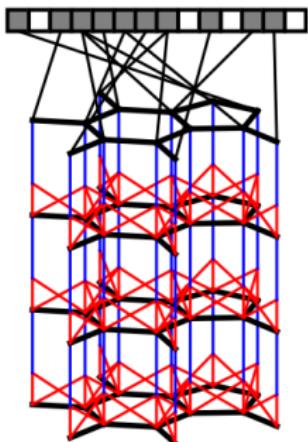
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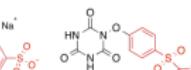
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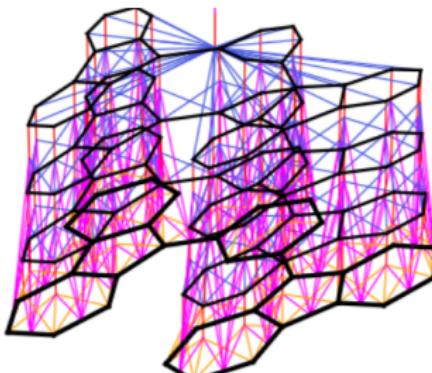
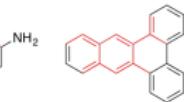
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Fragments most activated by toxicity feature on SR-MMP dataset



Fragments most activated by toxicity feature on NR-AHR dataset



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- 5 atom-level featurization can be very effective for total energies

# Multiple linear regression



## Multiple linear regression

Linear models give  $\hat{y}$  as linear function of the data matrix of  $X$ :

$$\hat{y}_{MLR}(x^*) = \sum_{j=1}^d w_j x_j^* + w_0$$

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$$\hat{y}_{MLR}(x^*) = \sum_{j=1}^d w_j x_j^* + w_0 = [1 \quad x_1^* \quad \dots \quad x_d^*] \begin{bmatrix} w_0 \\ w_1 \\ \vdots \\ w_d \end{bmatrix}$$

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We can write this in a matrix form as well:

$$\hat{y}_{MLR}(X) = \begin{bmatrix} 1 & x_1^{(1)} & x_2^{(1)} & \dots & x_d^{(1)} \\ \vdots & & & & \vdots \\ 1 & x_1^{(n)} & x_2^{(n)} & \dots & x_d^{(n)} \end{bmatrix} \begin{bmatrix} w_0 \\ w_1 \\ \vdots \\ w_d \end{bmatrix} = Xw$$

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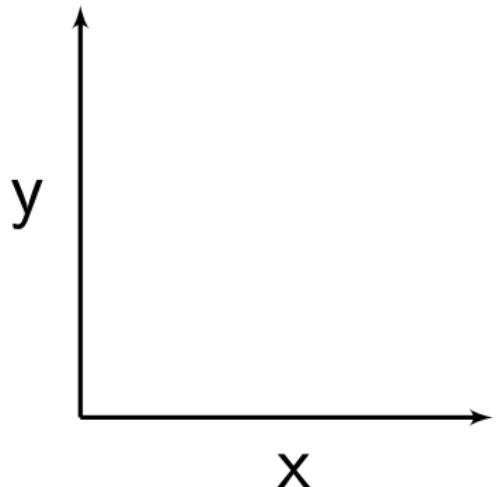
Notice how we handle the constant terms

## Multiple linear regression II

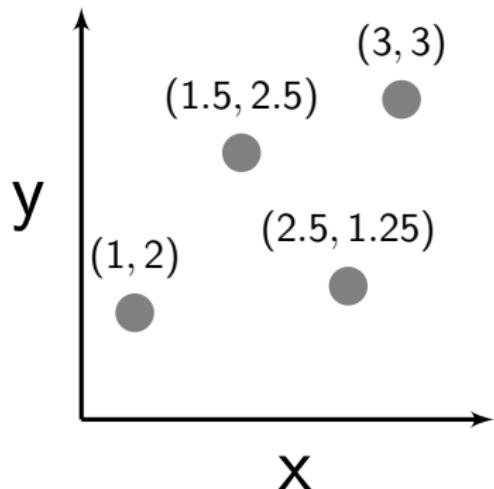
Let's solve our regularized least-squares problem:

$$\begin{aligned}
 w &= \arg \min_{w \in \mathbb{R}^p} \frac{1}{n} \|y_{data} - Xw\|_2^2 + \lambda \|w\|_2^2 \\
 &= \frac{1}{n} (y_{data} - Xw)^T (y_{data} - Xw) + \lambda w^T w \\
 \frac{\partial \mathcal{L}}{\partial w} &= -\frac{2}{n} X^T (y_{data} - Xw) + 2\lambda w = 0 \\
 \implies (\lambda I + X^T X)w &= X^T y_{data} \\
 w &= (\lambda I + X^T X)^{-1} X^T y_{data}
 \end{aligned}$$

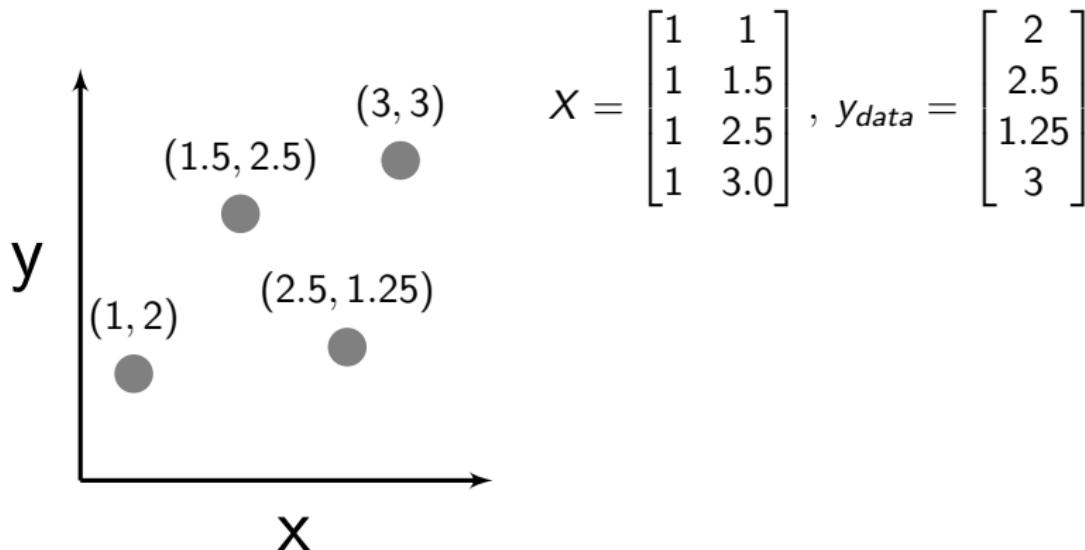
# Simple example in 1D



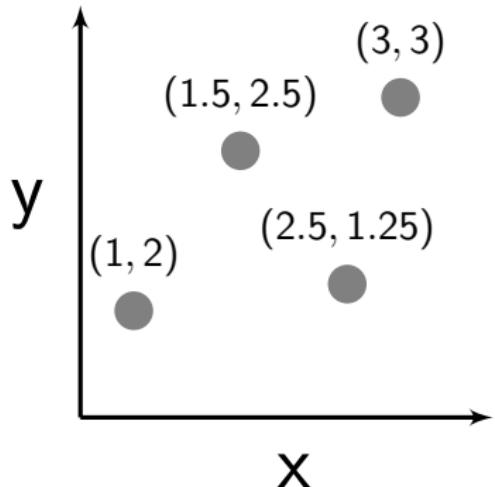
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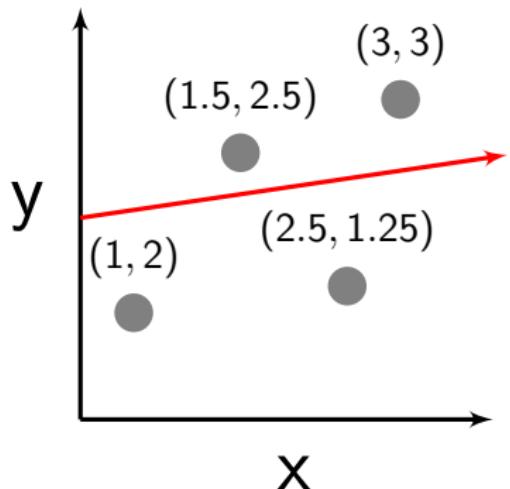
## Simple example in 1D



$$X = \begin{bmatrix} 1 & 1 \\ 1 & 1.5 \\ 1 & 2.5 \\ 1 & 3.0 \end{bmatrix}, \quad y_{data} = \begin{bmatrix} 2 \\ 2.5 \\ 1.25 \\ 3 \end{bmatrix}$$

$$w = (X^T X + \lambda I)^{-1} X^T y_{data}$$

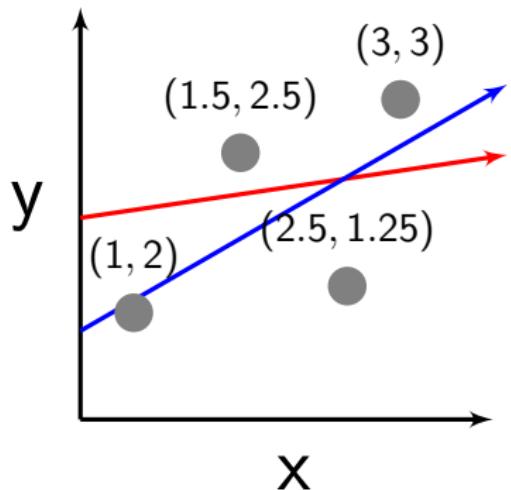
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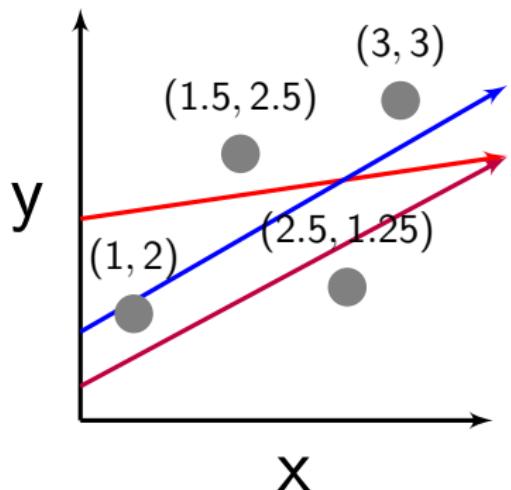
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$$\begin{aligned} w &= (X^T X + \lambda I)^{-1} X^T y_{data} \\ &= \begin{bmatrix} 0.82 \\ 0.58 \end{bmatrix} (\lambda = 1.0) \end{aligned}$$

