

Machine learning and chemistry

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under the supervision of Professor Heather J. Kulik

for the most recent version and demos: github.com/jpjanet/ML-chem-workshop
this revision: `fafcc26fd21e2c6dcc9da2a0c233d8fbac5f60e7` on branch `master`



Rise of the (chemical) machines

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Rise of the (chemical) machines

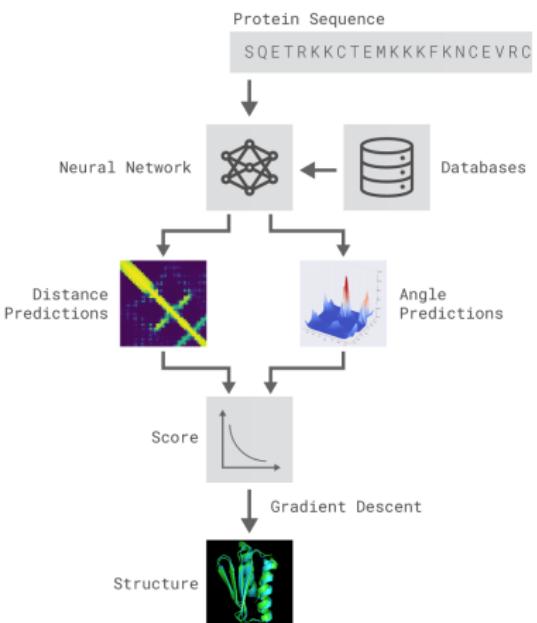
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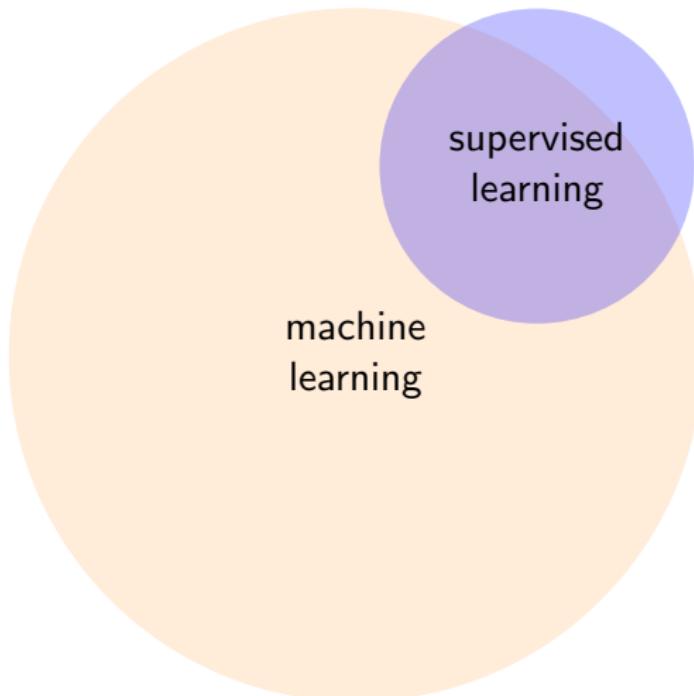
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This is probably a bit strong, but all scientists generate data as a product. ML provides new, powerful ways to exploit their that information.

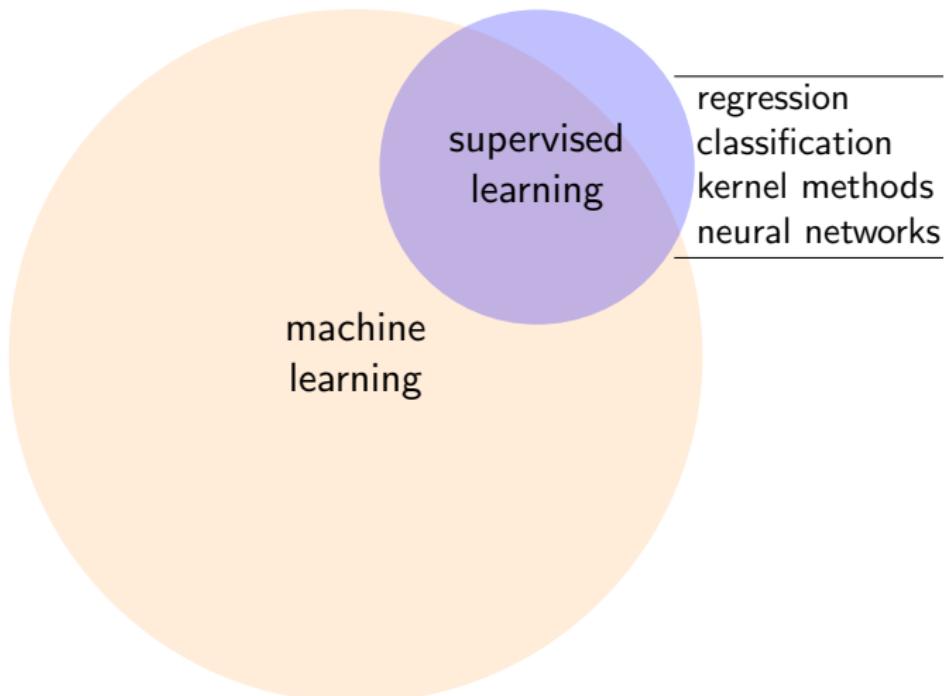
Types of machine learning

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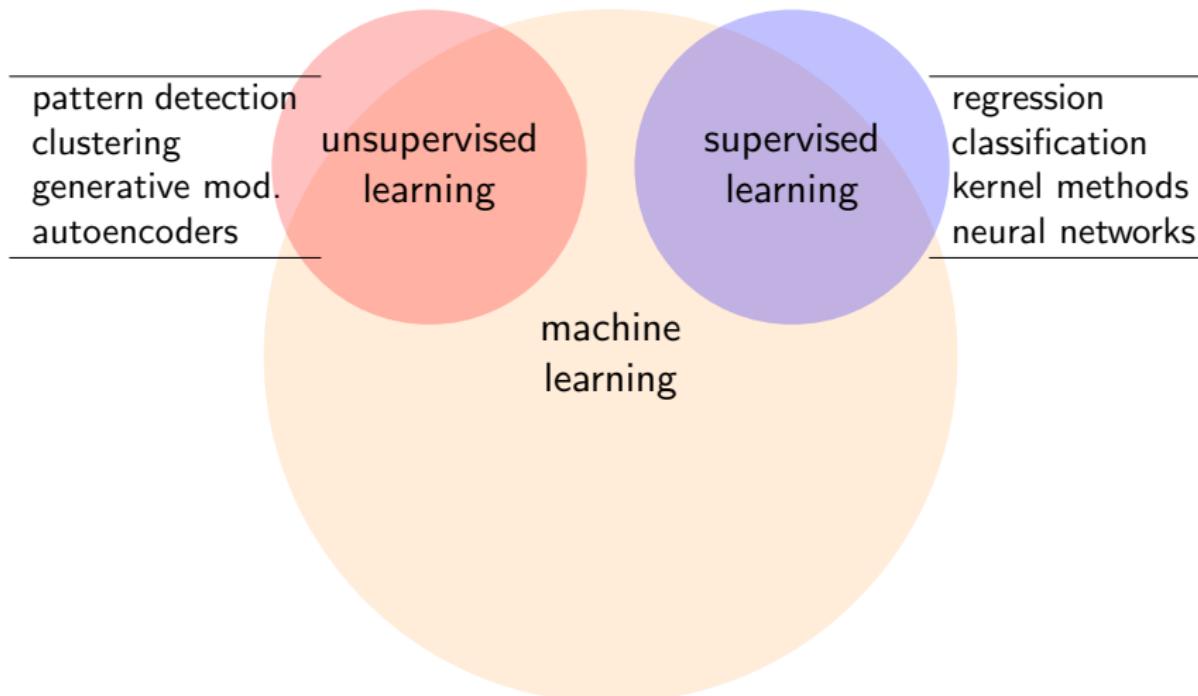
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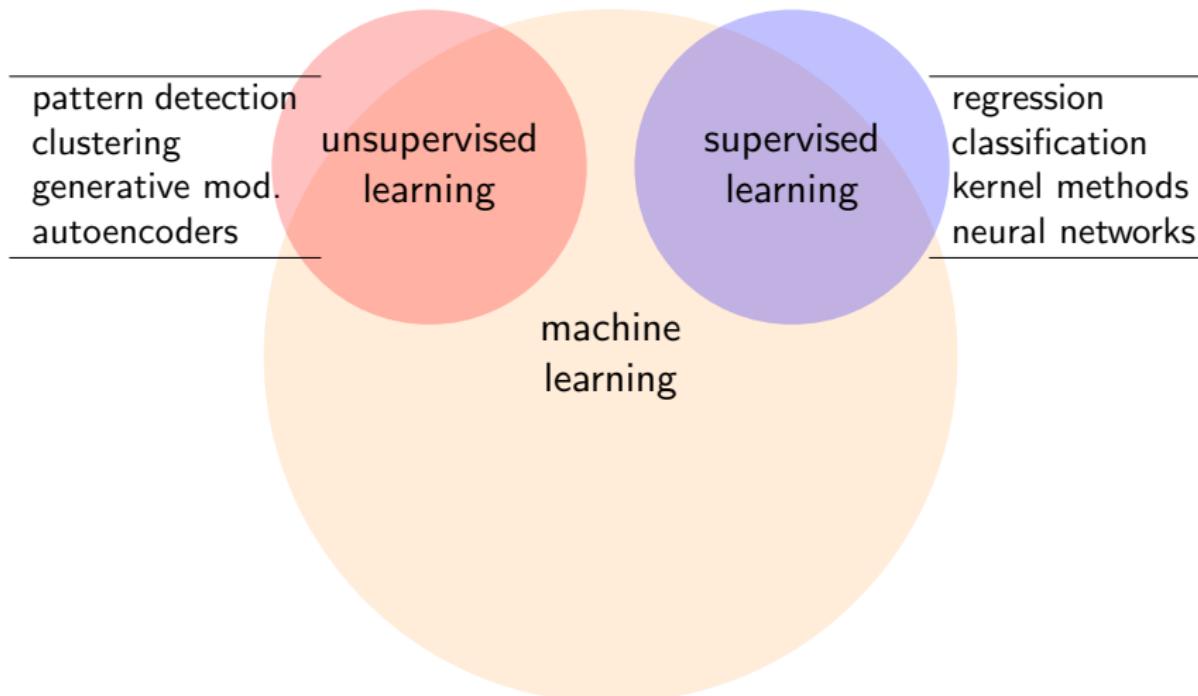
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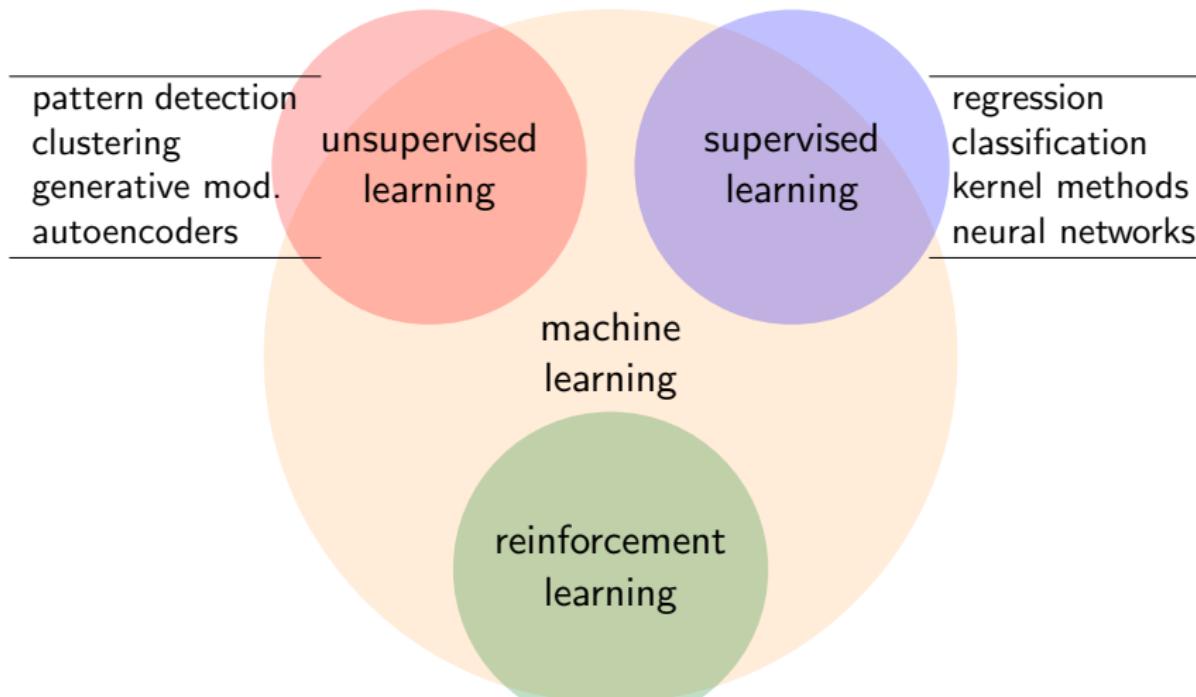
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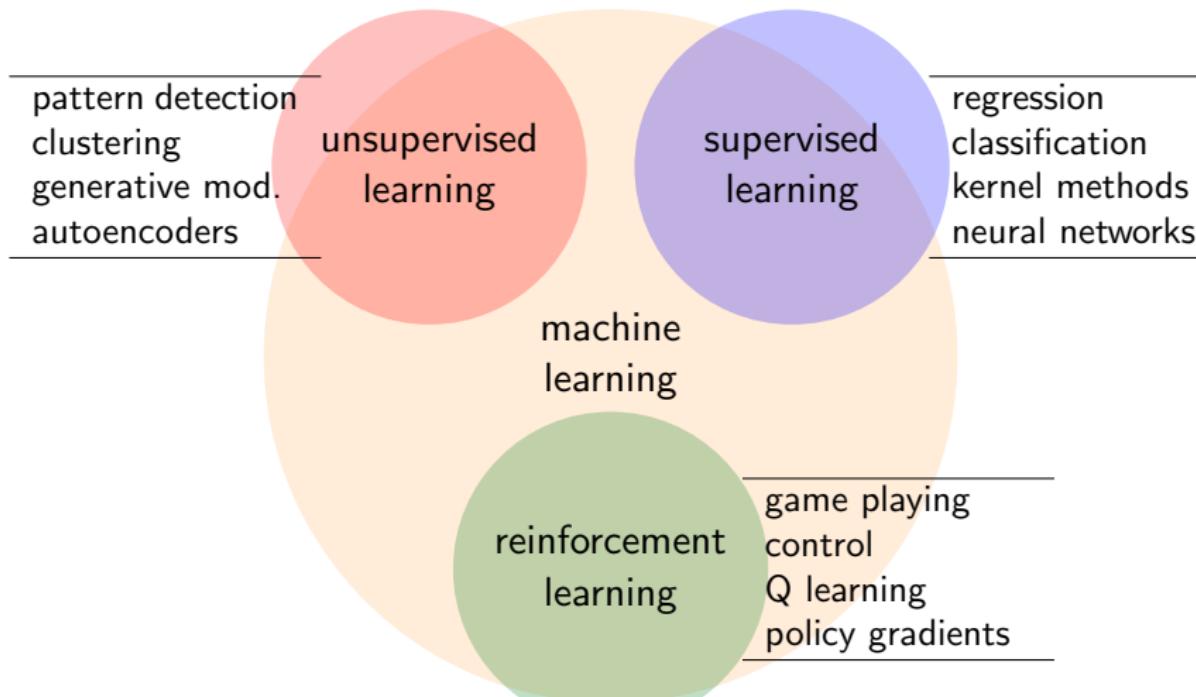
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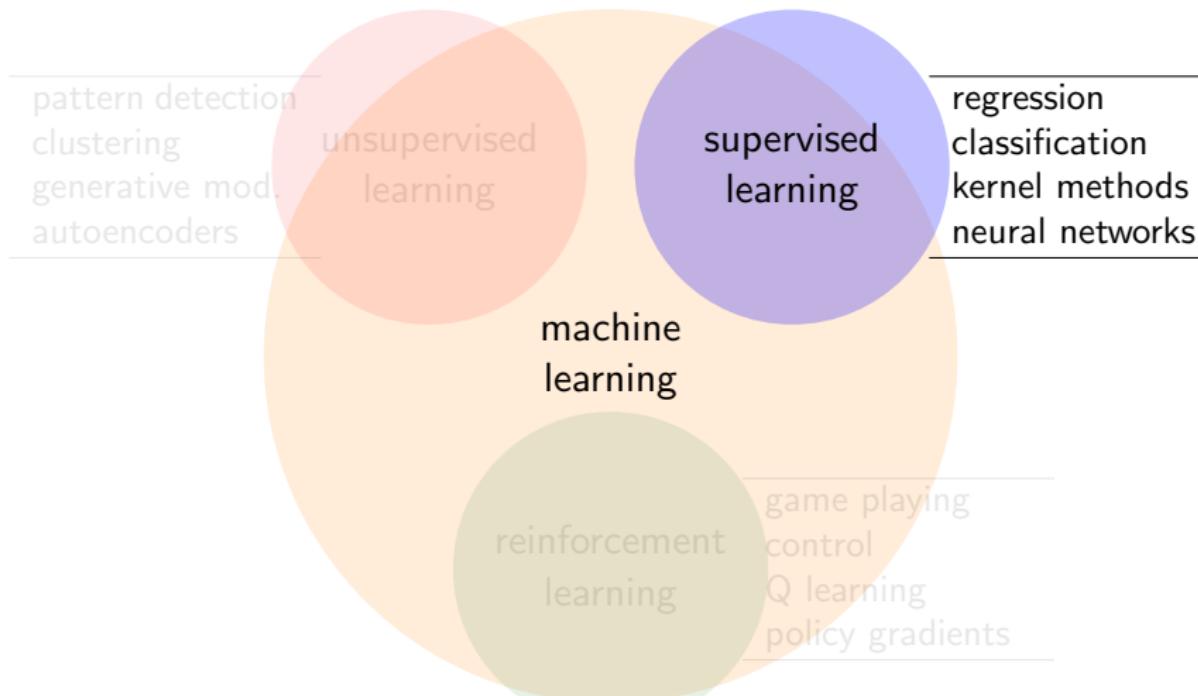
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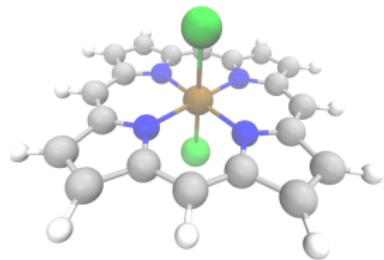
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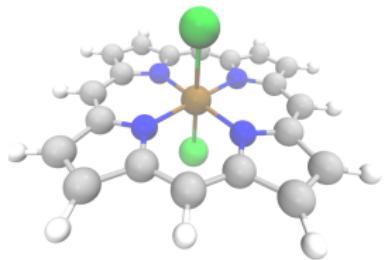
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Why ML in chemistry?

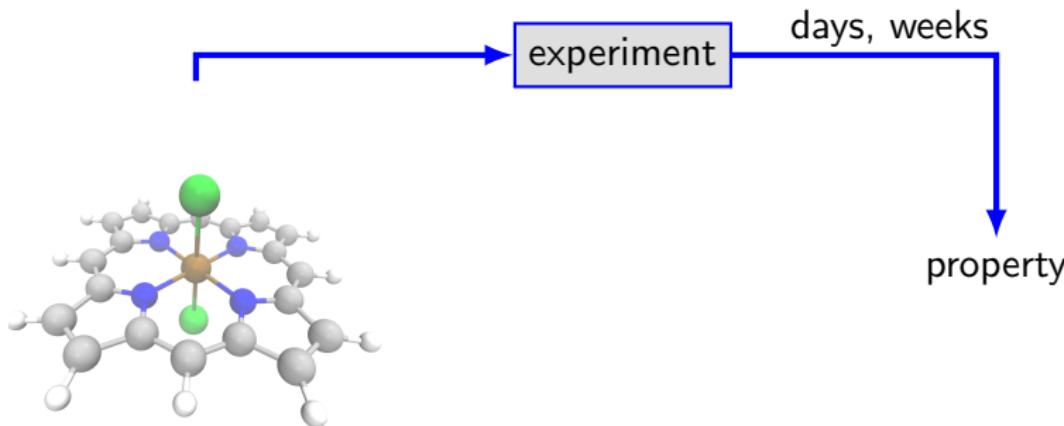


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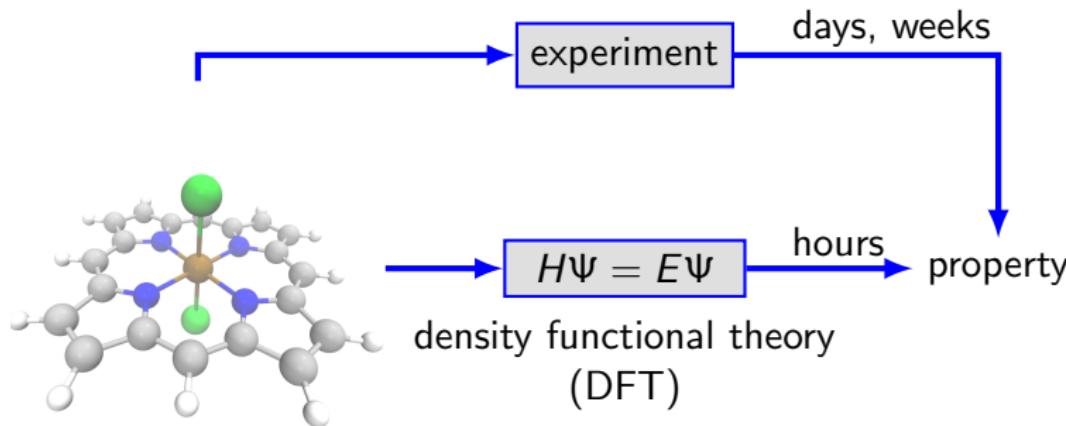


property

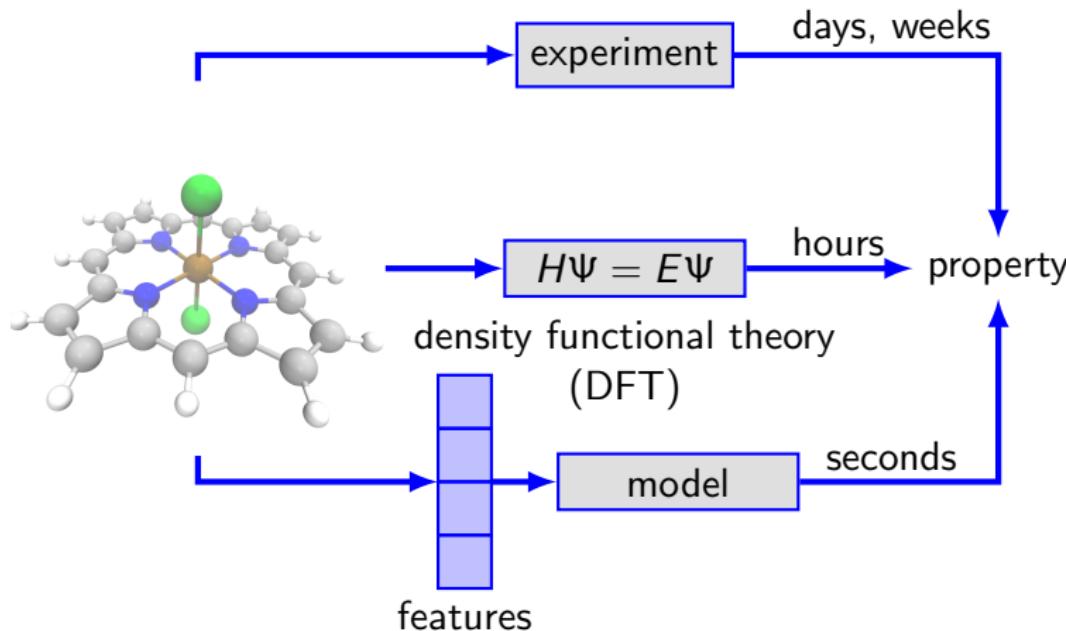
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Structure of this talk

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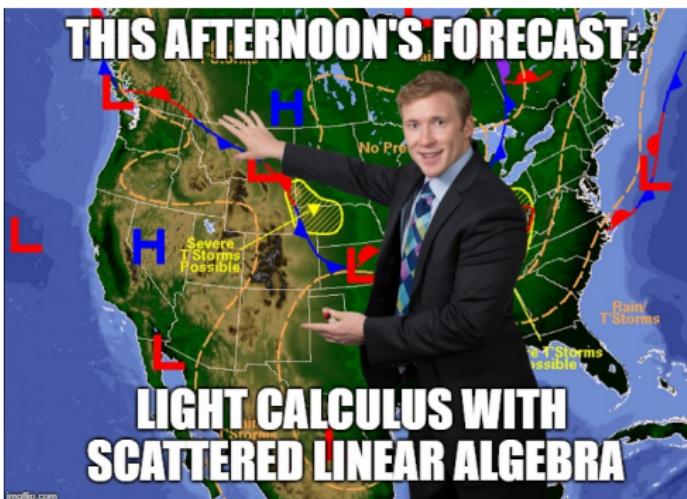
Please ask questions throughout!

Disclaimer

Warning: this talk contains some *light* mathematics.

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Some useful notation:

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

The goal of statistical learning

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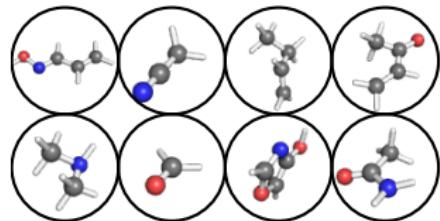
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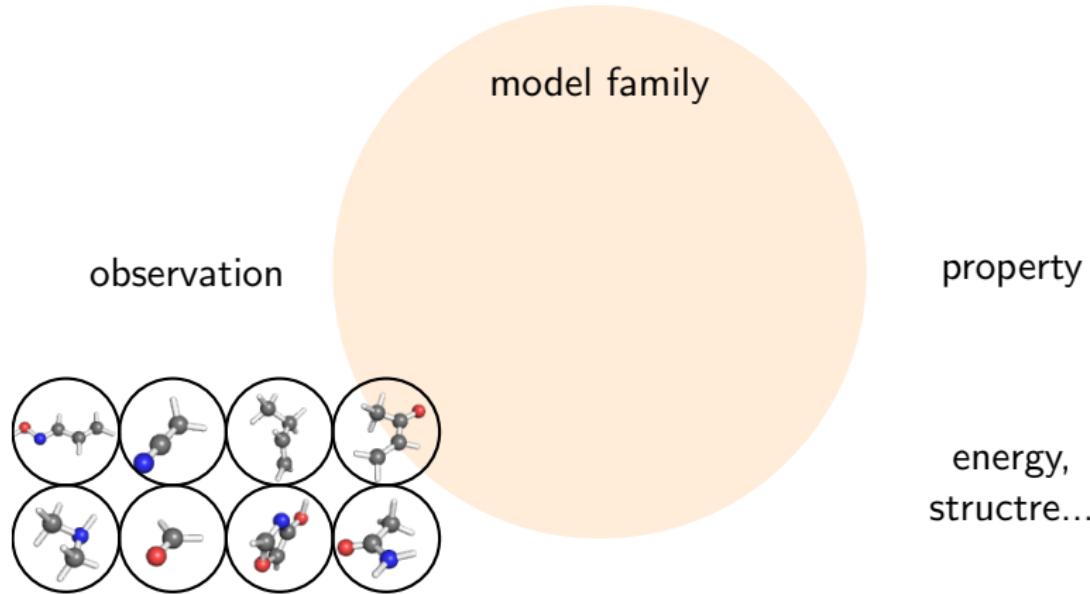
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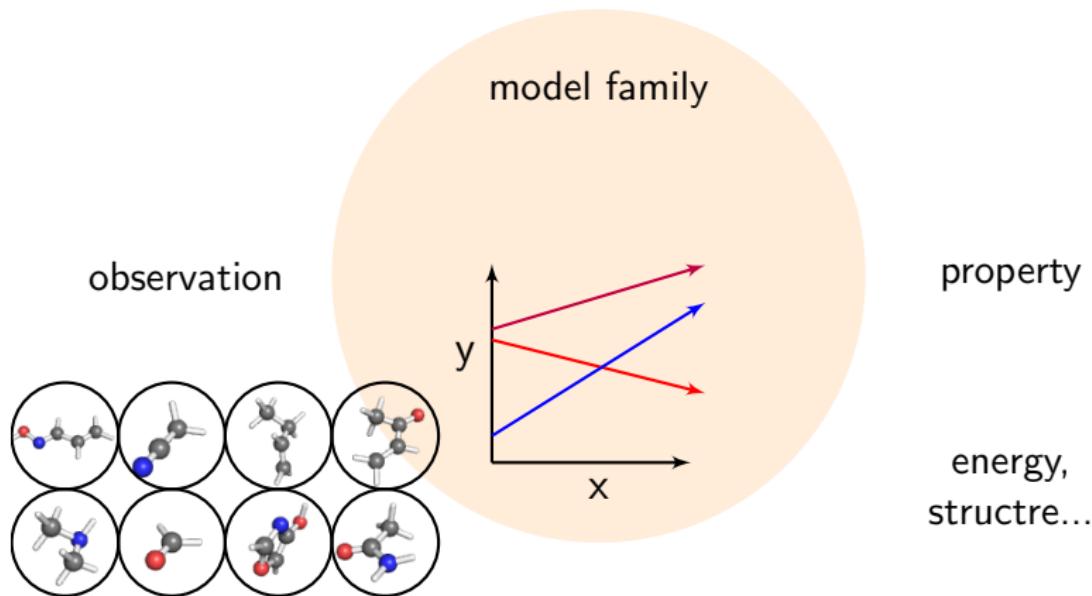


energy,
structre...

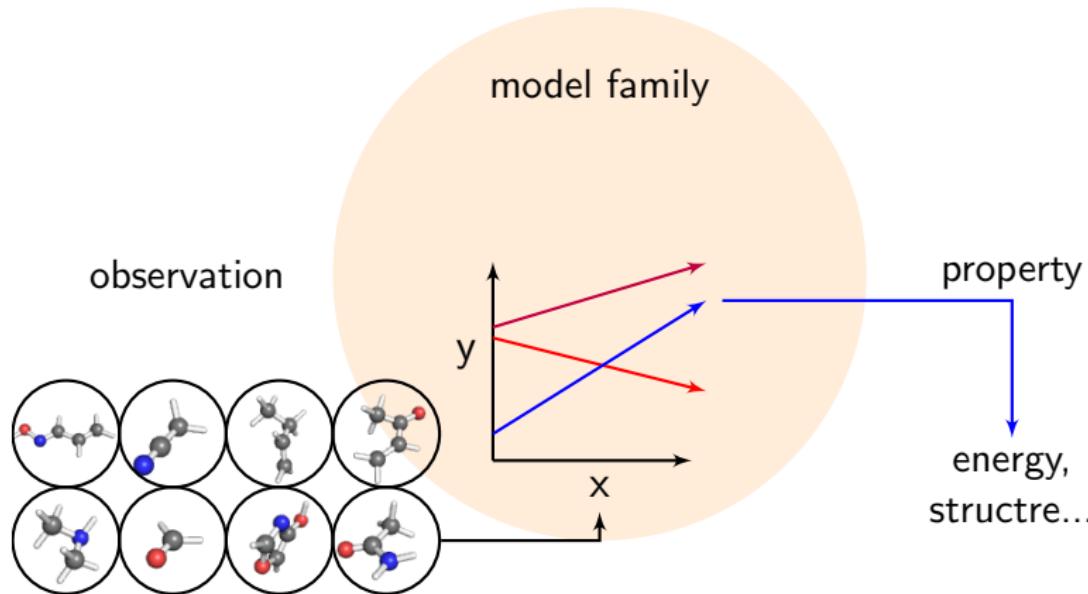
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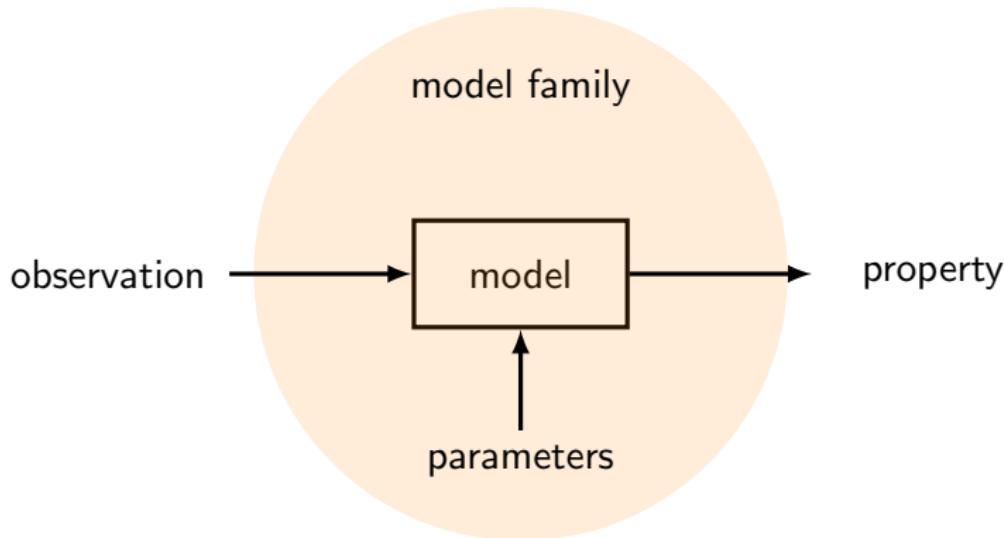
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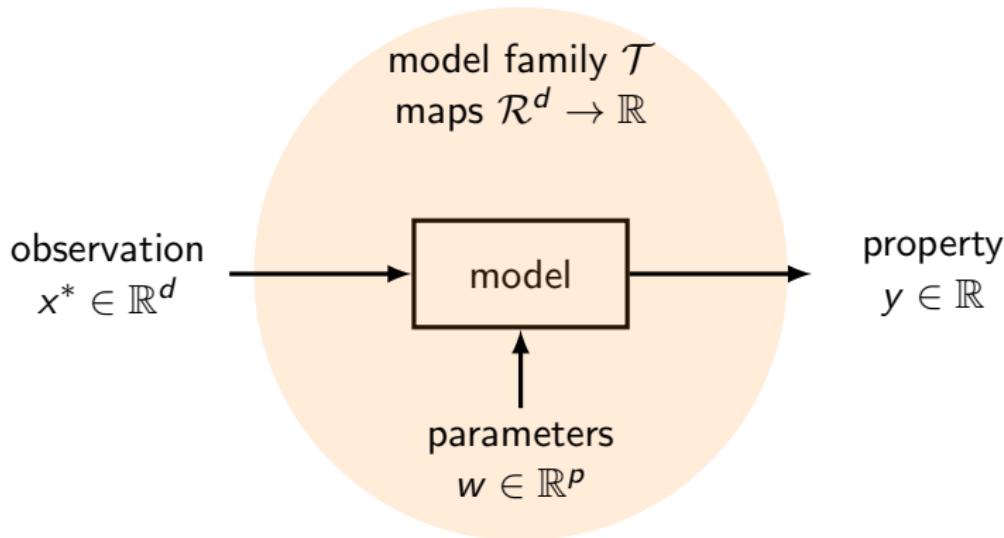
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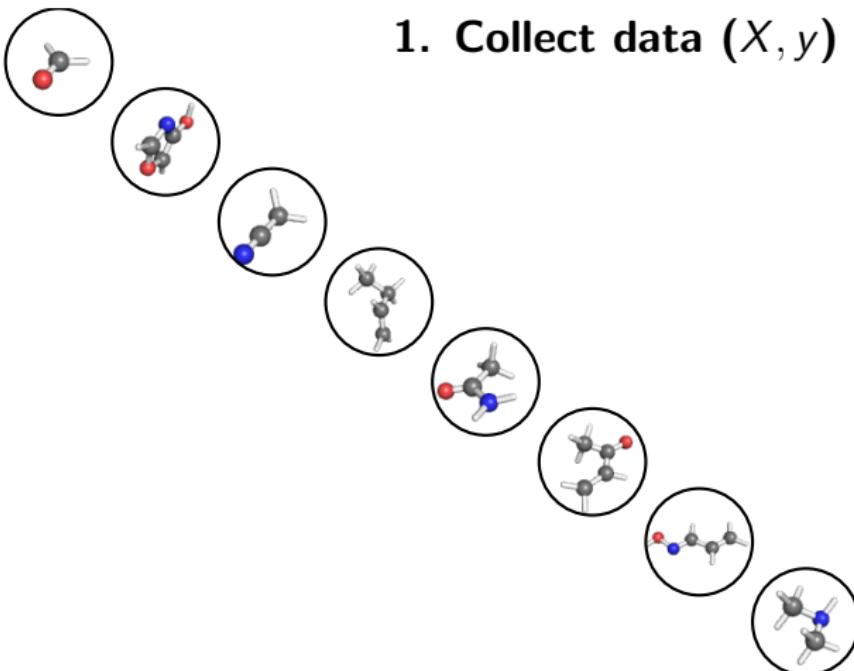