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$$\begin{aligned} w &= (X^T X + \lambda I)^{-1} X^T y_{data} \\ &= \begin{bmatrix} 0.32 \\ 0.54 \end{bmatrix} (\lambda = 10) \end{aligned}$$

## The linear kernel

We can rewrite our result to express  $w = X^T a$  for  $a \in \mathbb{R}^n$  (shift of basis).

$$\hat{y}_{MLR}(x^*) = x^* w = \sum_{j=1}^d x_j^* w_j$$

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$$\begin{aligned}\hat{y}_{MLR}(x^*) &= x^* \textcolor{blue}{w} = \sum_{j=1}^d x_j^* \textcolor{blue}{w_j} \\ &= x^* \textcolor{blue}{X^T a} = \begin{bmatrix} x_1^* & \dots & x_d^* \end{bmatrix} \begin{bmatrix} x_1^{(1)} & \dots & x_1^{(n)} \\ \vdots & & \vdots \\ x_d^{(1)} & \dots & x_d^{(n)} \end{bmatrix} \begin{bmatrix} a_1 \\ \vdots \\ a_n \end{bmatrix} \\ &= \sum_{i=1}^n x_i^* \textcolor{blue}{x_i^T a_i}\end{aligned}$$

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We can rewrite our result to express  $w = X^T a$  for  $a \in \mathbb{R}^n$  (shift of basis).

$$\begin{aligned}\hat{y}_{MLR}(x^*) &= x^* \mathbf{w} = \sum_{j=1}^d x_j^* w_j \\ &= x^* \mathbf{X}^T \mathbf{a} = [x_1^* \quad \dots \quad x_d^*] \begin{bmatrix} x_1^{(1)} & \dots & x_1^{(n)} \\ \vdots & & \vdots \\ x_d^{(1)} & \dots & x_d^{(n)} \end{bmatrix} \begin{bmatrix} a_1 \\ \vdots \\ a_n \end{bmatrix} \\ &= \sum_{i=1}^n x^* \mathbf{x}_i^T \mathbf{a}_i = \sum_{i=1}^n k(x^*, x_i) a_i\end{aligned}$$

The term  $k(x^*, x_i) = x^* x_i^T = \langle x^*, x_i \rangle$  is the **linear kernel**.

## The linear kernel II

The matrix  $K_{i,j} = \langle x_i, x_j \rangle$  is called the (linear) **kernel matrix**.

We can write the solution of the regression problem in this form – it is **exactly equivalent**:

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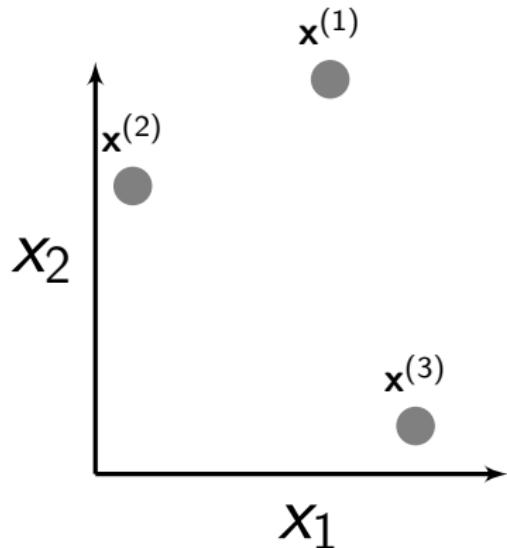
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The prediction at any new point is proportional to the inner product of each training point and the new point:

$$\hat{y}_{MLR}(x^*) = \sum_{i=1}^n k(x^*, x_i) a_i = \sum_{i=1}^n k\langle x^*, x_i \rangle a_i$$