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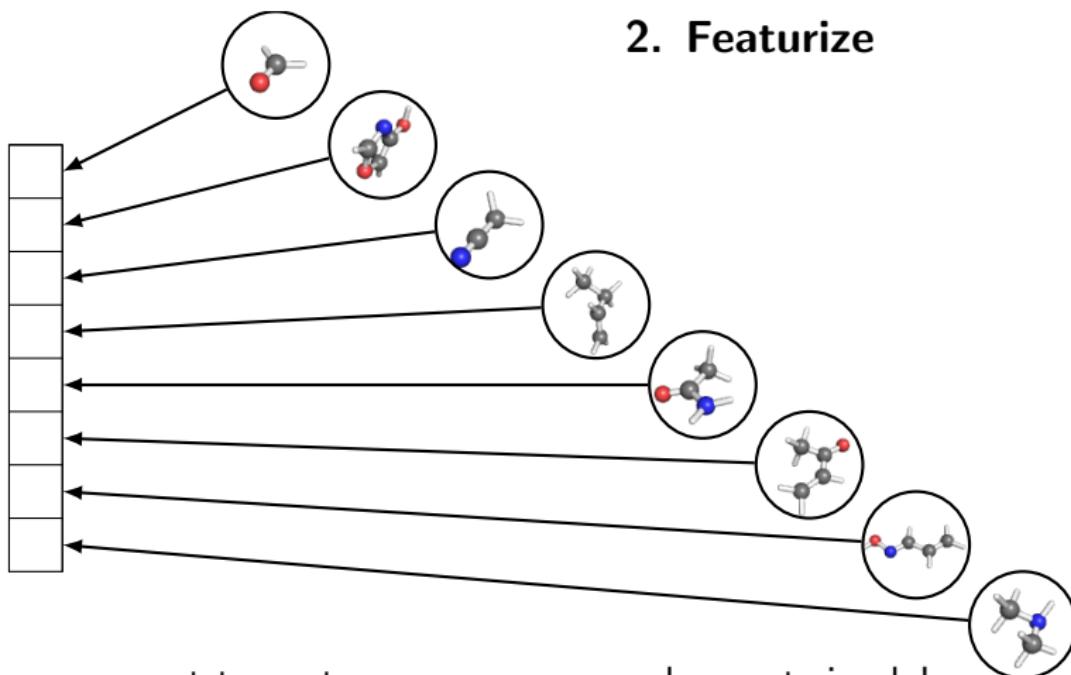


Overview of supervised learning

1. Collect data (X, y)



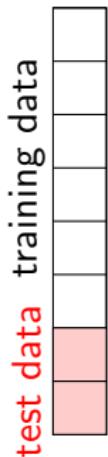
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convert to vectors, preprocess, scale – not simple!

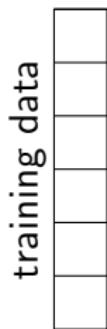
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3. Partition data

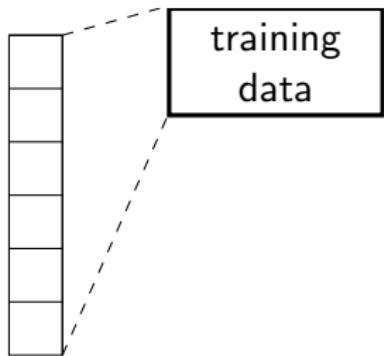


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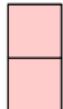
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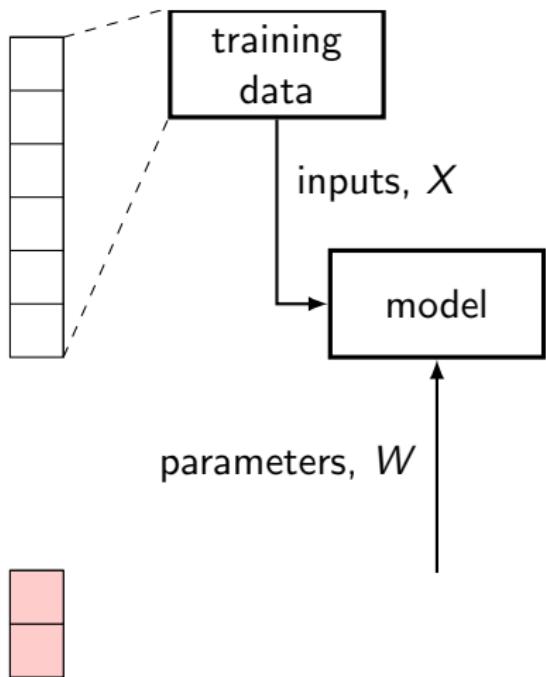
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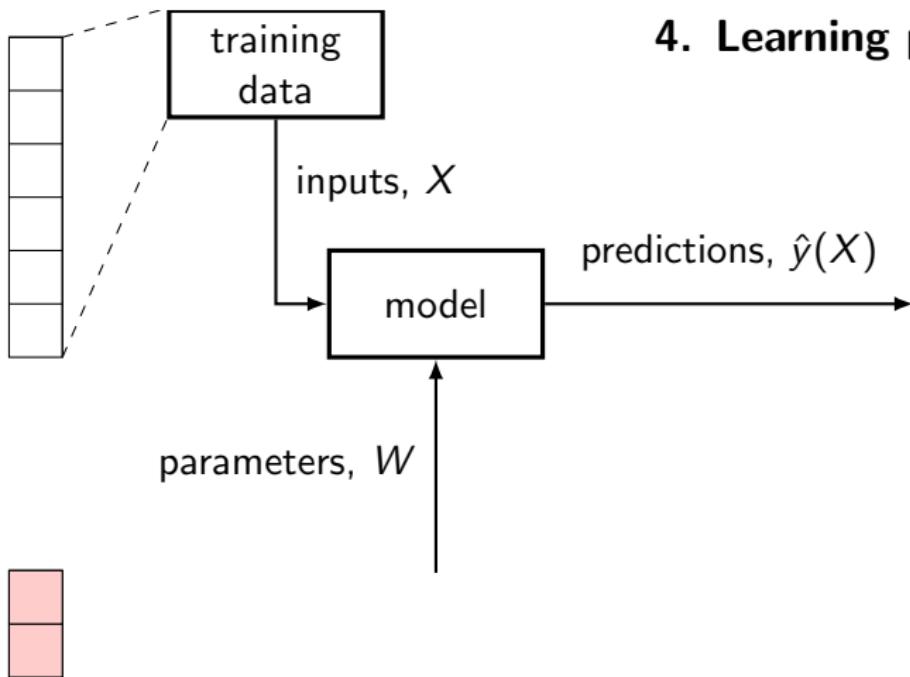


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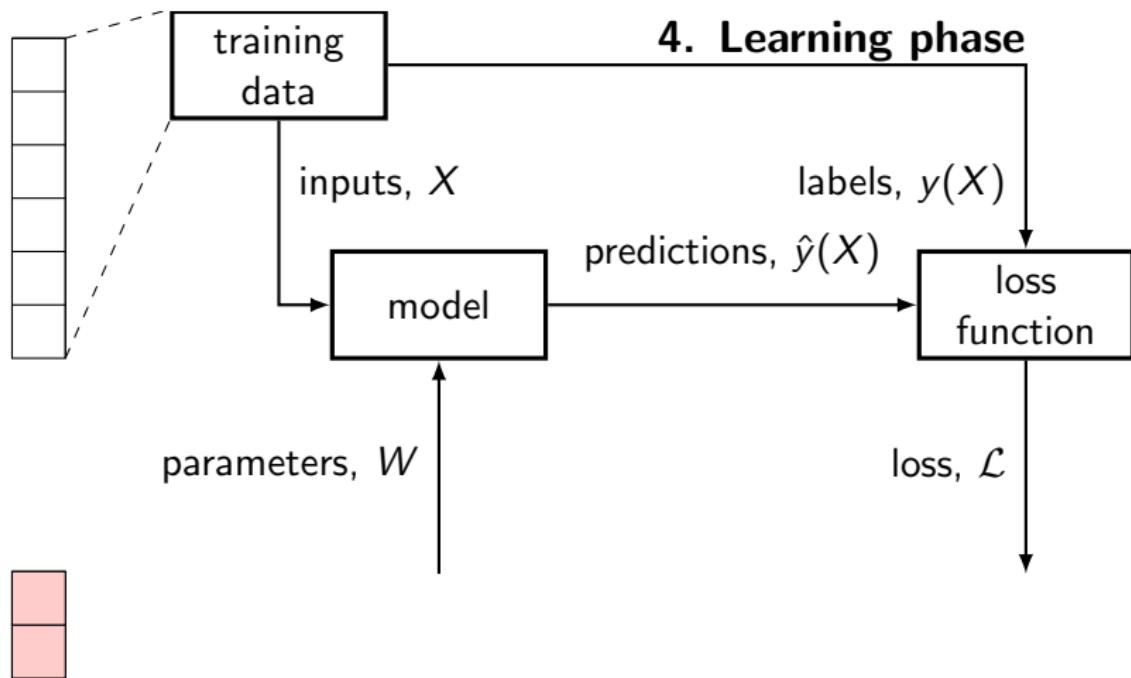
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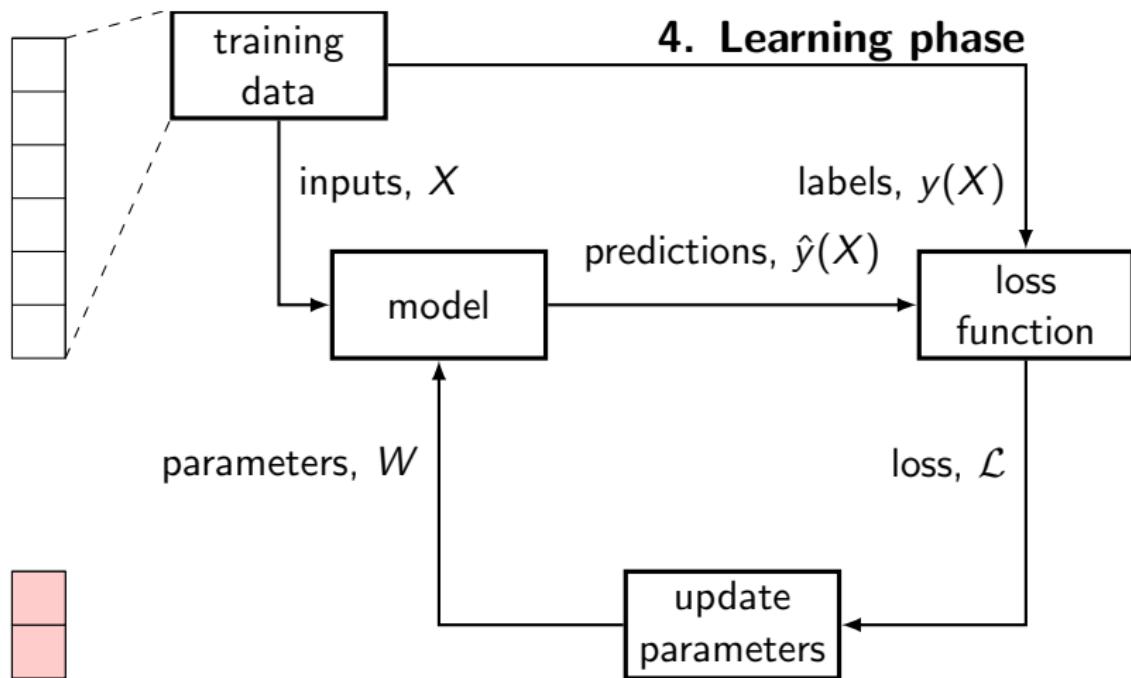


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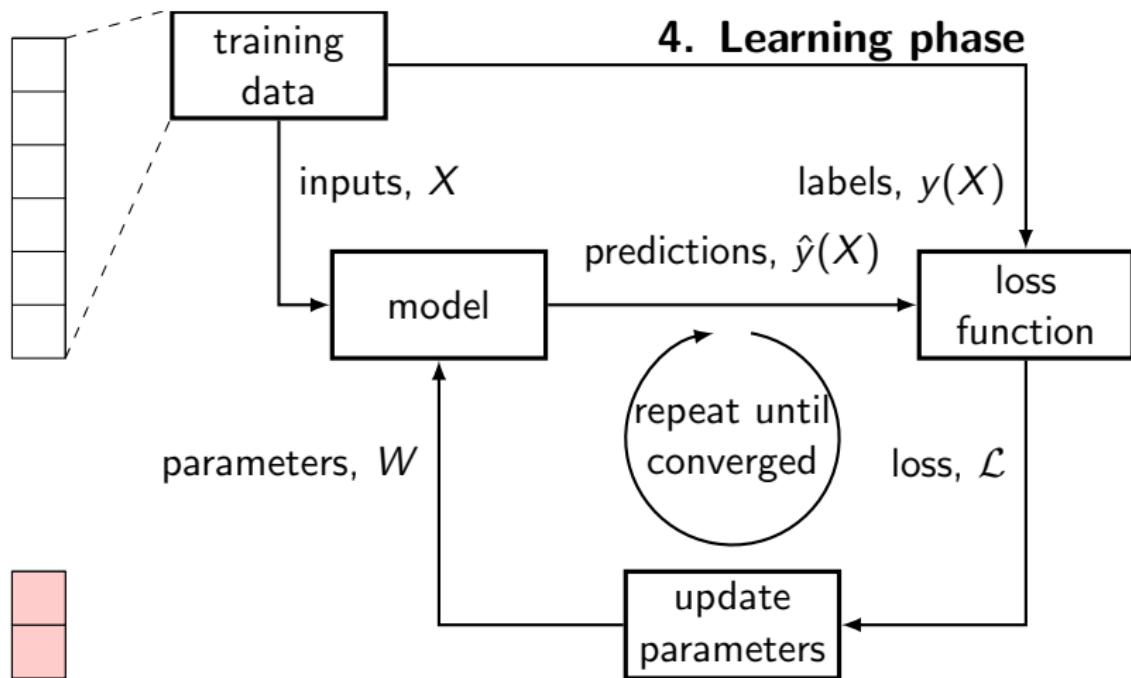
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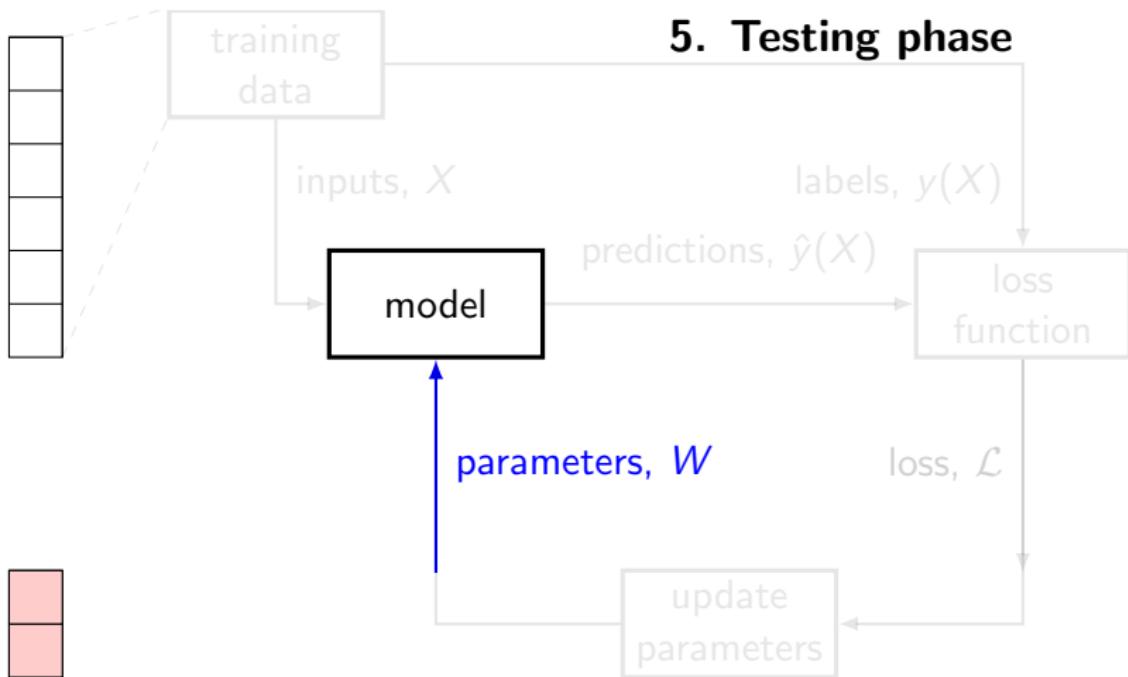
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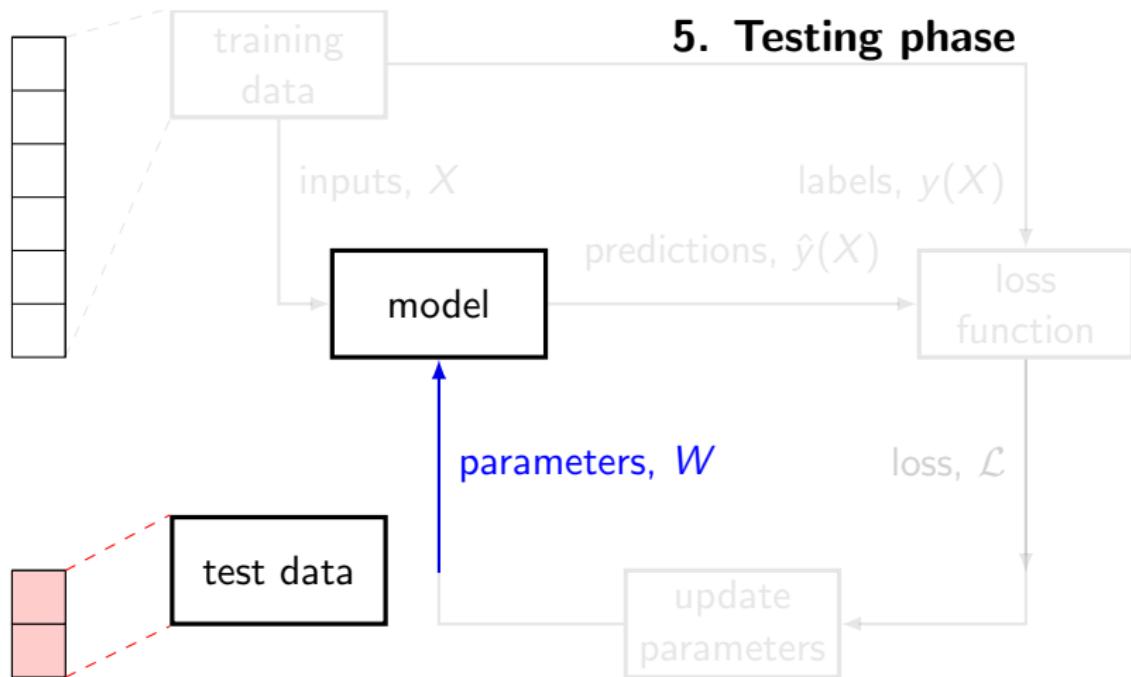
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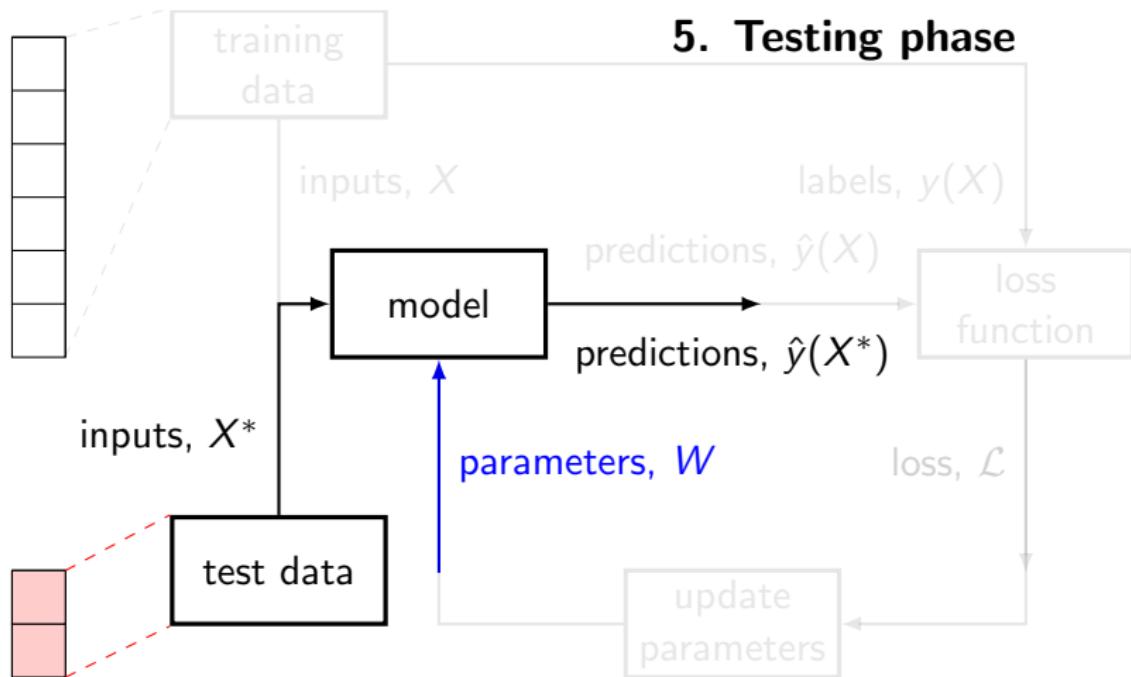
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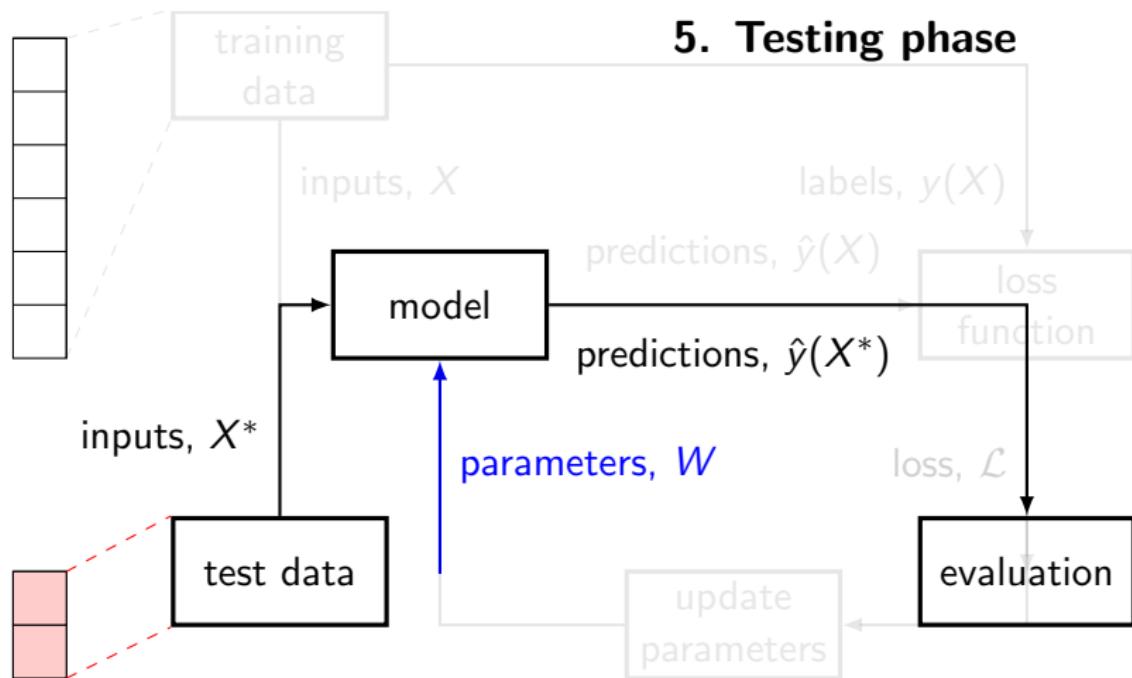
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Risk and generalization - I