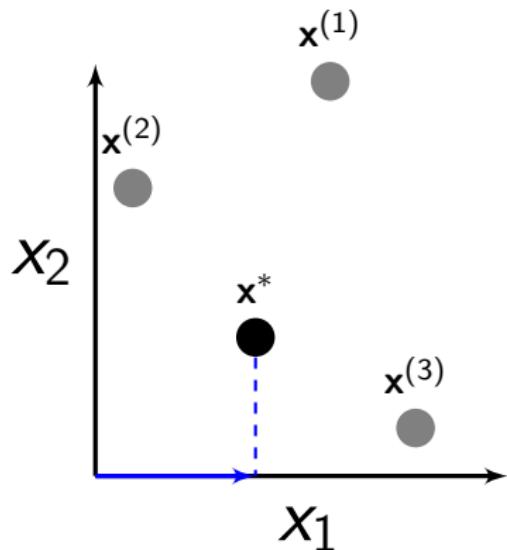
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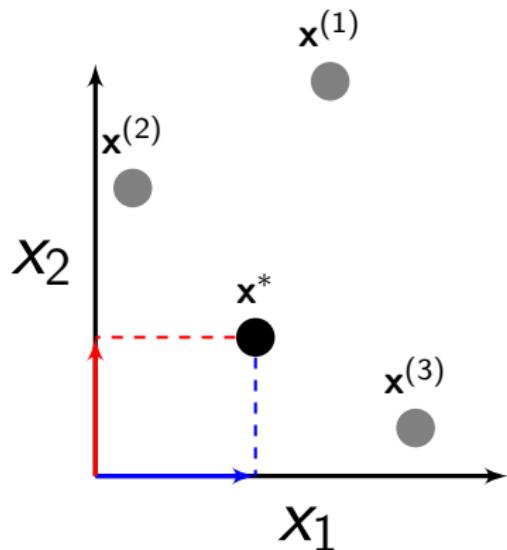
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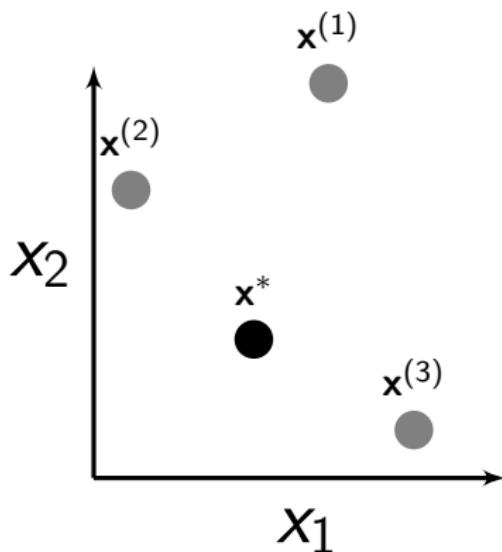
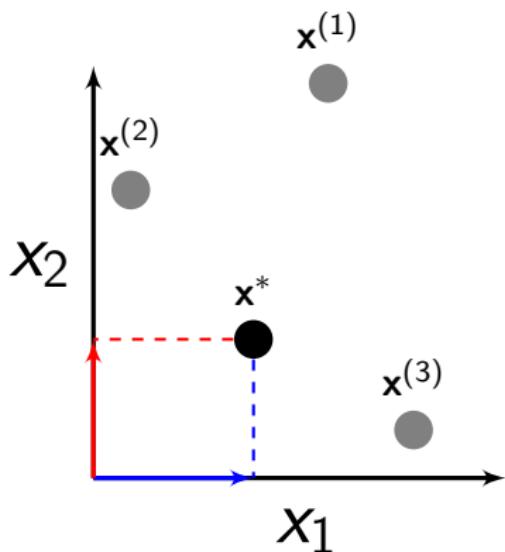
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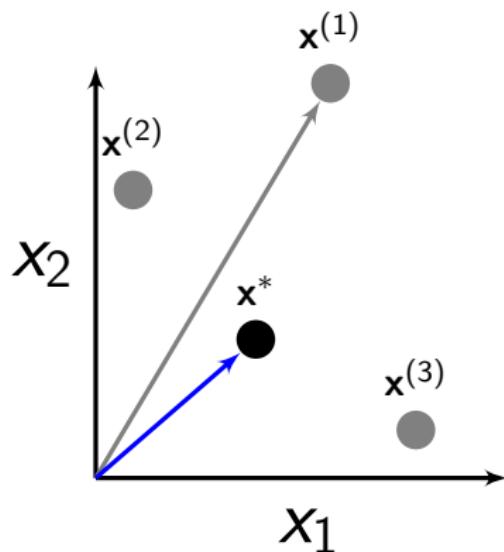
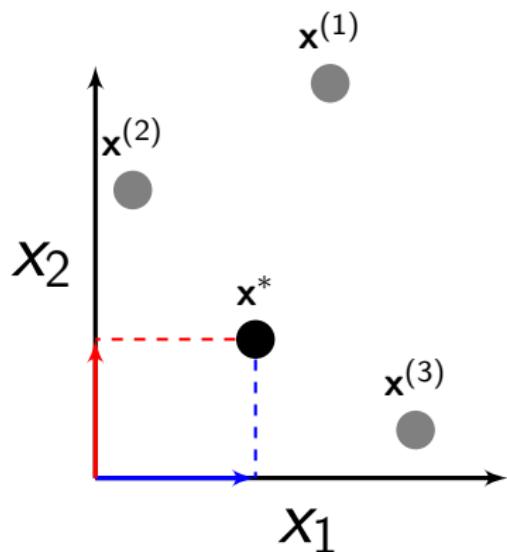
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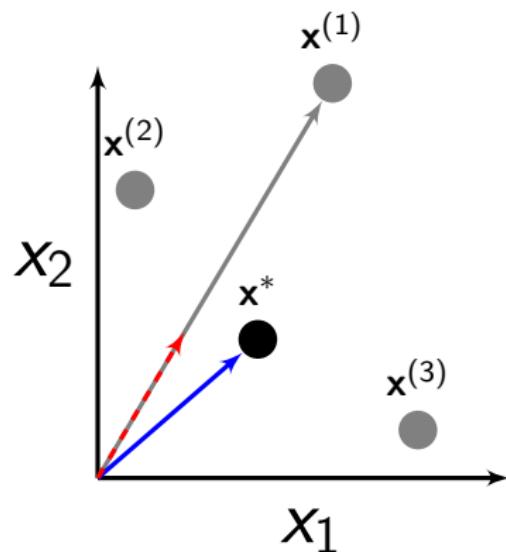
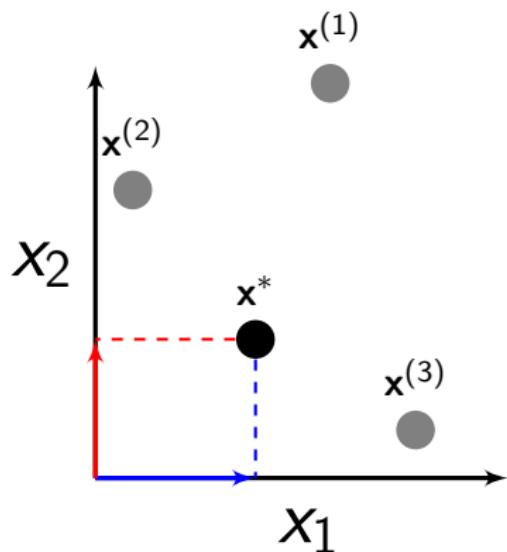
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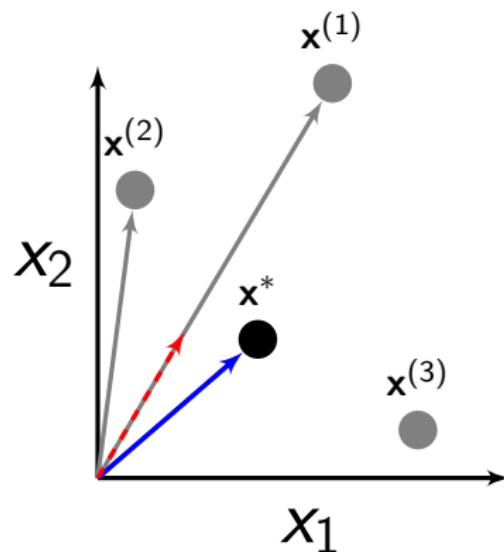
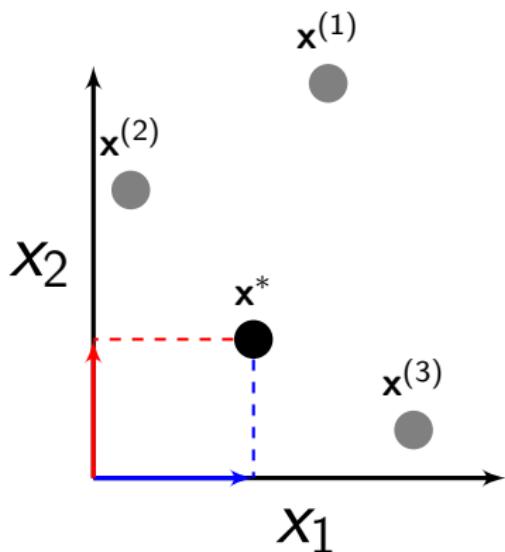
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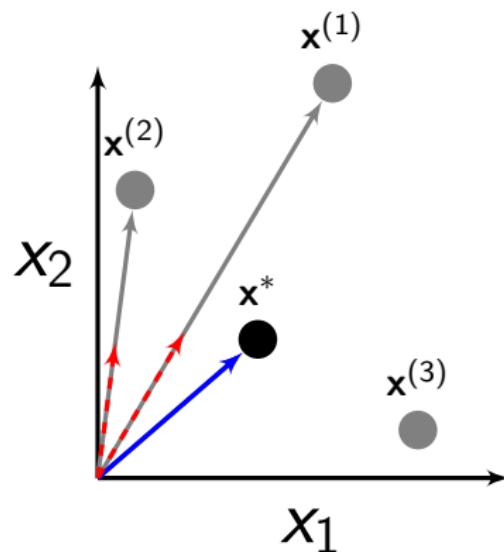
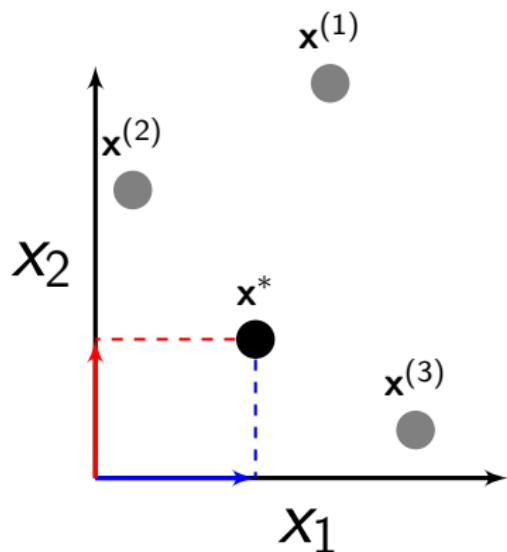
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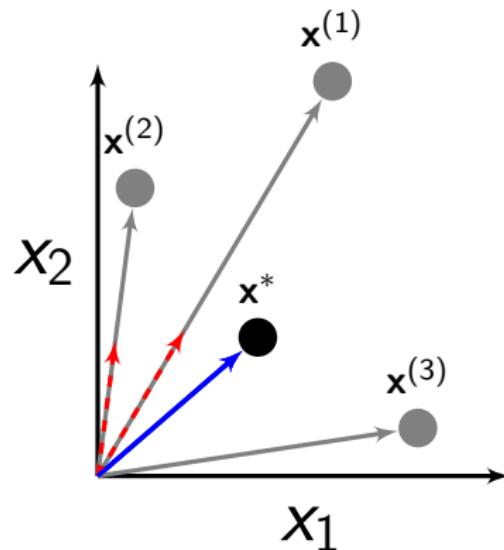
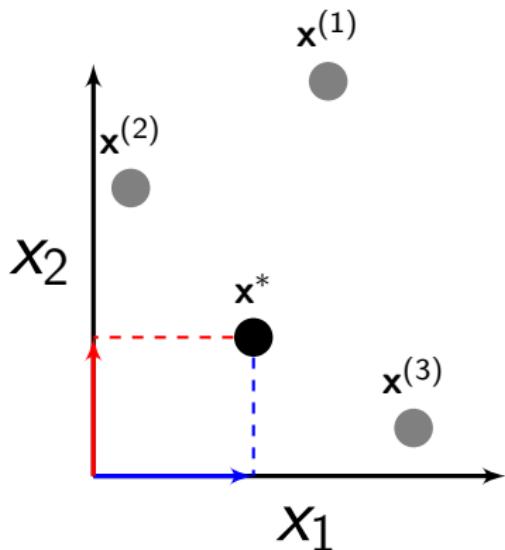
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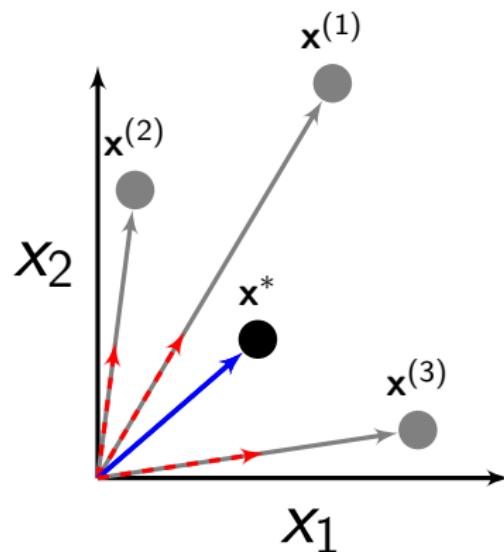
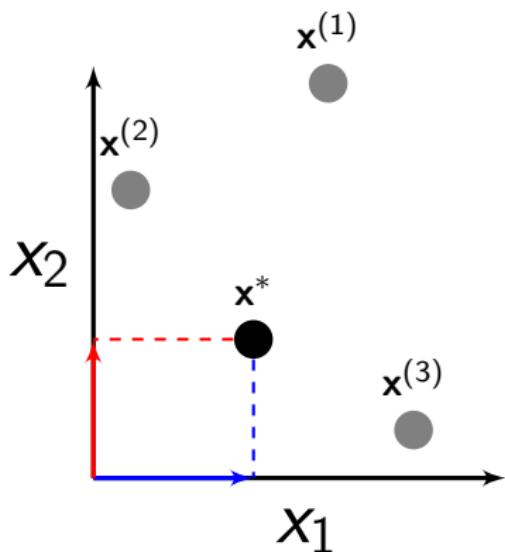
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Notice that this is *linear* in  $w$  for a 'lifted' feature space,  $\varphi(X)$ :

$$y_{QUAD}(x) = \varphi(X)w$$

$$= \begin{bmatrix} 1 & \sqrt{2}x_1^{(1)} & \sqrt{2}x_2^{(1)} & \sqrt{2}x_1^{(1)}x_2^{(1)} & (x_1^{(1)})^2 & (x_2^{(1)})^2 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 1 & \sqrt{2}x_1^{(n)} & \sqrt{2}x_2^{(n)} & \sqrt{2}x_1^{(n)}x_2^{(n)} & (x_1^{(n)})^2 & (x_2^{(n)})^2 \end{bmatrix} \begin{bmatrix} w_1 \\ \vdots \\ w_6 \end{bmatrix}$$

except the dimension has increased from  $\mathbb{R}^{n \times 2} \rightarrow \mathbb{R}^{n \times 6}$

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by direct analogy to the previous slides, there is also a kernel form:

$$\hat{y}(x^*) = \sum_{i=1}^n k(x^*, x_i) a_i$$

$$k(x^*, x_i) = \langle \varphi(x_i), \varphi(x_j) \rangle$$

$$= \begin{bmatrix} 1 & \sqrt{2}x_1^{(i)} & \dots & (x_1^{(i)})^2 & (x_2^{(i)})^2 \end{bmatrix} \begin{bmatrix} 1 \\ \sqrt{2}x_1^{(j)} \\ \vdots \\ (x_1^{(j)})^2 \\ (x_2^{(j)})^2 \end{bmatrix}$$

## The “kernel trick”

Notice that all that is required is vector products, i.e.