Our training data defines the *empirical risk*

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we choose the model to minimize $\mathcal{E}_{emp}(f)$ over all the models in \mathcal{T}

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We cannot expect that f^* is in \mathcal{T} . The best we can do is f^\dagger :

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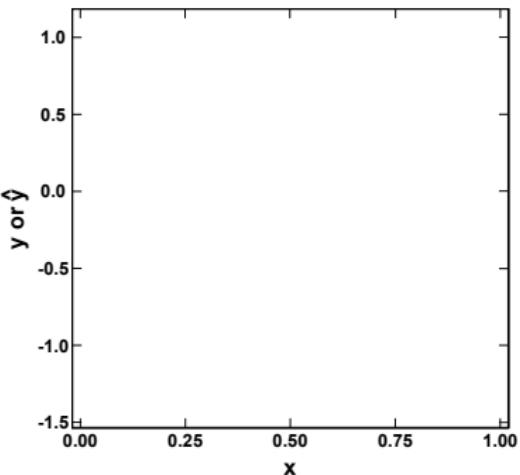
Conversely, a simple model will stop improving with more data past a certain point – where the approximation error dominates.

Risk and generalization - IV

Let us use **polynomials** to estimate:

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

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



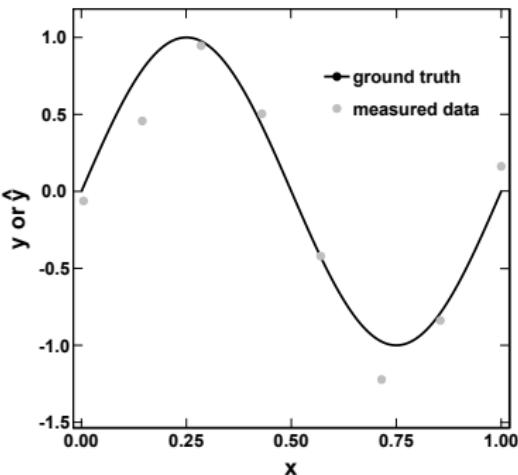
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Assume 8 measurements with noise $\mathcal{N}(0, 0.2)$



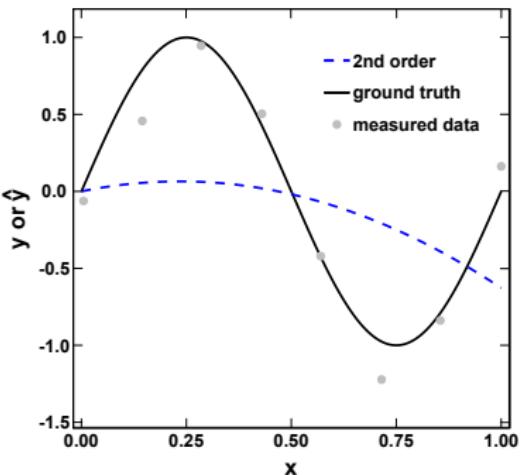
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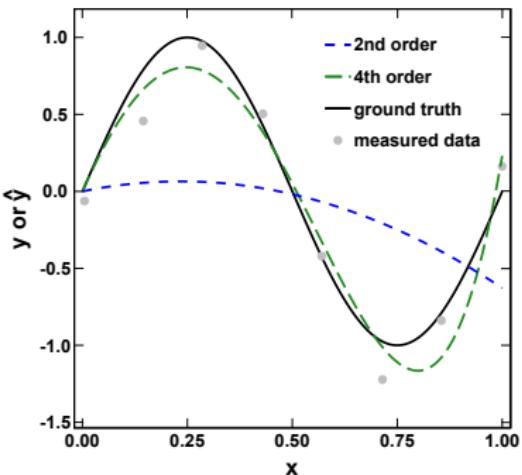
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Start with degree 2...What happens when we increase the order?

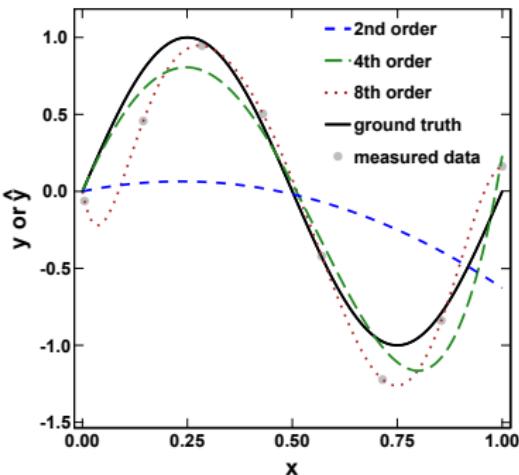


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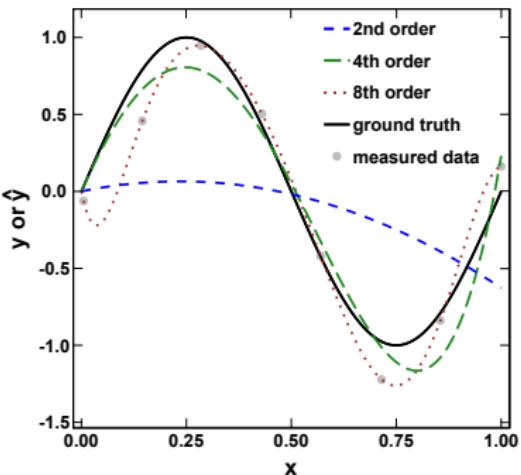
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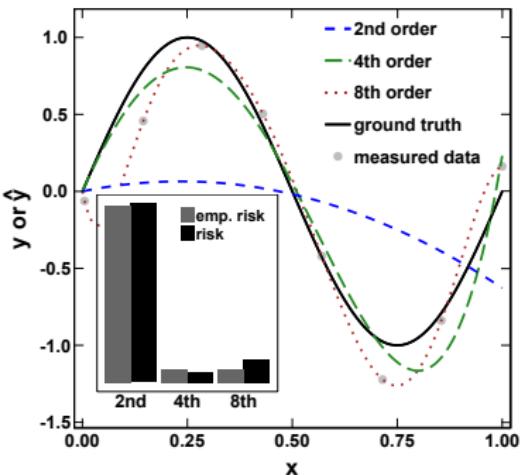
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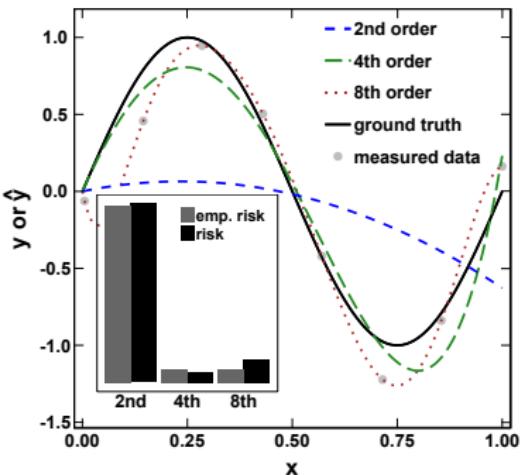


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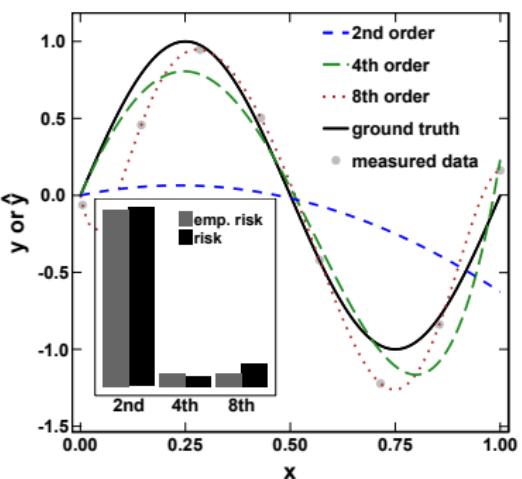
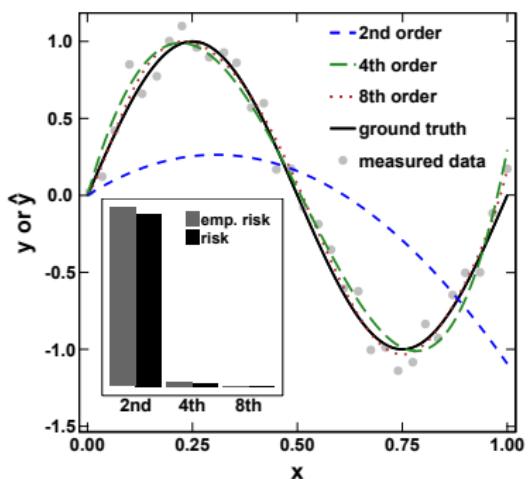
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What happens if we add more data?

Risk and generalization - IV



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Adapting model complexity to fit the problem is necessary. However, it is not obvious how to do this in a controlled way. Hence, we need a way prevent over-fitting that is applicable to many different types of model – **regularization**.

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We choose to **penalize terms with large weights**, i.e. complicated functions.

Controlling Complexity

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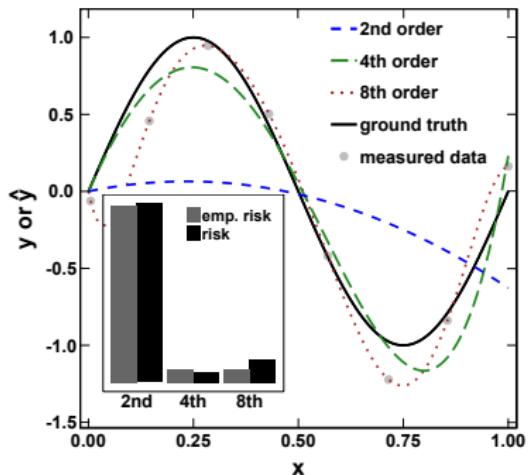
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- This makes empirical errors worse.
- This *can* improve generalization/excess risk.

Controlling Complexity

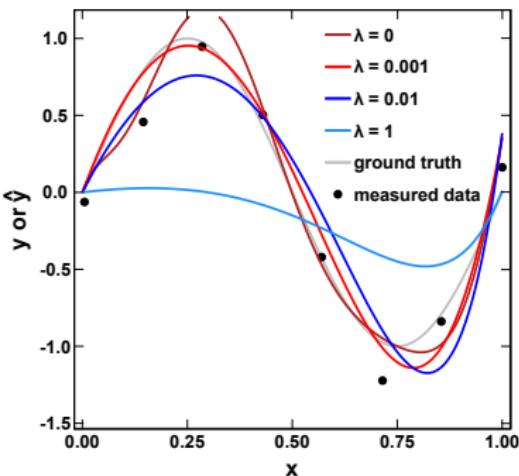
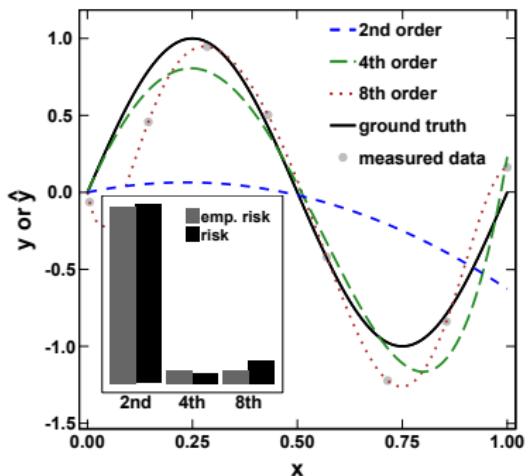
Let's return to our previous example:



Remember: larger λ = simpler, flatter model.

Controlling Complexity

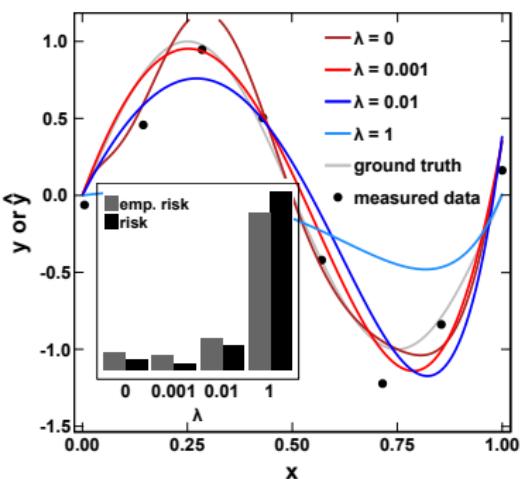
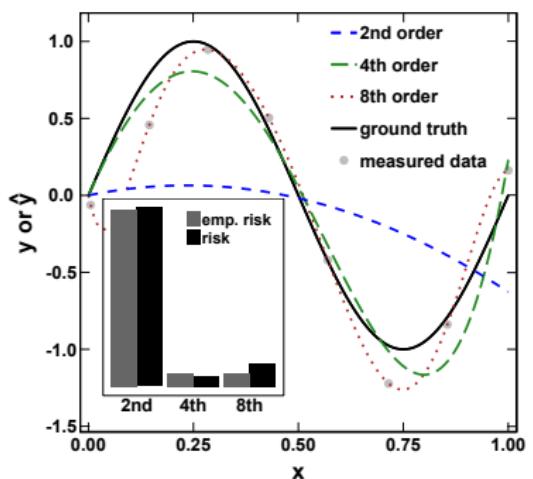
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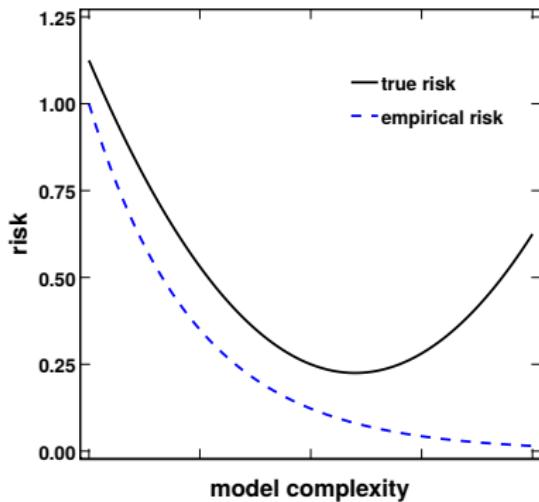
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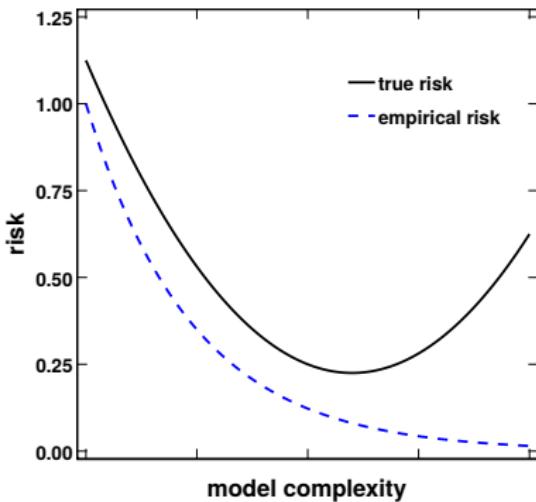


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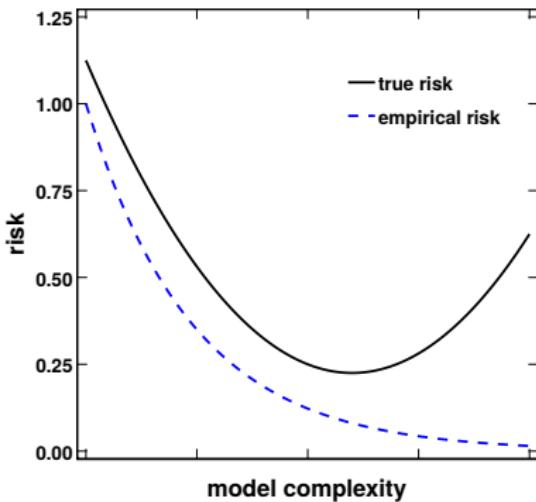


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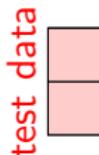
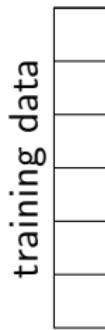
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Controlling Complexity

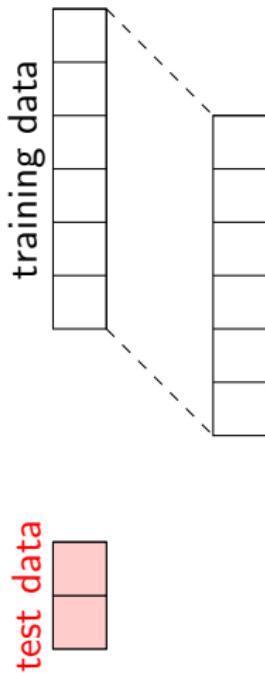


None of this helps us understand how complicated our model should be. Unfortunately, **errors on our training data cannot tell us the answer**

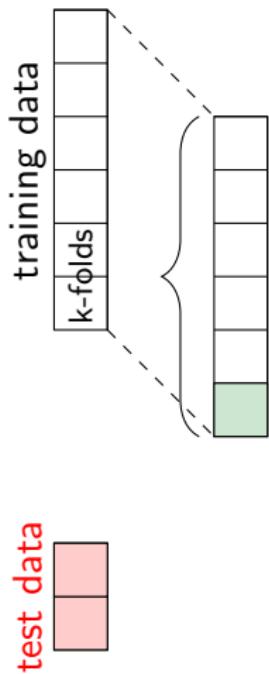
(Cross)-validation



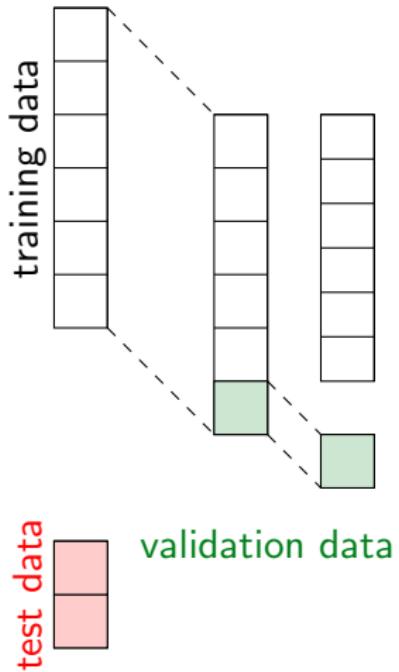
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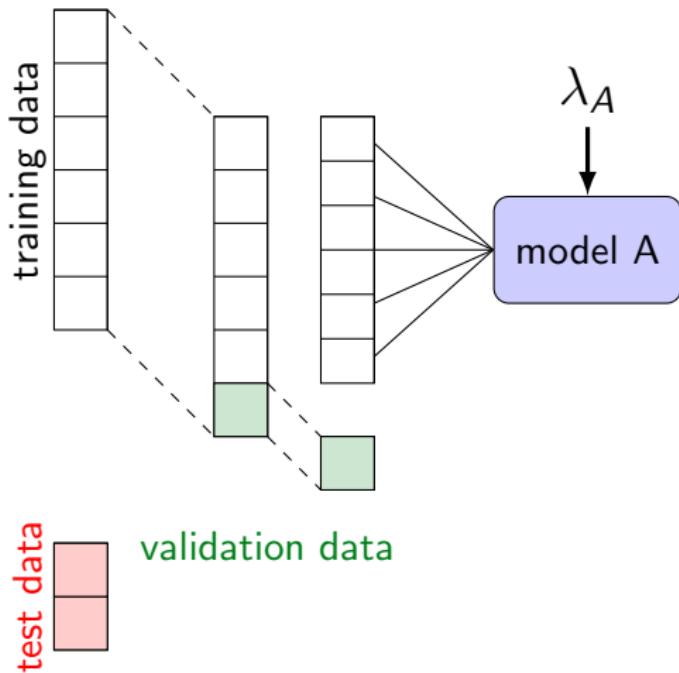
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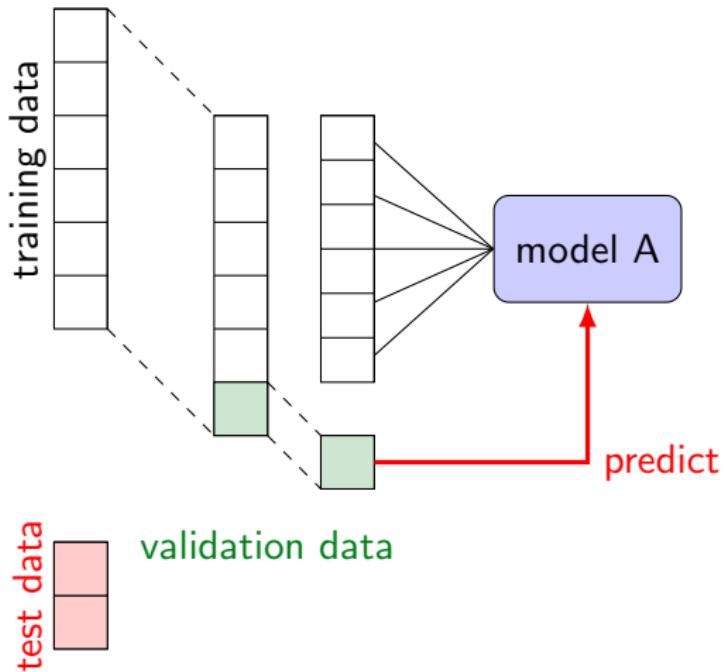
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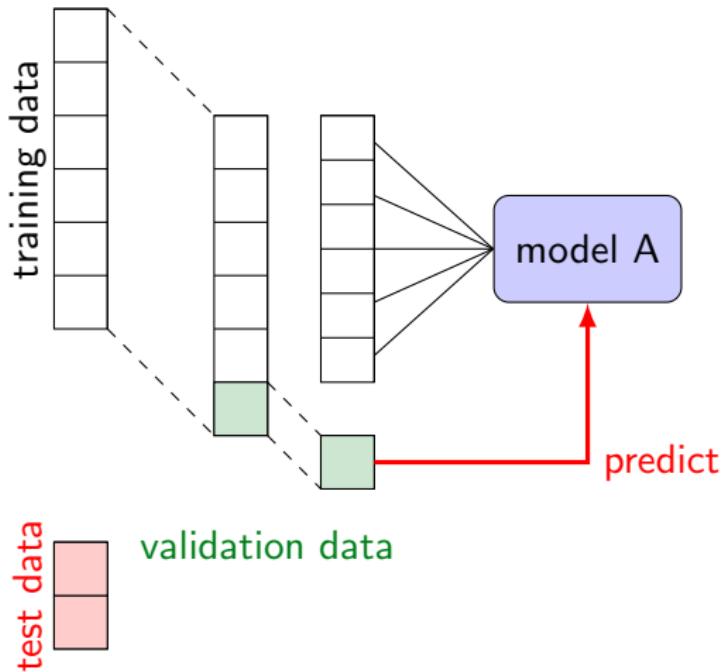
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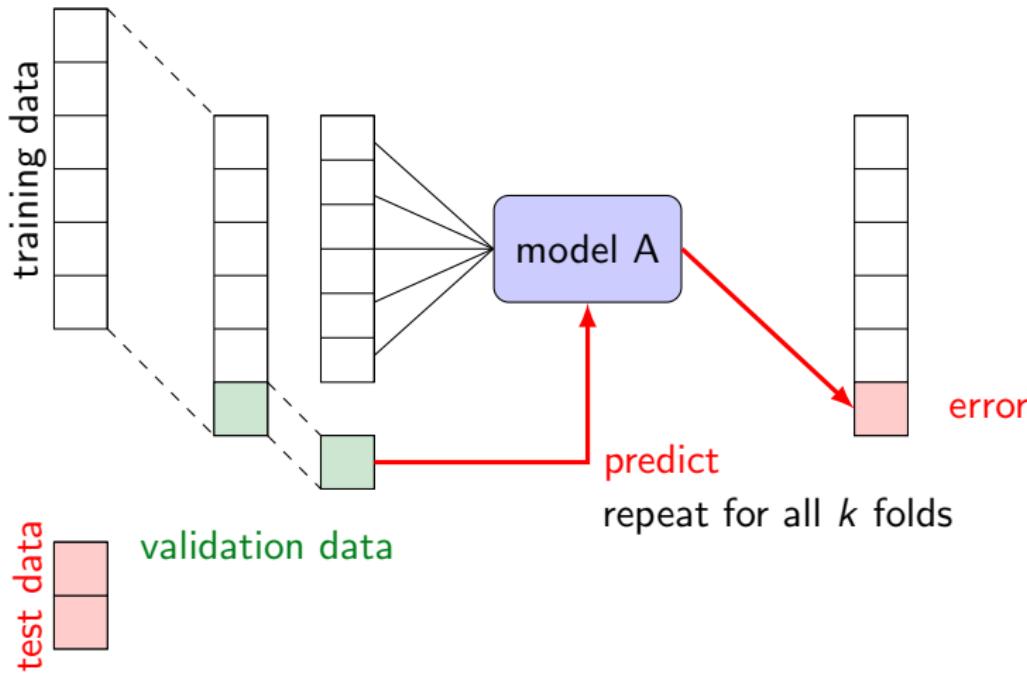
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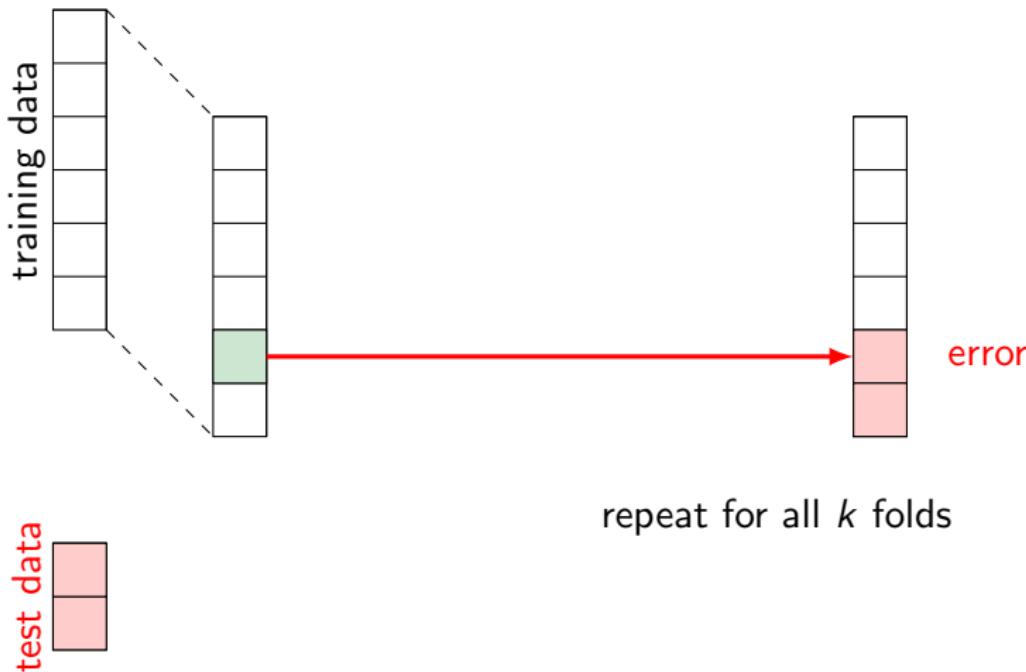
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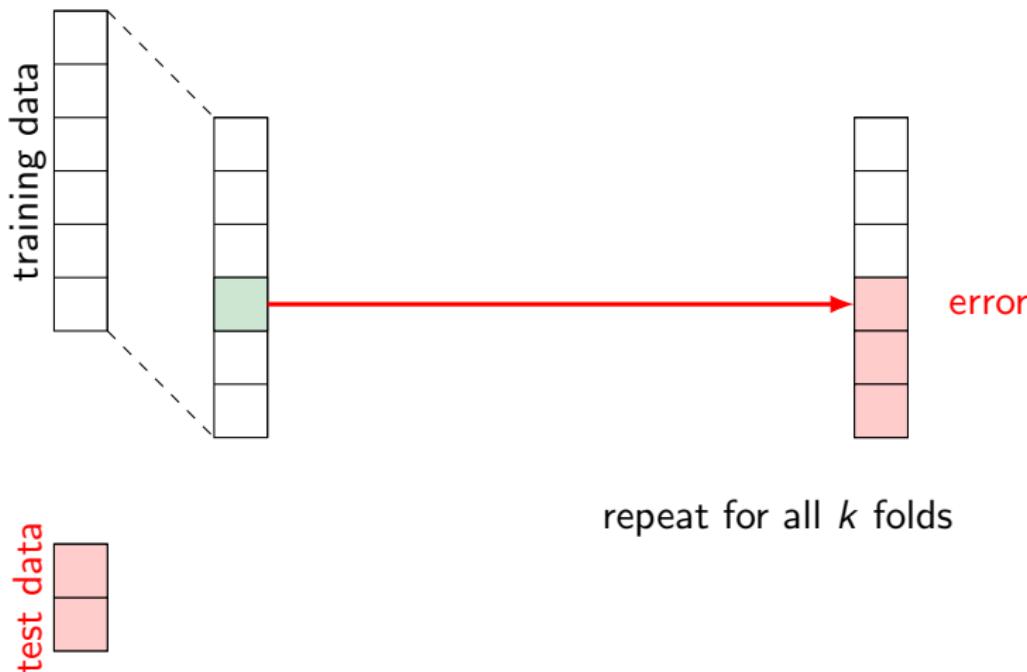
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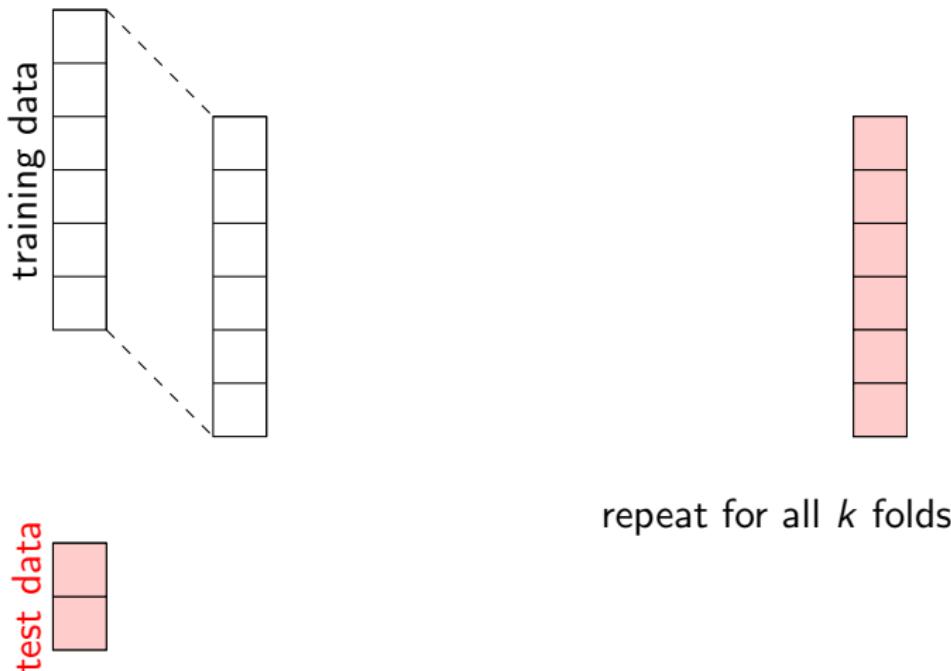
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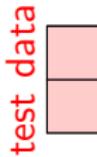
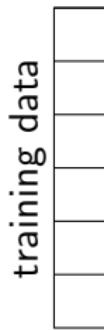
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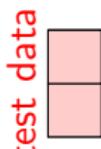
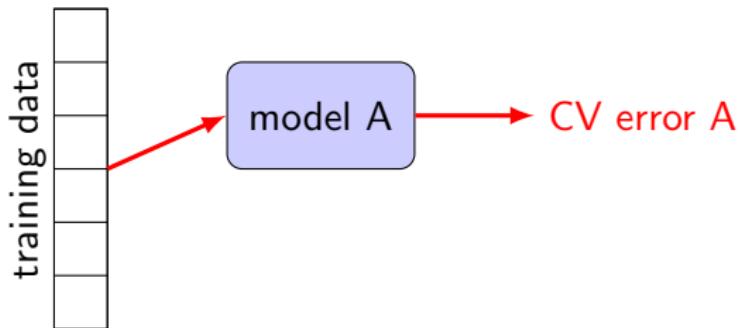
(Cross)-validation



average error =
CV error

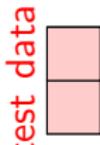
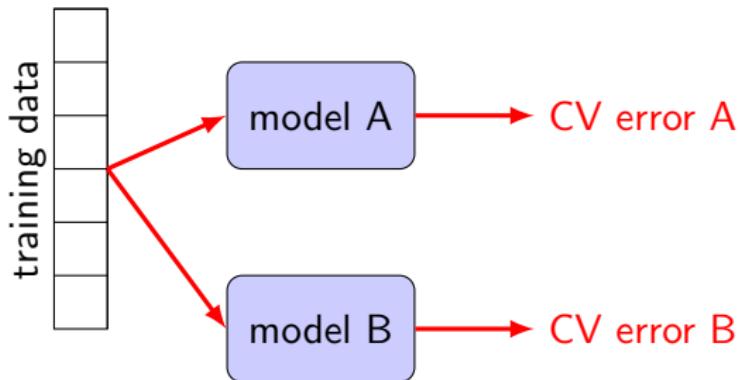
A vertical stack of 5 pink rectangular boxes, enclosed in a large curly brace, representing the cross-validation error.