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$$K_{i,j} = \left( (x^{(i)})^T x^{(j)} + 1 \right)^2 = (x_1^{(i)})^2 (x_1^{(j)})^2 + 2x_1^{(i)} x_1^{(j)} x_2^{(i)} x_2^{(j)} + \dots$$

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which can be computed entirely using vectors in  $\mathbb{R}^2$ , so we never have to allocate the (factorially large) feature space.

## Detailed example of nonlinear regression

jupyter notebook: [github.com/jpjanet/ML-chem-workshop/  
blob/master/notebooks/workshop\\_compare\\_models.ipynb](https://github.com/jpjanet/ML-chem-workshop/blob/master/notebooks/workshop_compare_models.ipynb)

# General kernels

Both kernel methods are the same except:

	linear	quadratic
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From the perspective of similarity, we can imagine arbitrary functions to be our kernel, without ever needing to know what the underlying feature map  $\varphi$  is.

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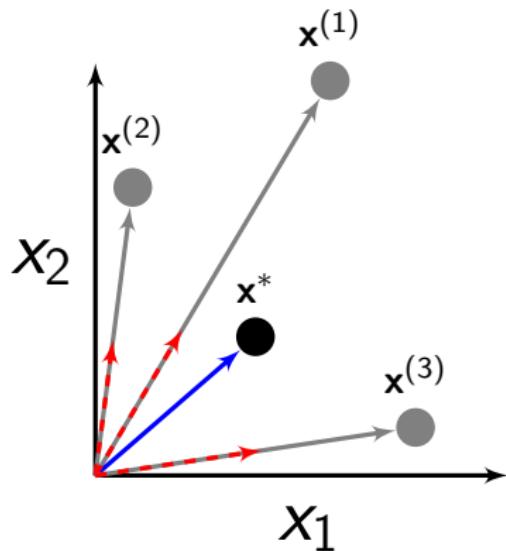
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Depends on  $\sigma$  to control non-locality.

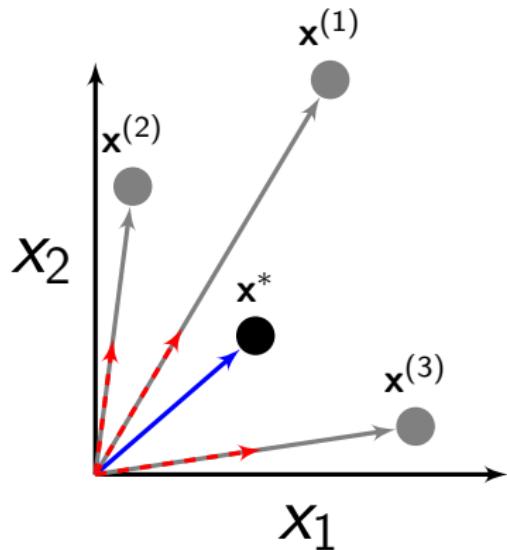
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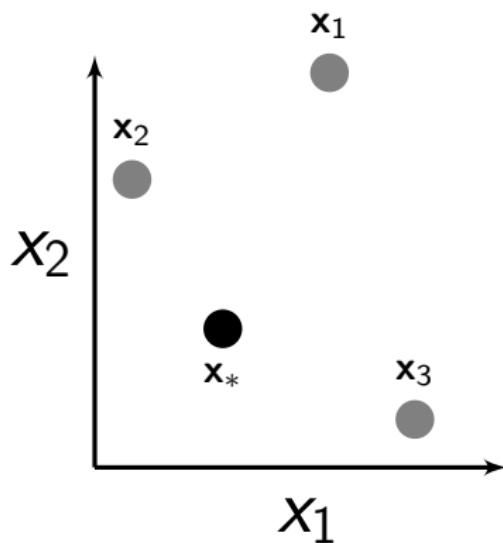


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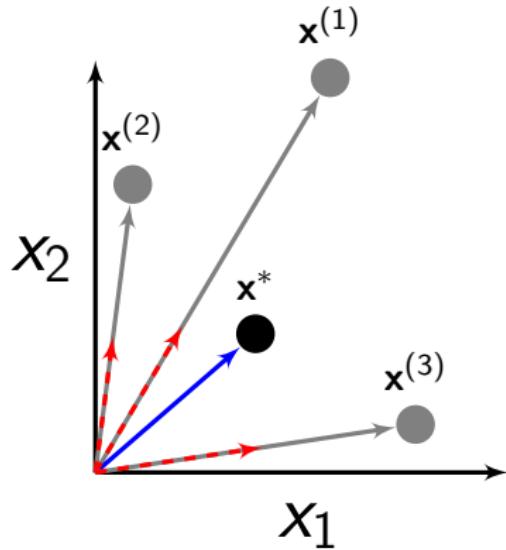
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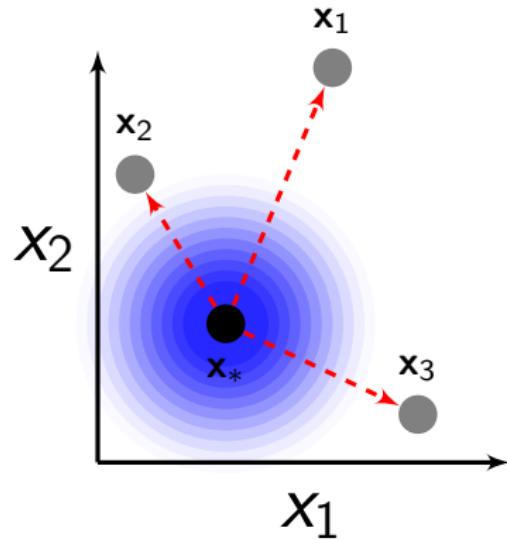
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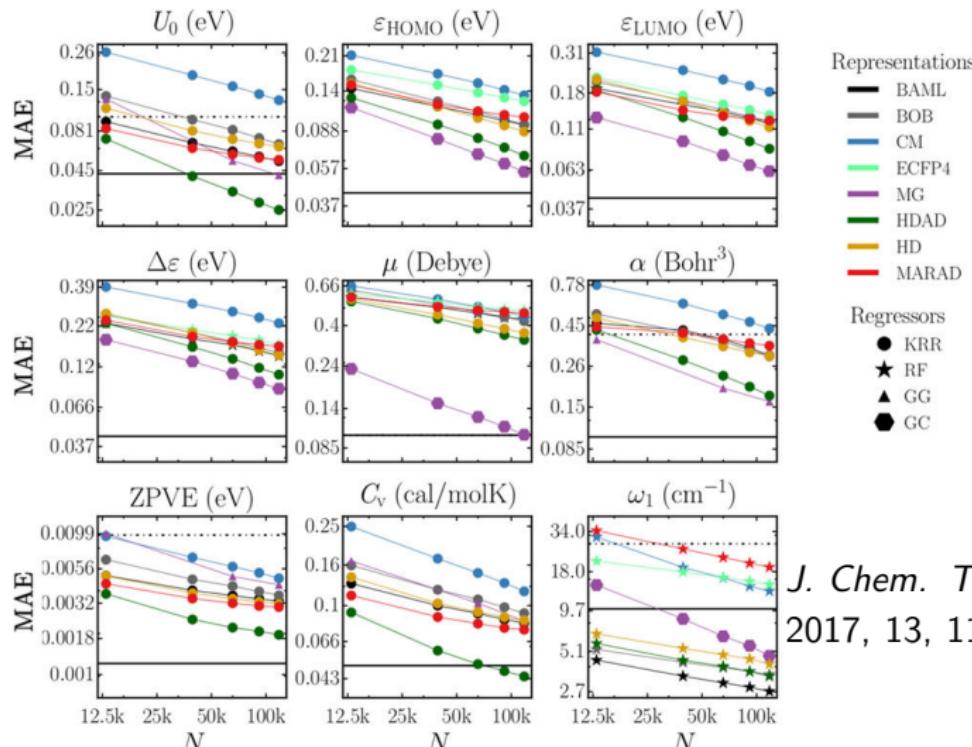
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- 4 check using cross-validation to choose  $\sigma$  and  $\lambda$

# KRR is widely used in chemistry



*J. Chem. Theory Comput.*  
2017, 13, 11, 5255–5264

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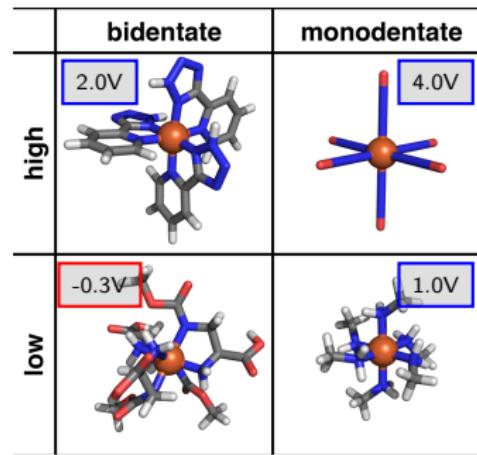
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# KRR example

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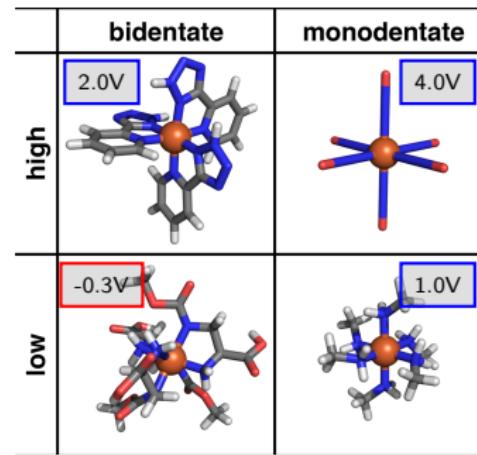
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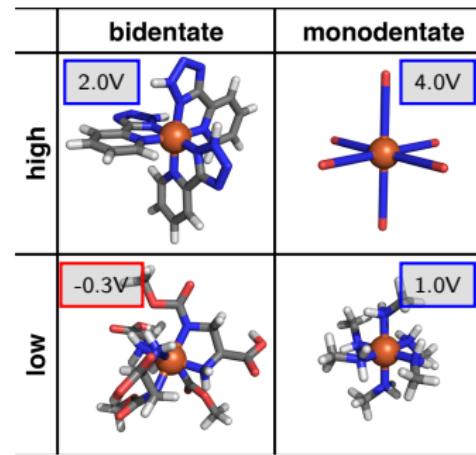


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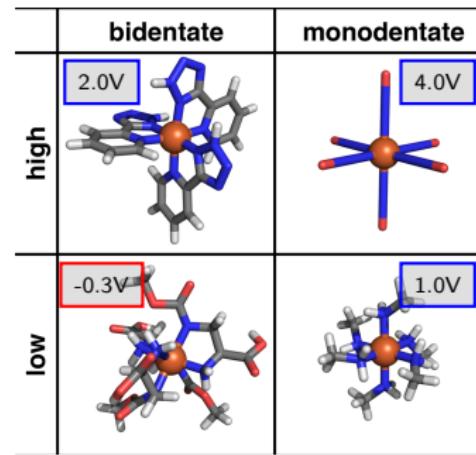


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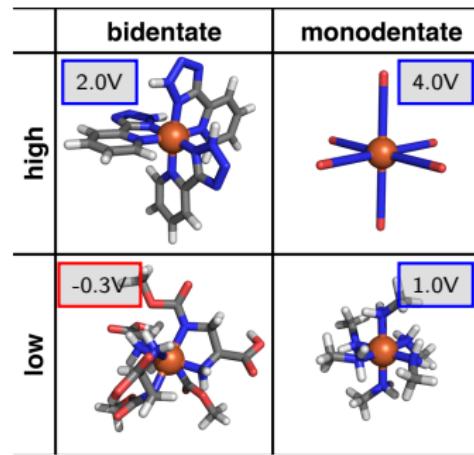
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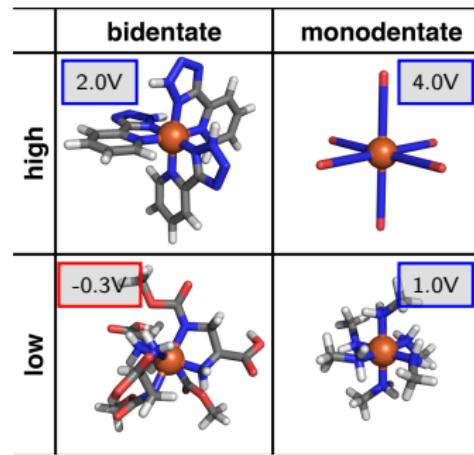
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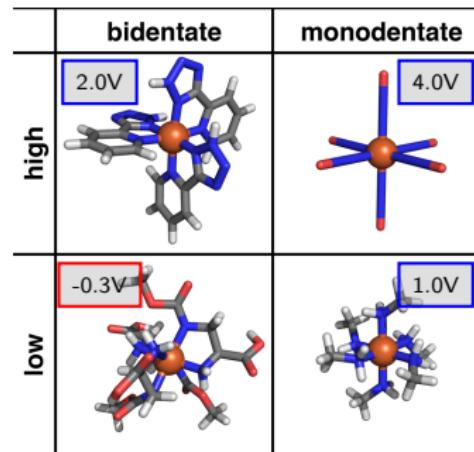
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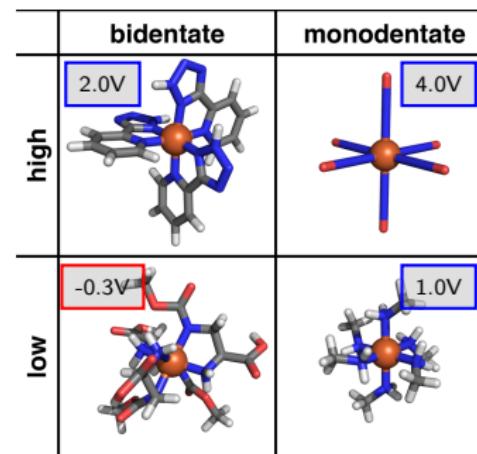
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<sup>5</sup>JP Janet et al. *Ind. Eng. Chem. Res.* 2017, 56, 17, 4898–4910

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Can use *autocorrelation* functions to describe how ligands and atoms are connected

$$\eta_{i,0} = p_i p_i$$

$$\eta_{i,k} = \sum_{i \neq j} p_i p_j \delta(d_{i,j} - d_k), \quad k \neq 0$$

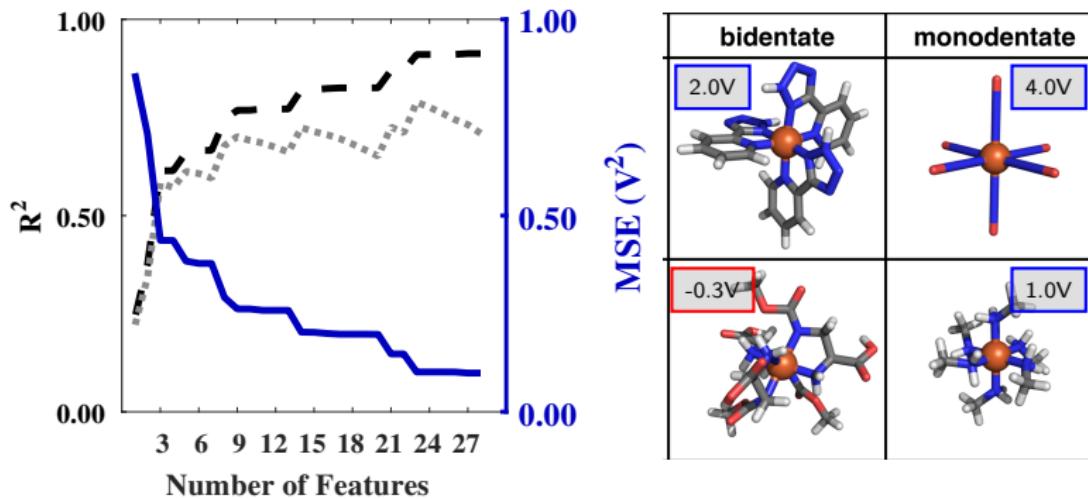
$$\text{AC}_k = \sum_i \eta_{i,k}$$

4 properties,  $k \in [0, 5]$   
 $\implies$  28 variables.

How to choose?

# Why do feature selection?

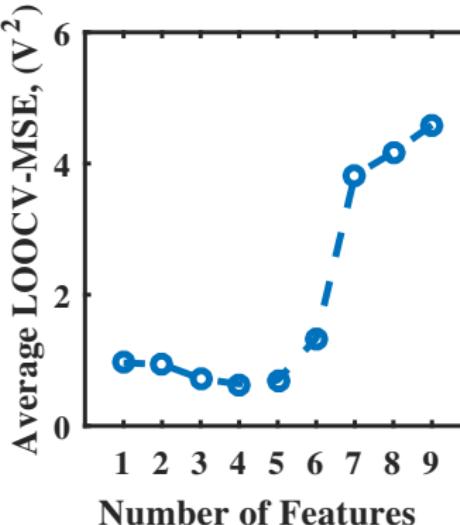
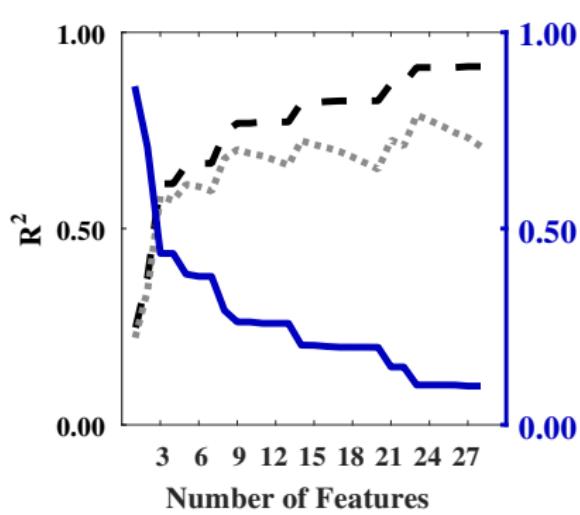
This can help explain what factors are important<sup>5</sup>:



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## How to pick important features?

Using unnecessary features can degrade model performance, so we want to able to pick the subset of variables that is best correlated with our objective, formally:

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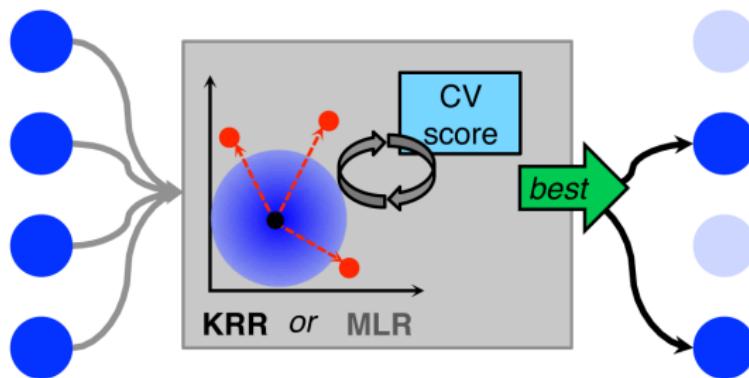
We don't know the optimal number upfront, and this is a combinatorial problem – possible for  $\leq 30$  dimensions or so, but rapidly becomes unfeasible.