(Cross)-validation



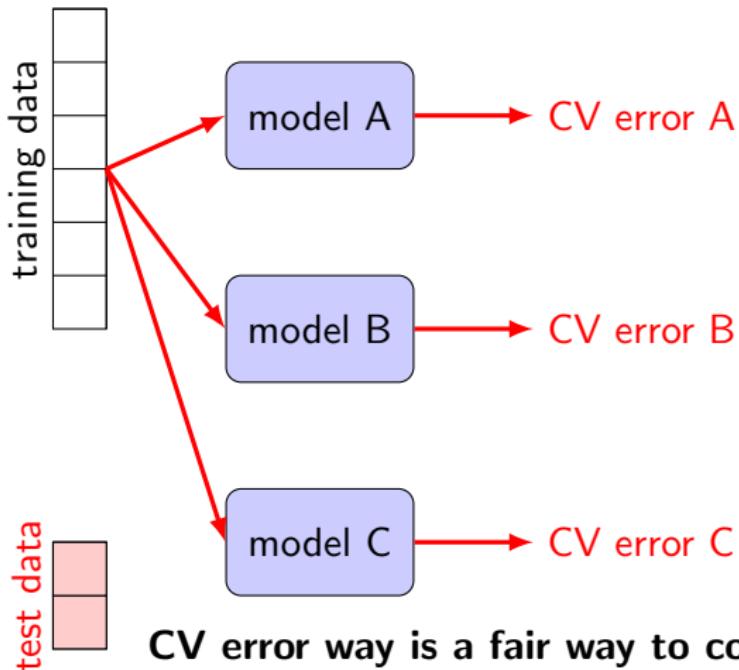
CV error way is a fair way to compare models

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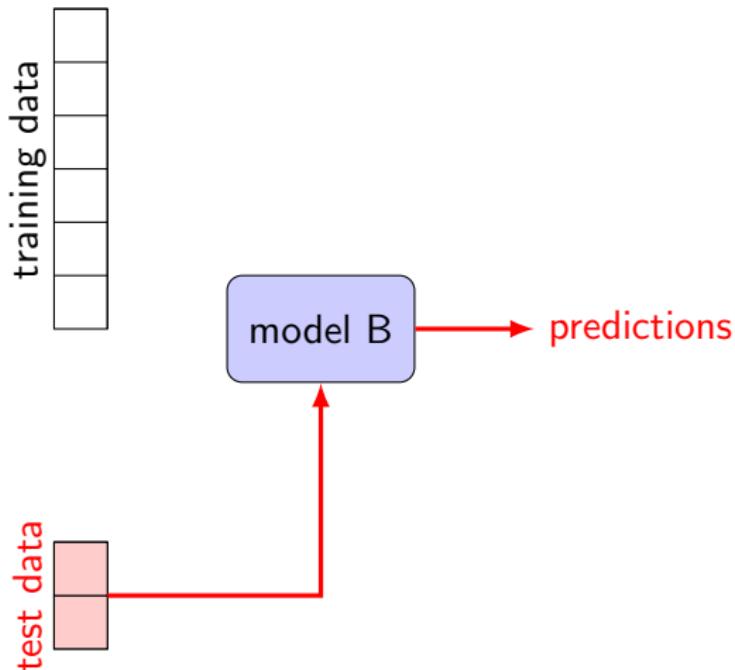


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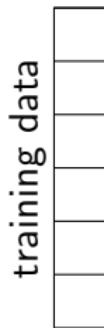
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Conclusion

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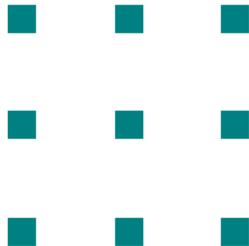
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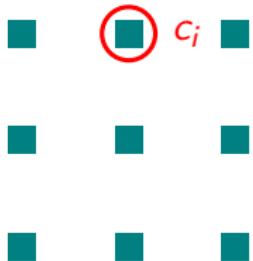
Deep neural networks (might) need better theories.

Purpose



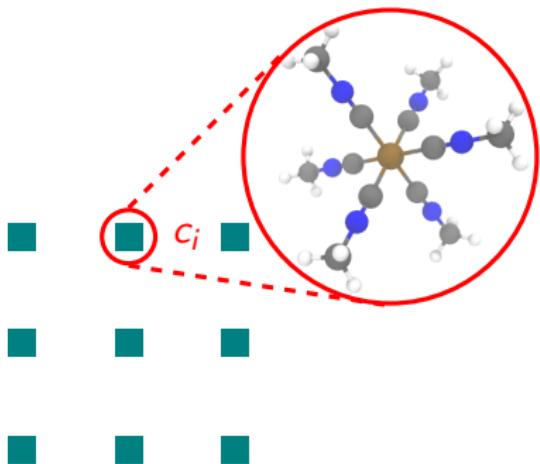
Chemical Space C_f

Purpose



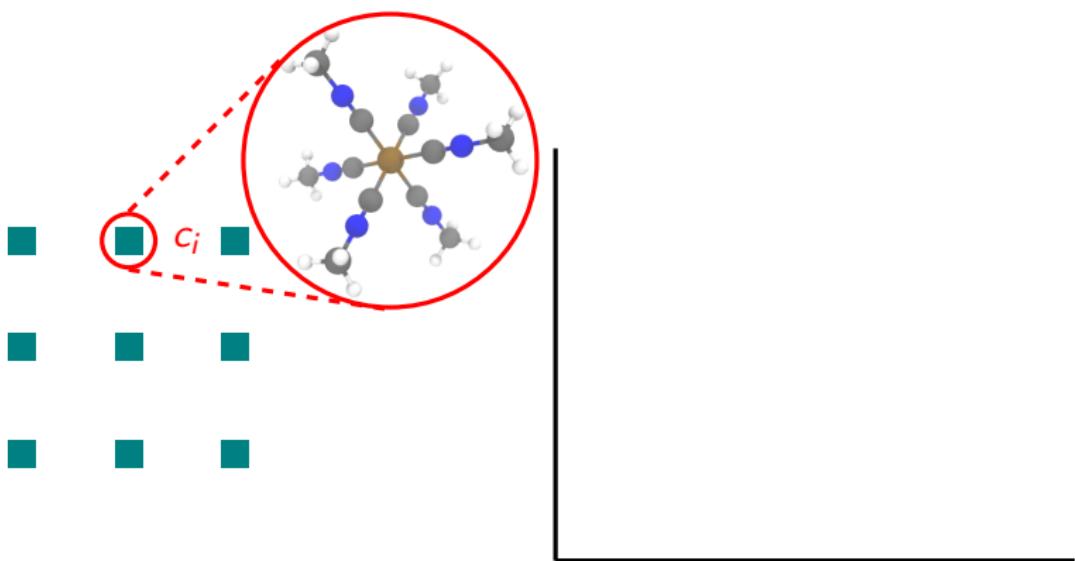
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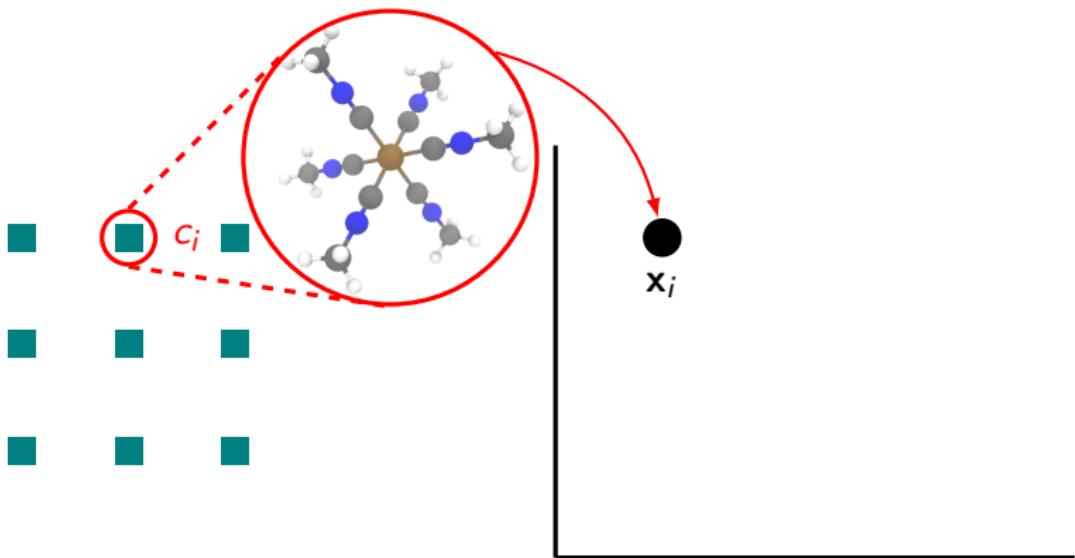
Purpose



Chemical Space C_f

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

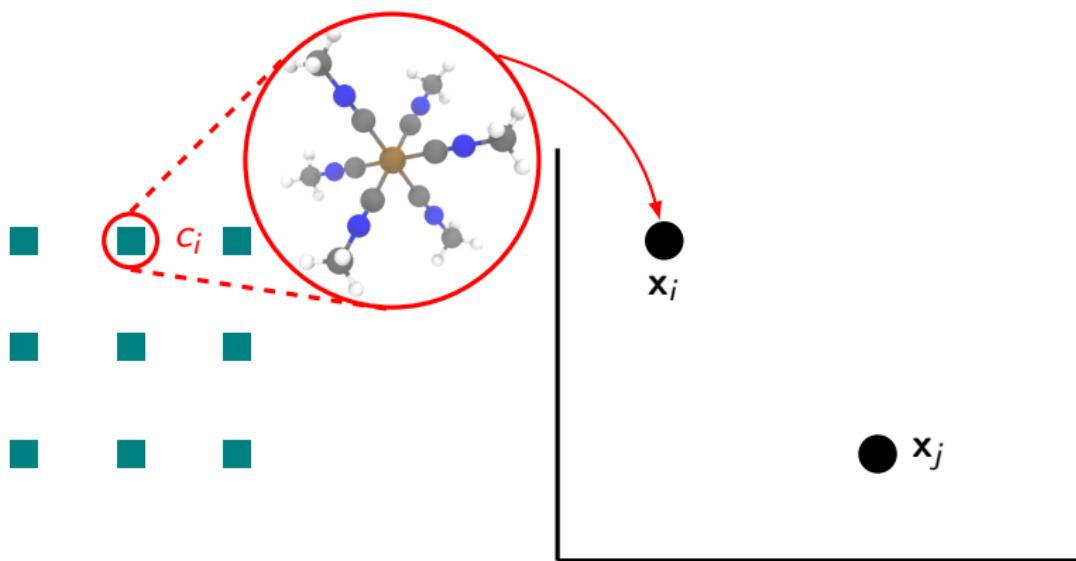
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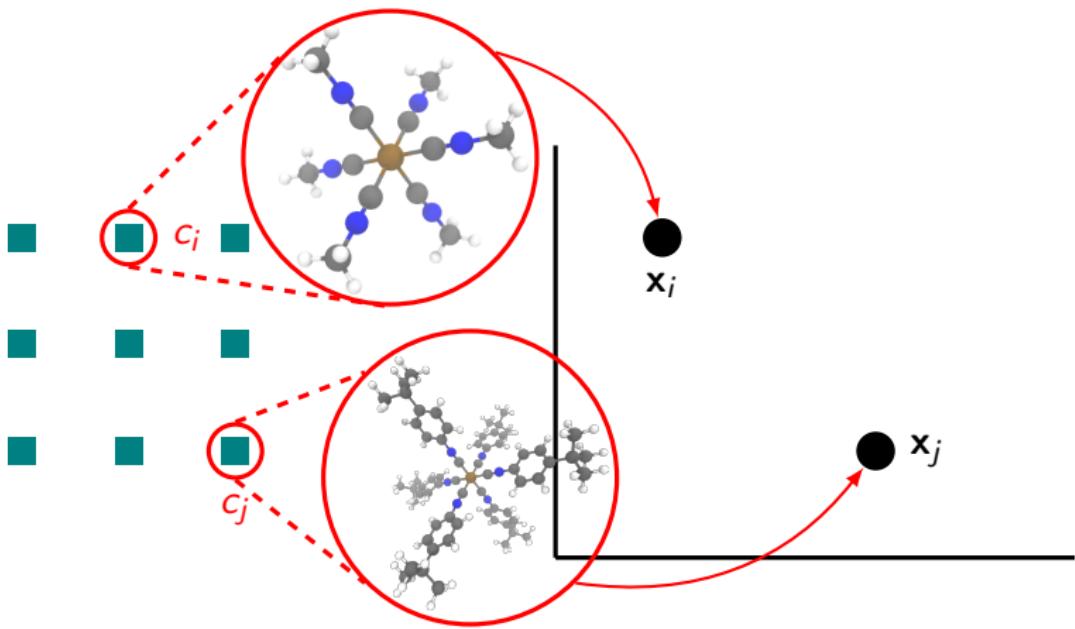
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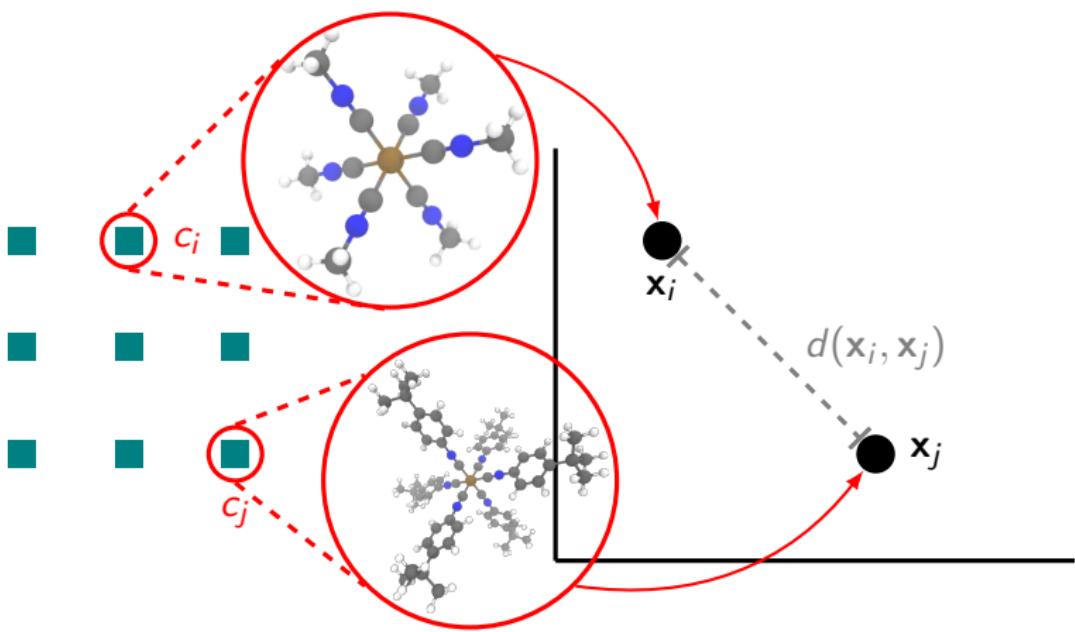
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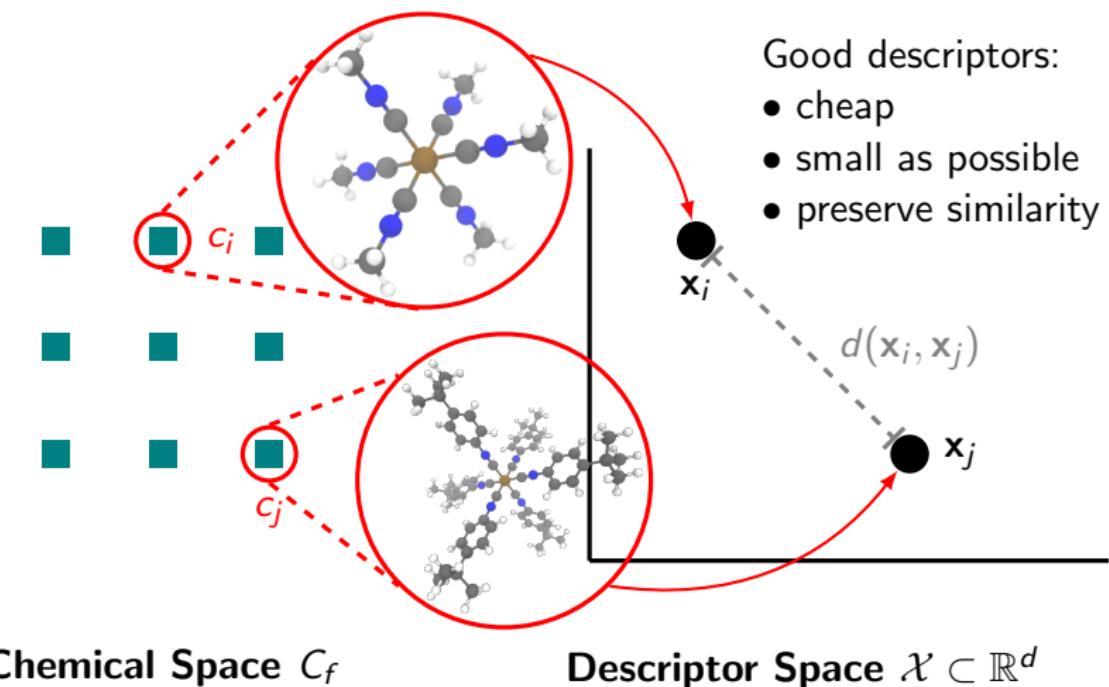
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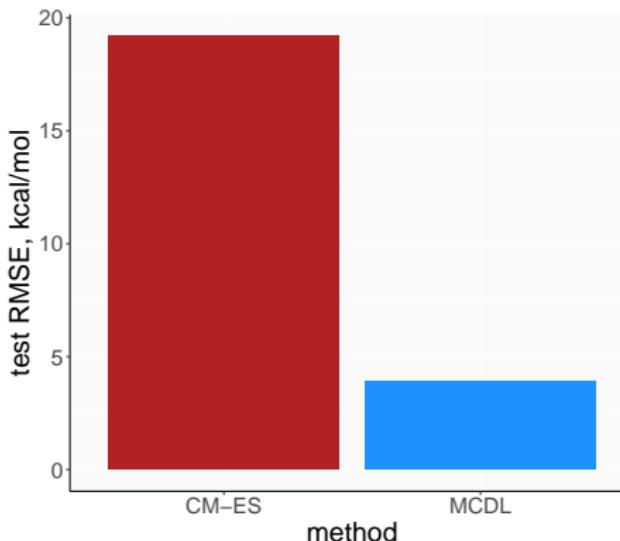