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Instead, we can do recursive feature addition/removal. Starting from all (or no) features, we test each feature and remove the one that improves performance most (**crucial to use CV error here**):

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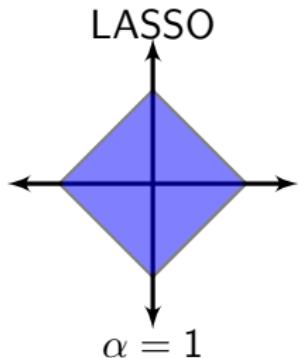
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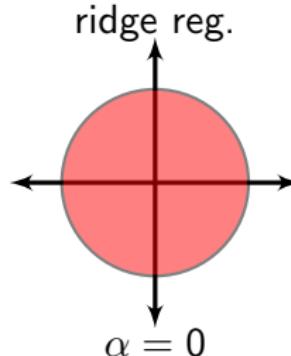
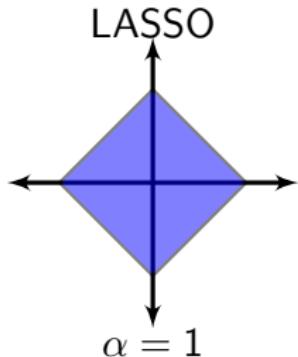
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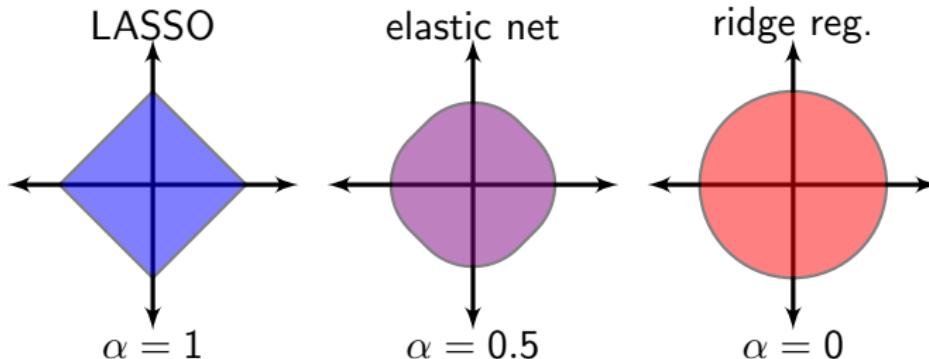
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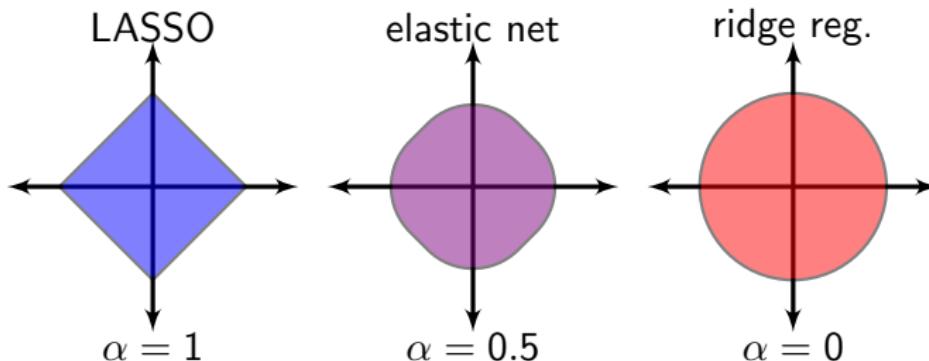
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Using even a small  $\alpha > 0$  ensures the minimization is stable.

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- 1 Feature selection techniques can help identify important features, for modeling and for interpretation
- 2 Iterative subset selection can be expensive since the model needs to be re-trained, including hyperparameters each time
- 3 LASSO/elastic net provide simple ways of extracting most important linear features

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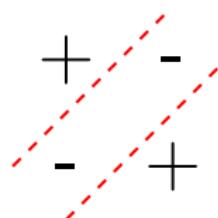
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Decision boundary

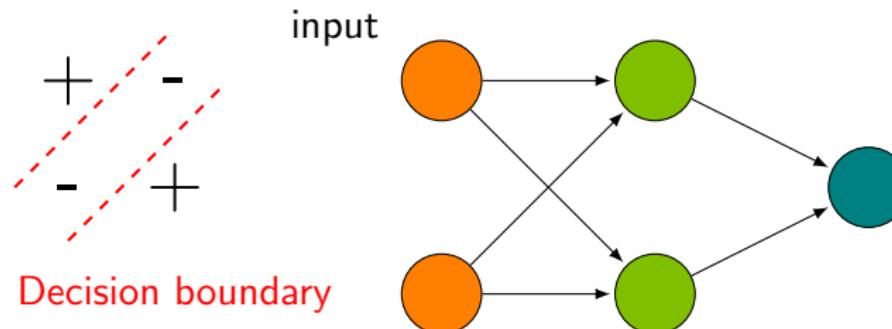
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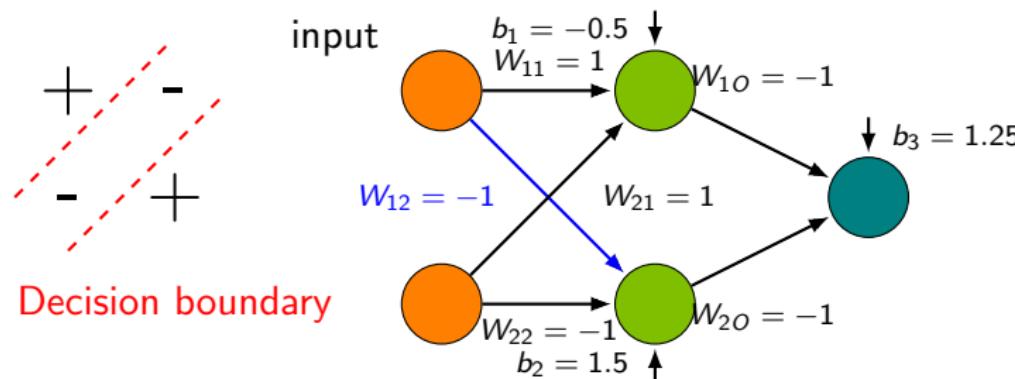
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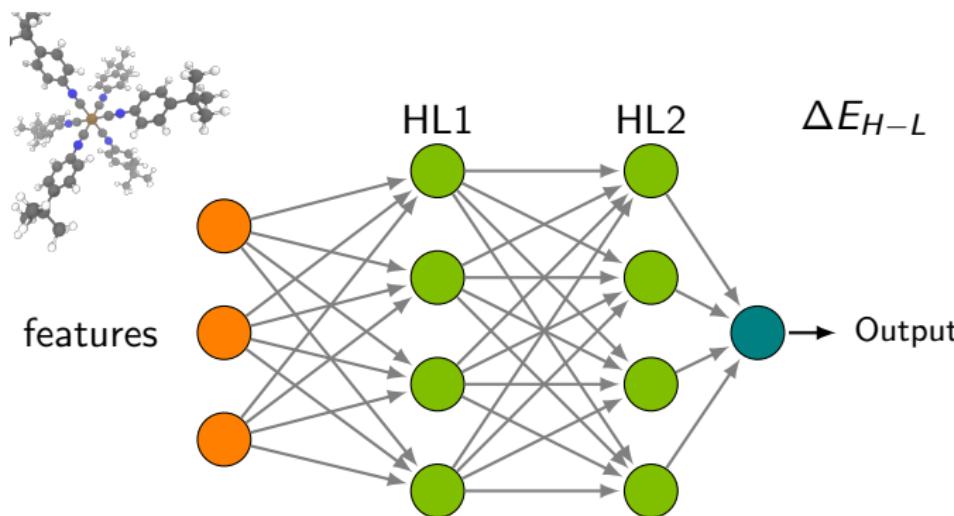
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# What do they look like?

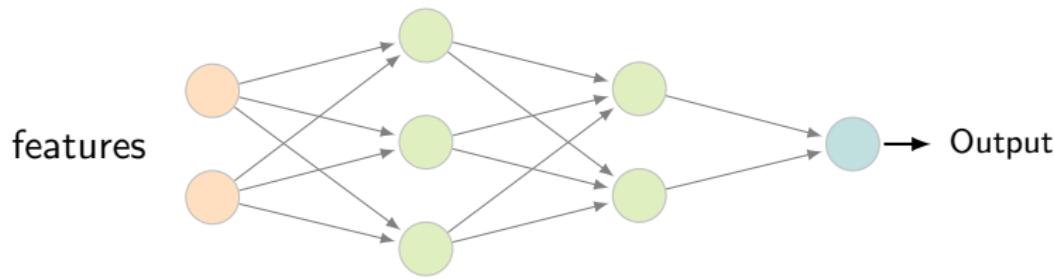


# Backpropagation (chain rule!)

Back-propagation updates neural network weights → example

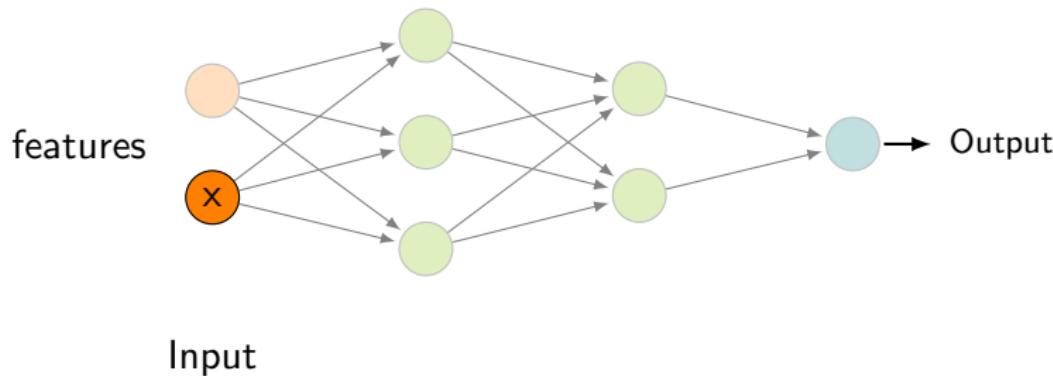
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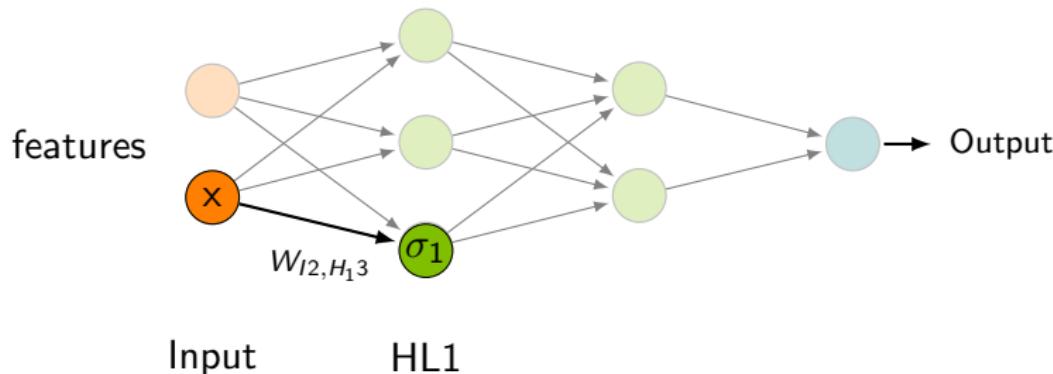
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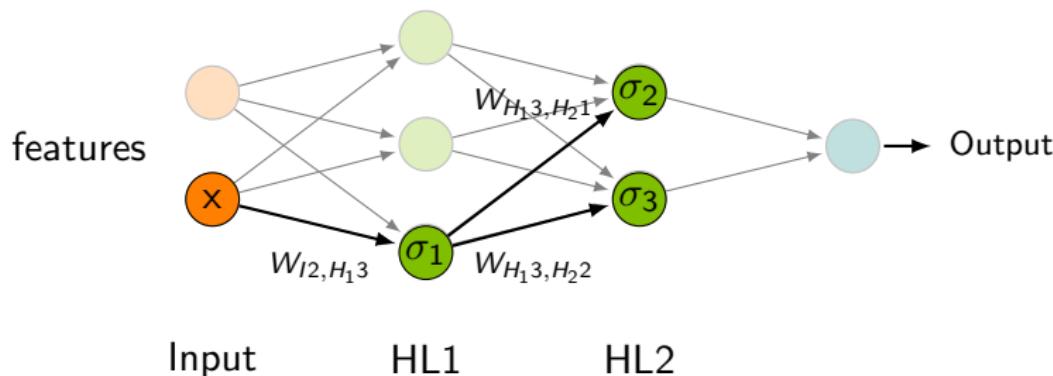
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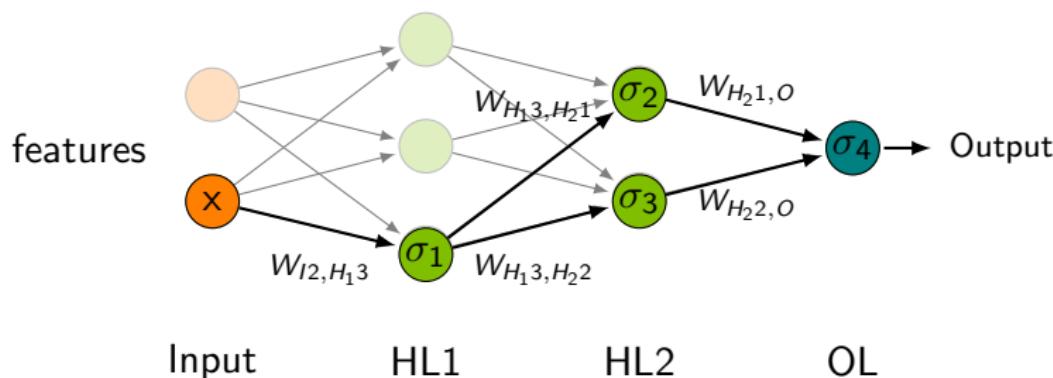
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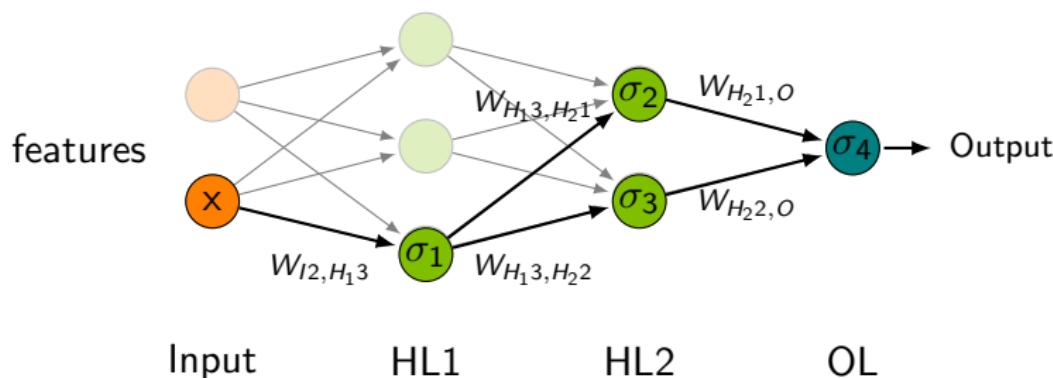
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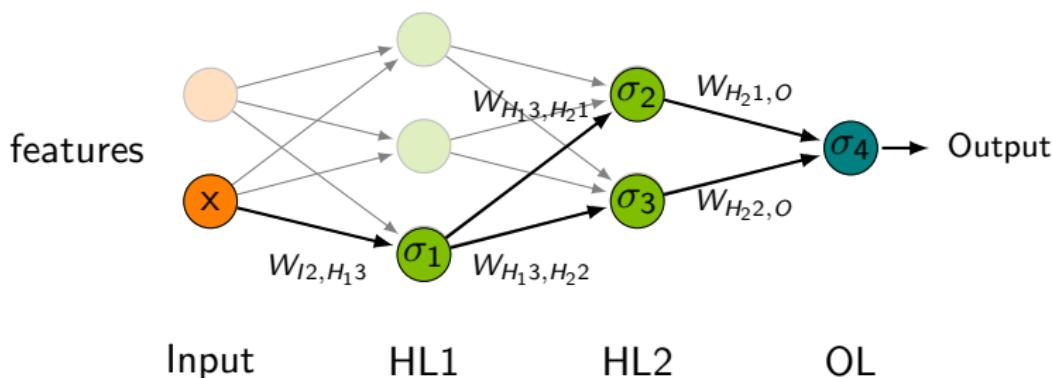
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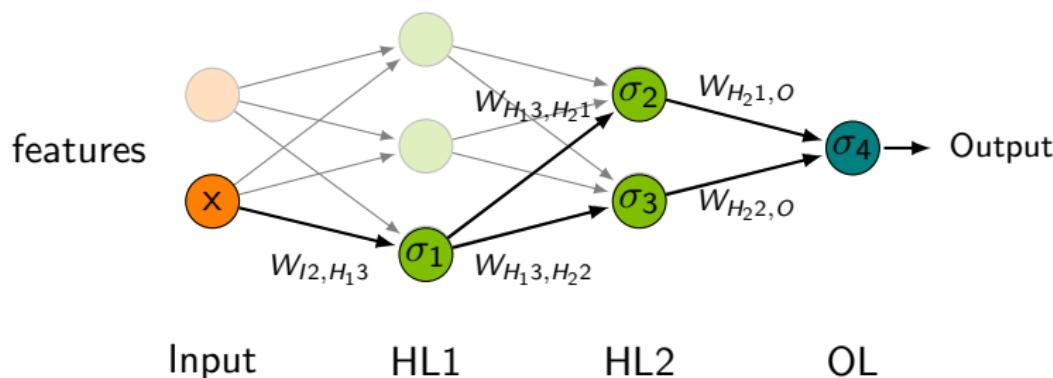
$$\text{Loss} \rightarrow \mathcal{L}(W) = \sum_{i=1}^N ((y_i - y_{pred})^2) + \lambda (\sum_{l=1}^L ||W_l||^2)$$



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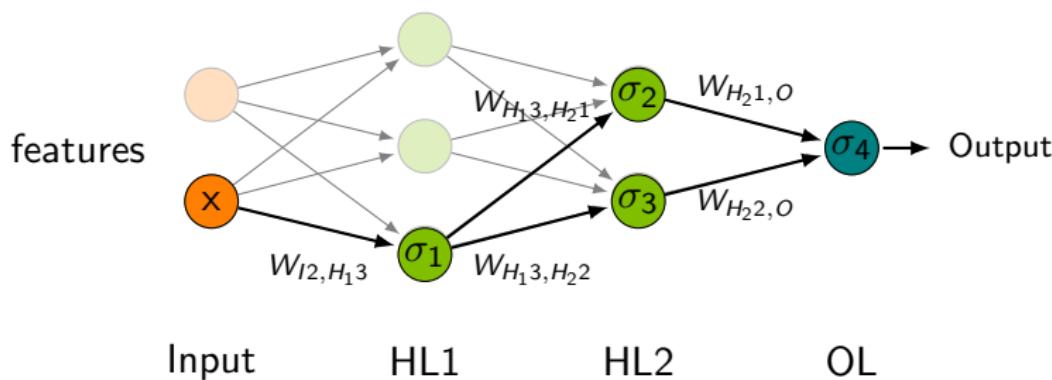
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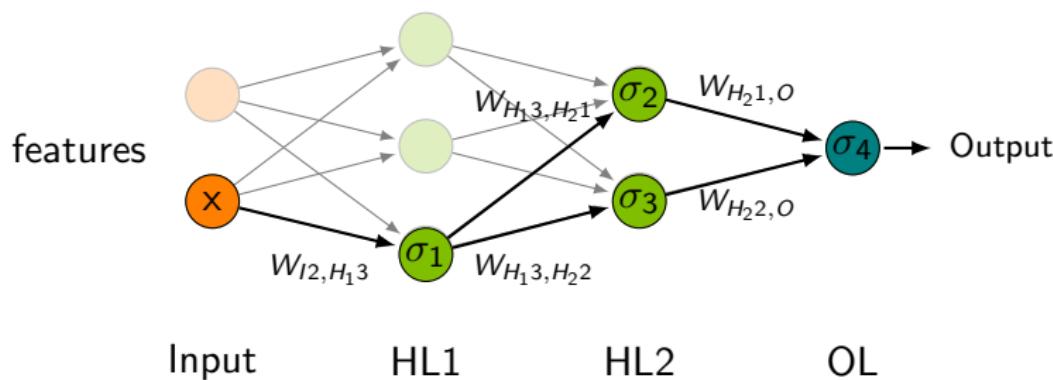
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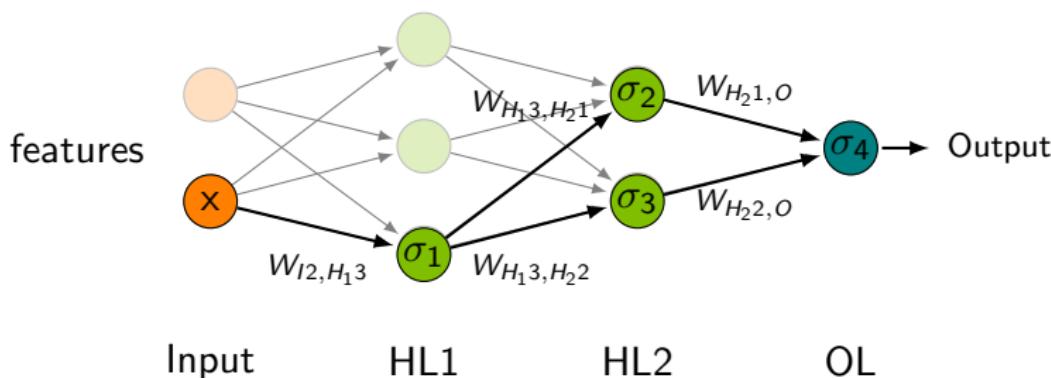
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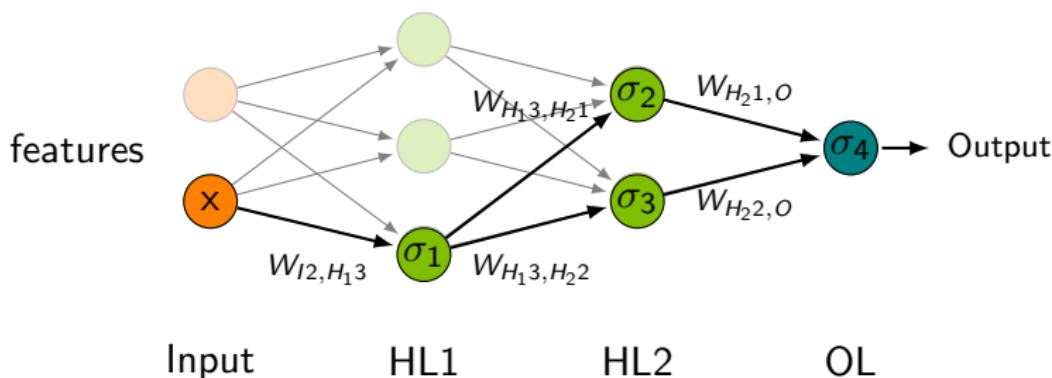