Why similarity is important

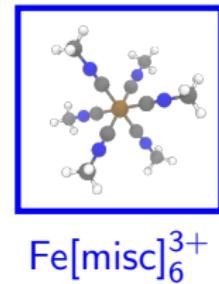
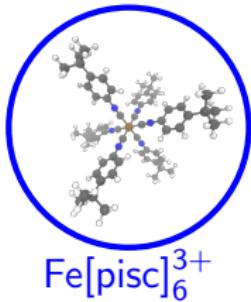
Different representations can have very different performance, particularly if they do not preserve notions of chemical similarity correctly:

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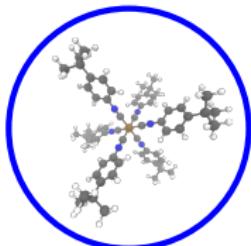
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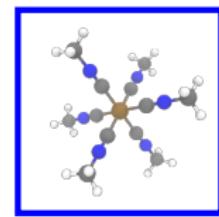


Why similarity is important



Fe[pisc]₆³⁺

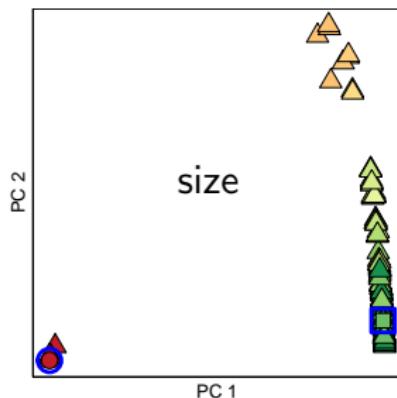
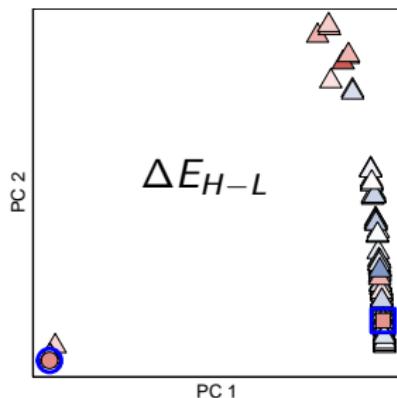
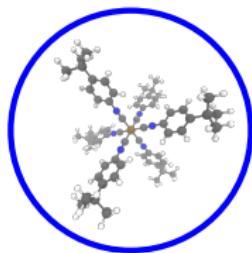
$$\Delta E_{H-L} = 37.7 \text{ kcal/mol}$$



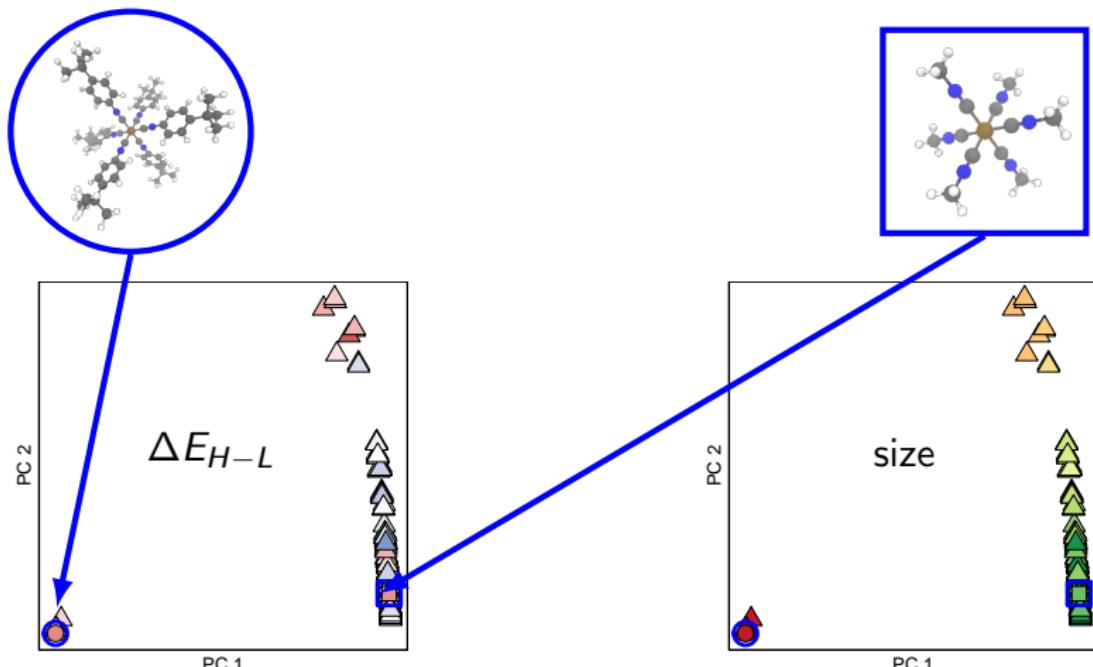
Fe[misc]₆³⁺

$$\Delta E_{\text{H-L}} = 40.7 \text{ kcal/mol}$$

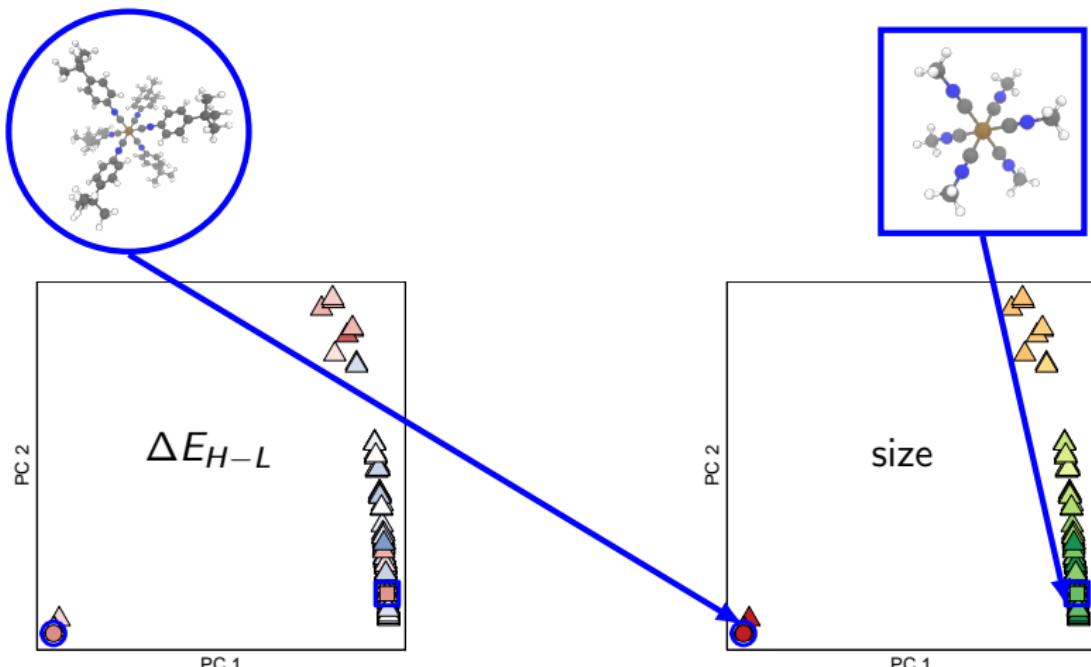
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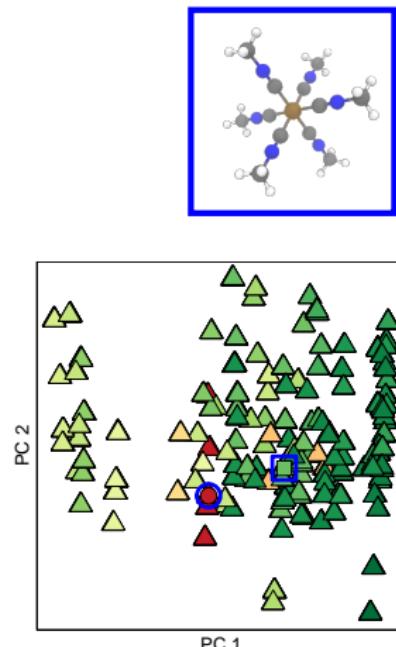
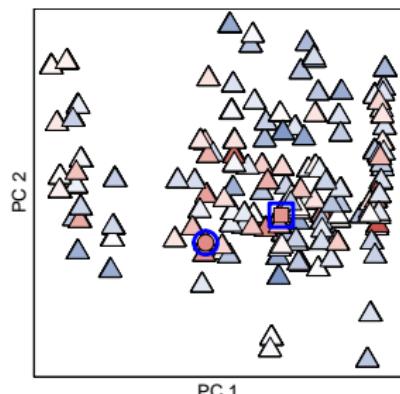
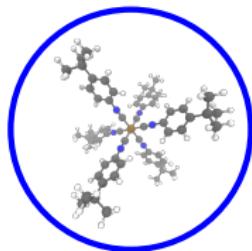
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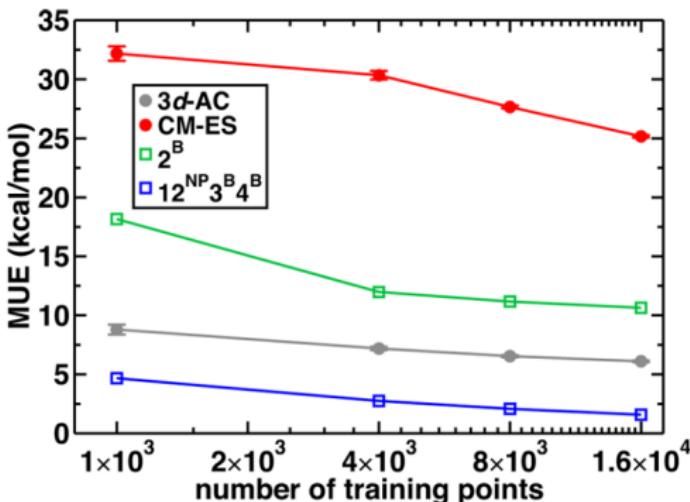


Why similarity is important

The richness of the representation also affects learning rate:

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Types of representation

complexity

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- considerable use in drug design
- no information related to molecular topology
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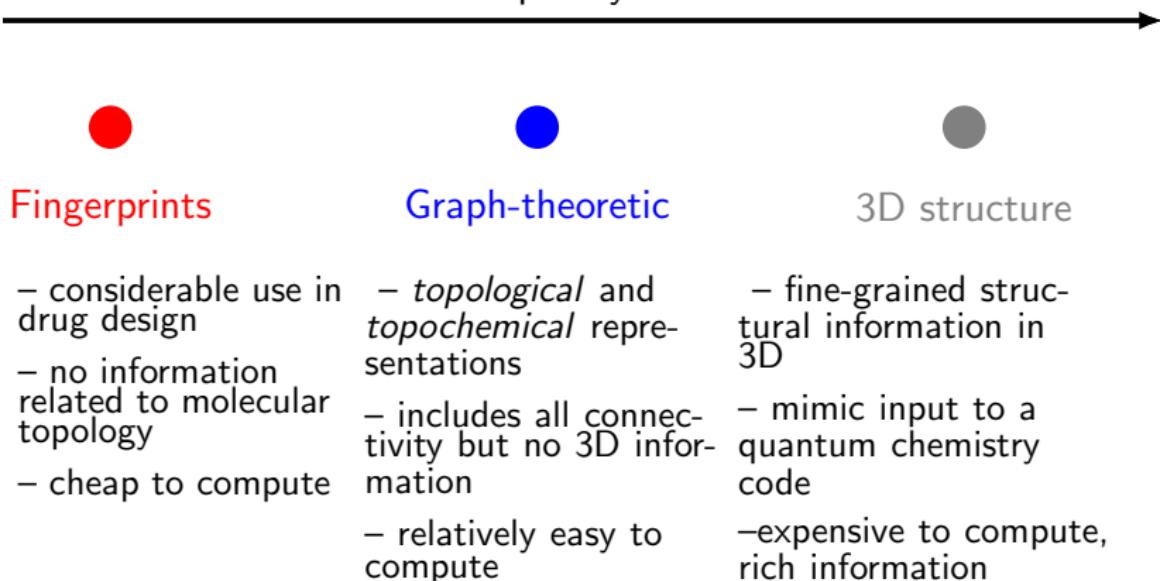


Graph-theoretic

- *topological* and *topochemical* representations
- includes all connectivity but no 3D information
- relatively easy to compute

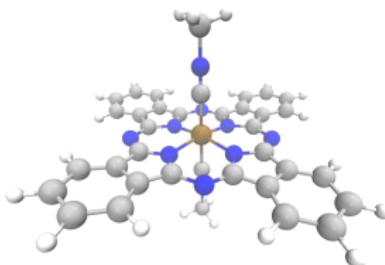
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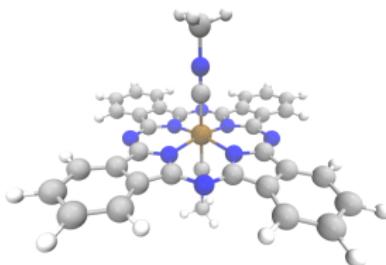
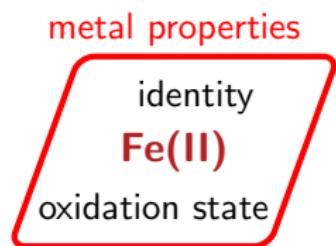
Ad-hoc properties

Sometimes, simple lists of atomic properties are sufficient, especially if informed by domain knowledge:



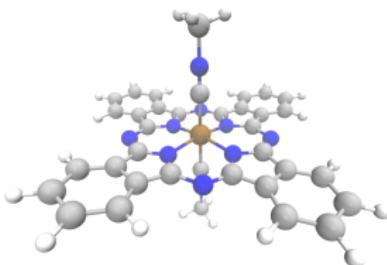
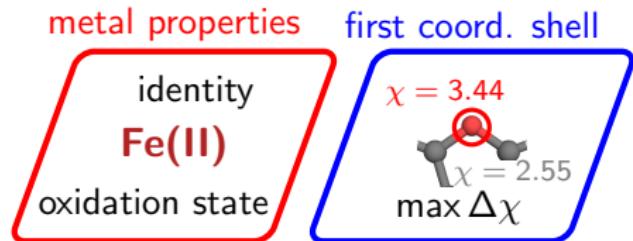
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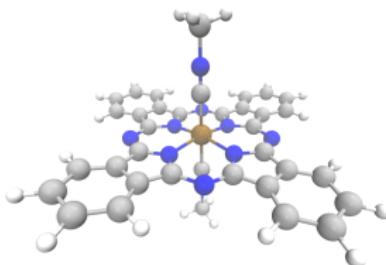
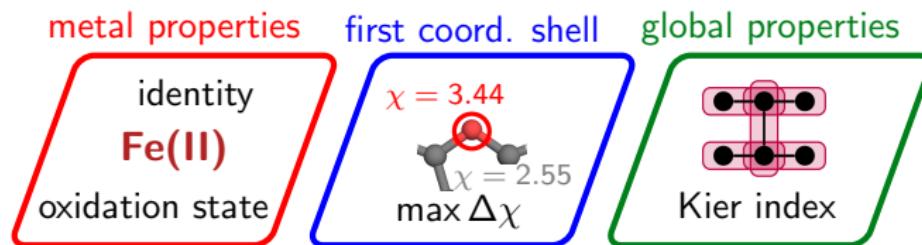
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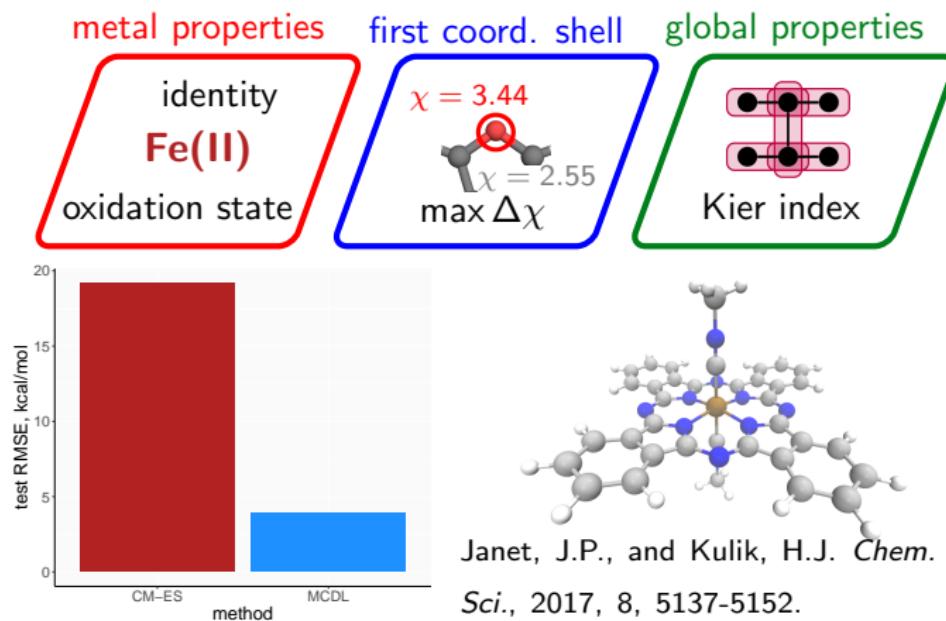
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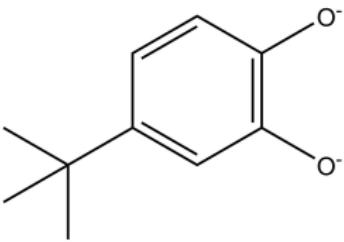