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$$\left( \frac{\partial \sigma_1}{\partial z_1} \right) \left( \frac{\partial z_1}{\partial W_{I2, H_13}} \right) + \left( \frac{\partial z_4}{\partial W_{H_22, O}} \right) \left( \frac{\partial W_{H_22, O}}{\partial \sigma_3} \right) \left( \frac{\partial \sigma_3}{\partial z_3} \right) \left( \frac{\partial z_3}{\partial W_{H_13, H_22}} \right) \left( \frac{\partial W_{H_13, H_22}}{\partial \sigma_1} \right) \left( \frac{\partial \sigma_1}{\partial z_1} \right) \left( \frac{\partial z_1}{\partial W_{I2, H_13}} \right)$$



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$SGD \rightarrow \left( \frac{\partial Loss}{\partial W} \right) \rightarrow$  one/few examples  $\rightarrow$  MUCH noisier!  $\rightarrow$  less stuck

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**Recurrent**→ Layers that “store” information about previous times, thus commonly used in speech or handwriting recognition

# Interpretation as representation learning

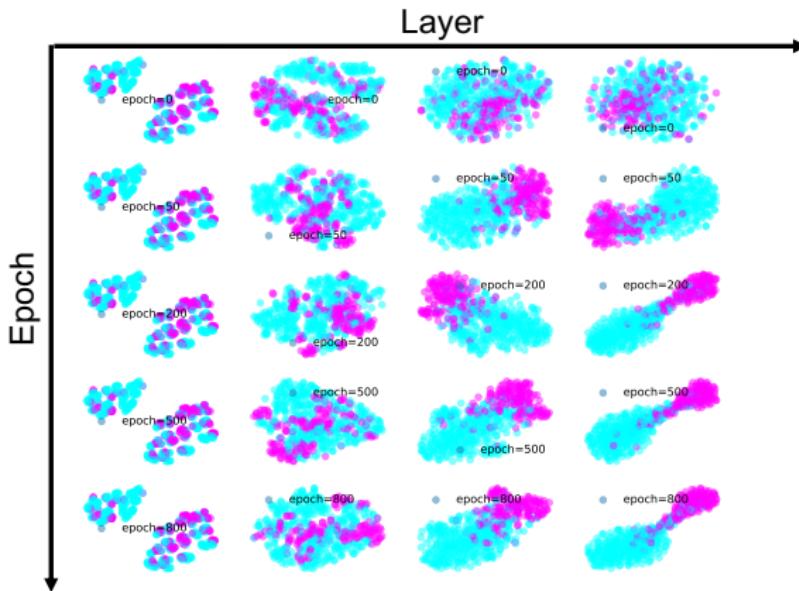
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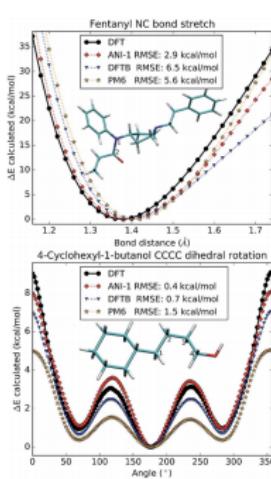
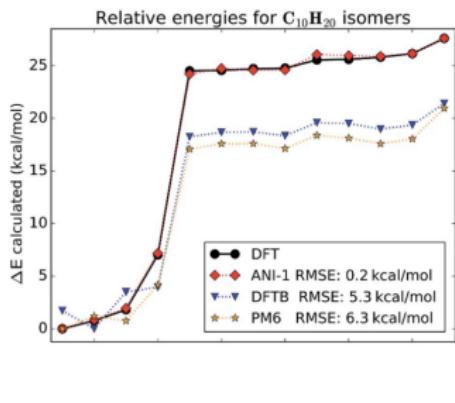
- 1 Neural network models provide model complexity 'on tap'
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## ANN example

jupyter notebook: [github.com/jpjanet/ML-chem-workshop/  
blob/master/notebooks/ANN.ipynb](https://github.com/jpjanet/ML-chem-workshop/blob/master/notebooks/ANN.ipynb)

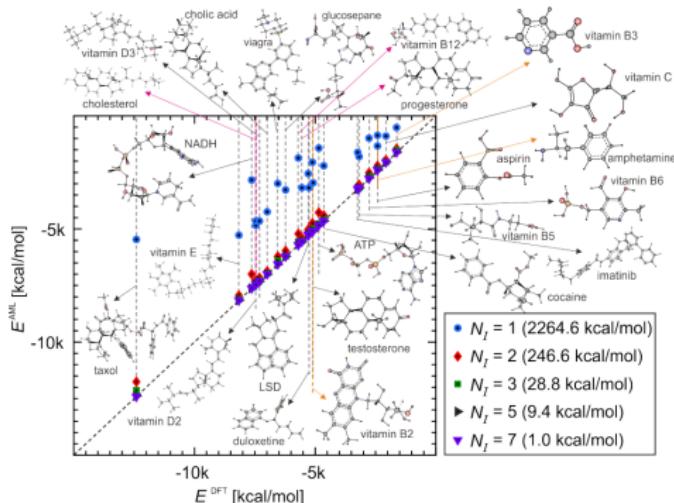
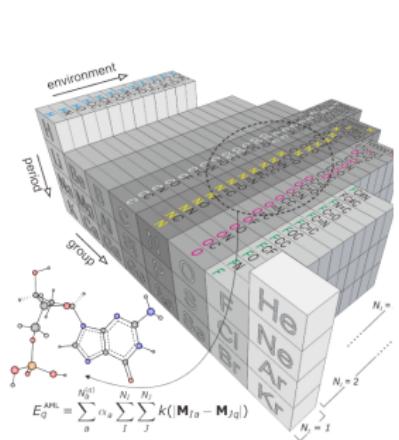
# Neural network potentials

Smith, J. S., Isayev, O., and Roitberg, A. E. ANI-1: an extensible neural network potential with DFT accuracy at force field computational cost. *Chem. Sci.*, 2017, 8, 3192-3203.



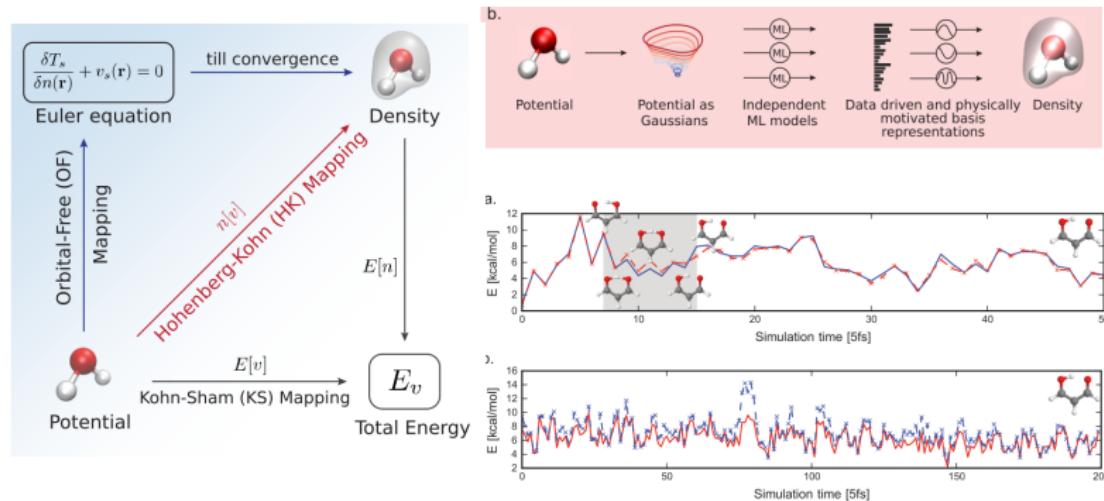
# Property predictions

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