Fingerprints and the low-information limit

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

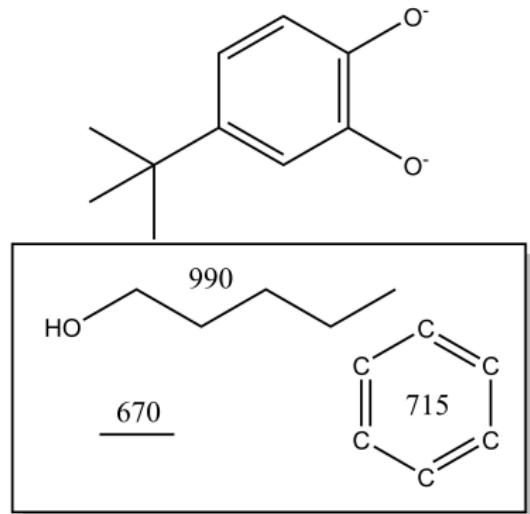
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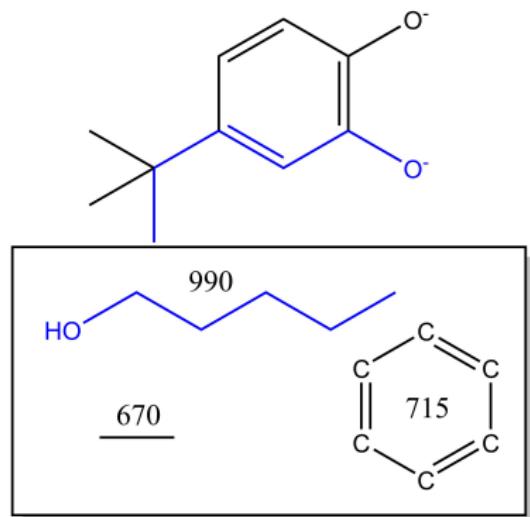
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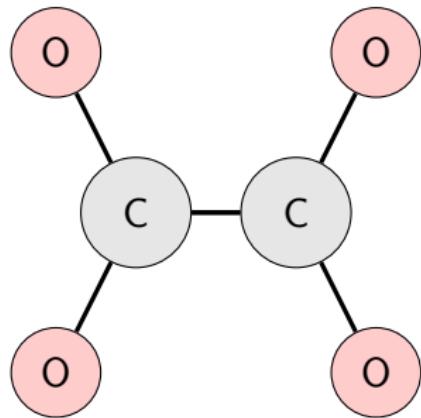
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Molecular graphs

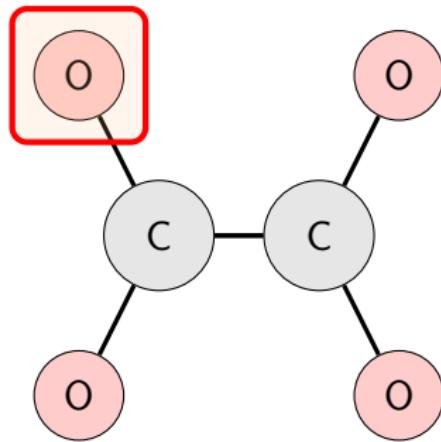
Based on autocorrelations¹



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

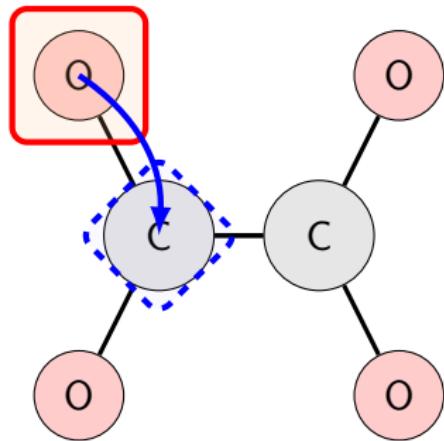
Molecular graphs

Based on autocorrelations and modified for TMCs⁴



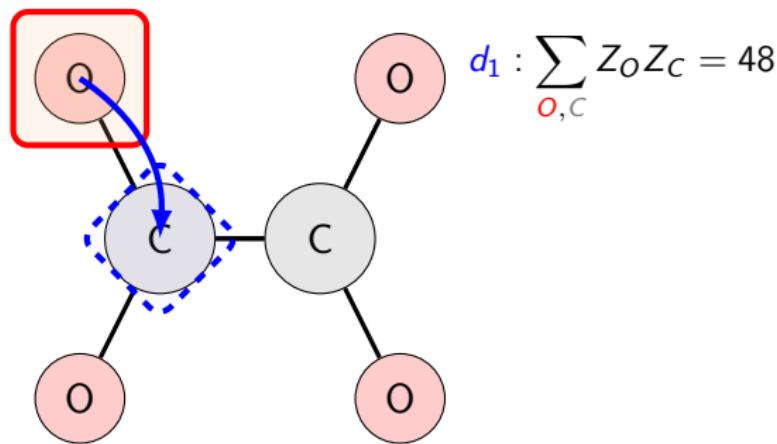
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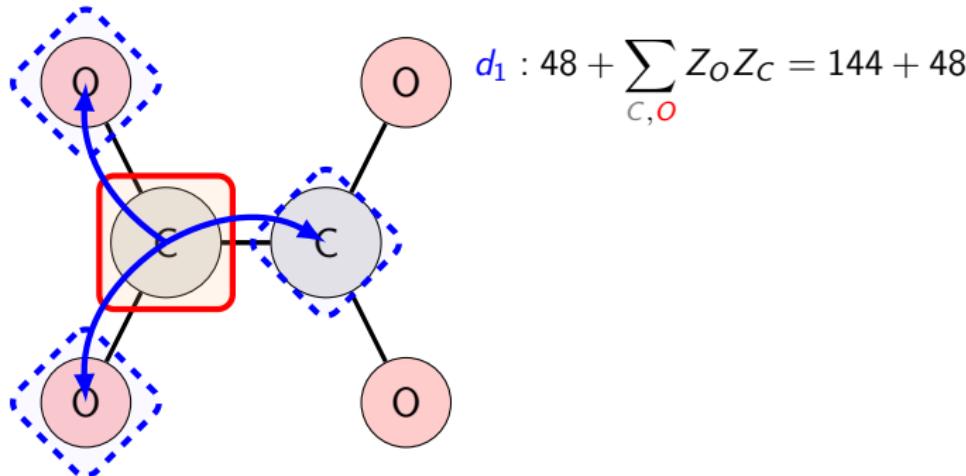
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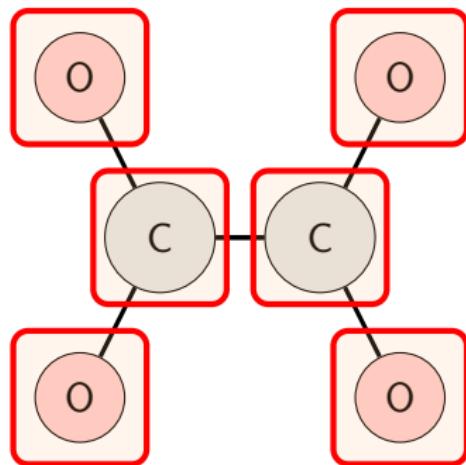
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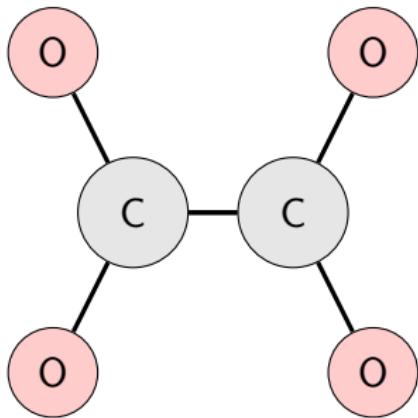
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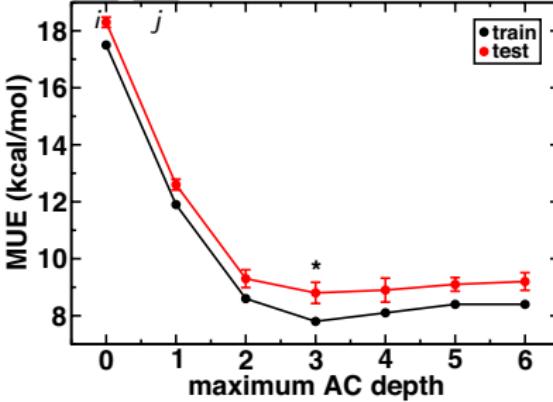
$$d_1 : \sum_i \sum_j Z_i Z_j \delta(d_{i,j}, 1)$$

Molecular graphs

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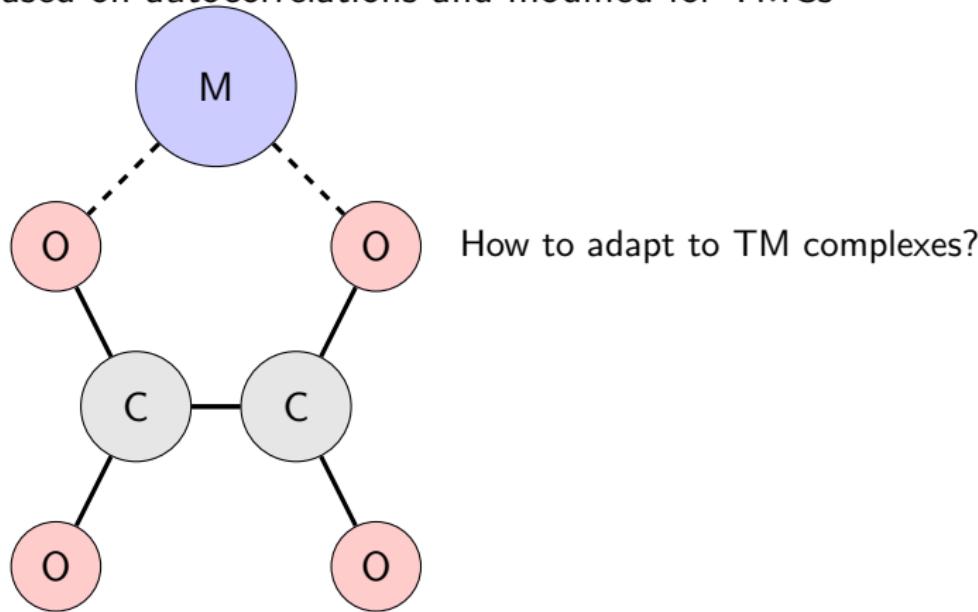
$$d_x : \sum_i \sum_j Z_i Z_j \delta(d_{ij}, x)$$



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

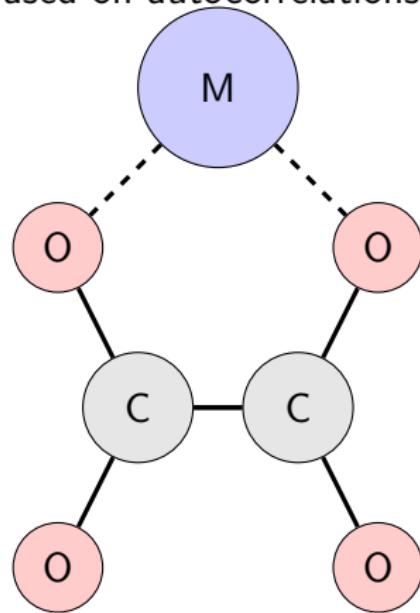
Molecular graphs

Based on autocorrelations and modified for TMCs⁴



Molecular graphs

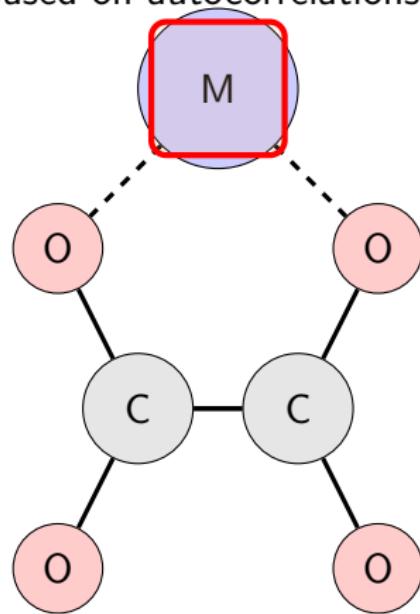
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How to adapt to TM complexes?
restrict the scope to focus on
near-metal atoms

Molecular graphs

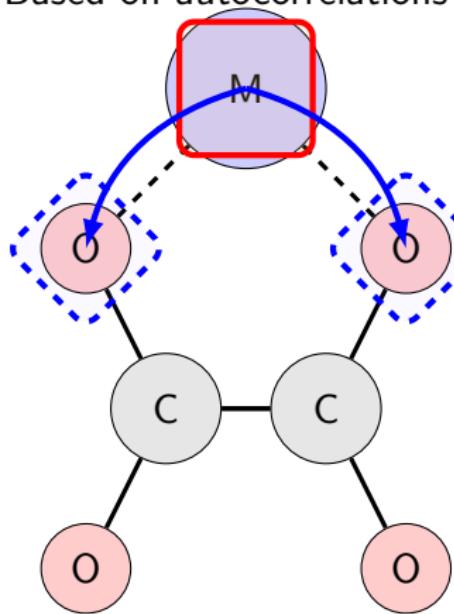
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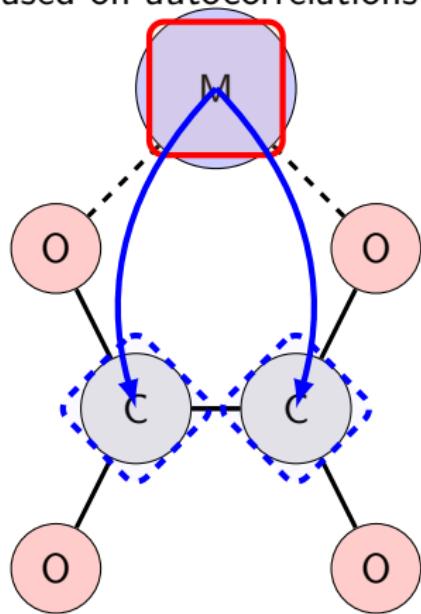
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$$d_1 : \sum_{M,O} Z_M Z_O$$

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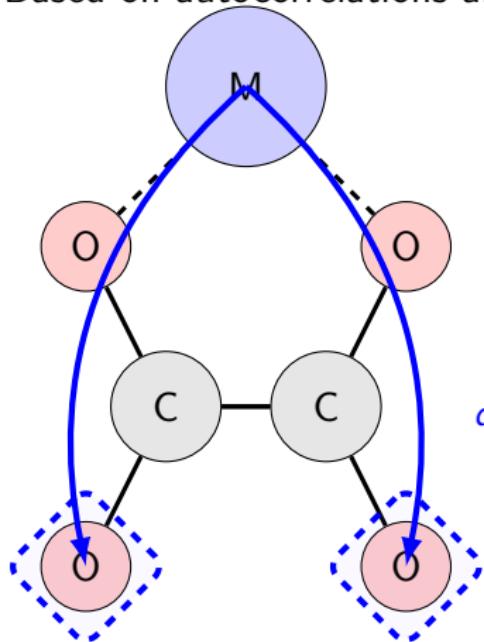
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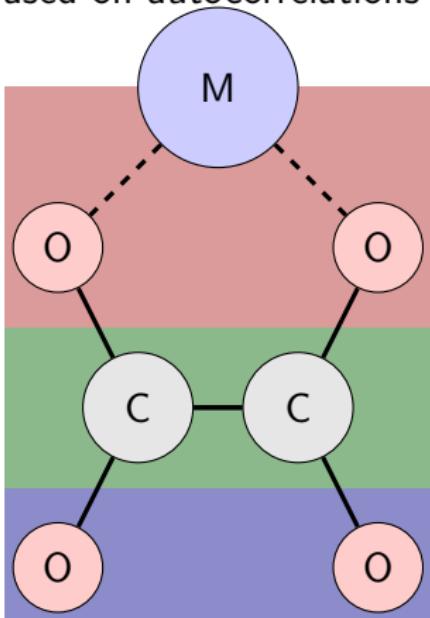
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$$d_3 : \sum_{M,O} Z_M Z_O$$

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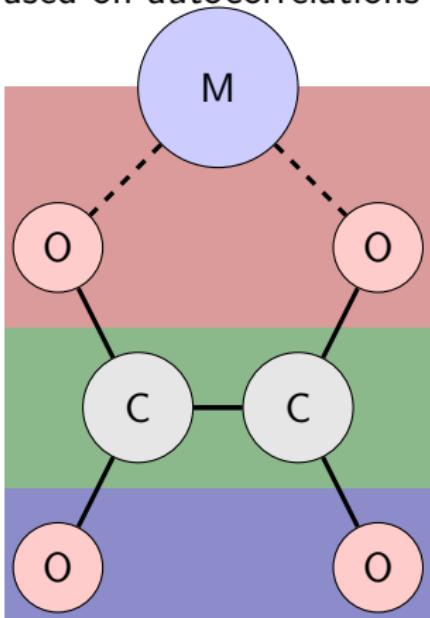


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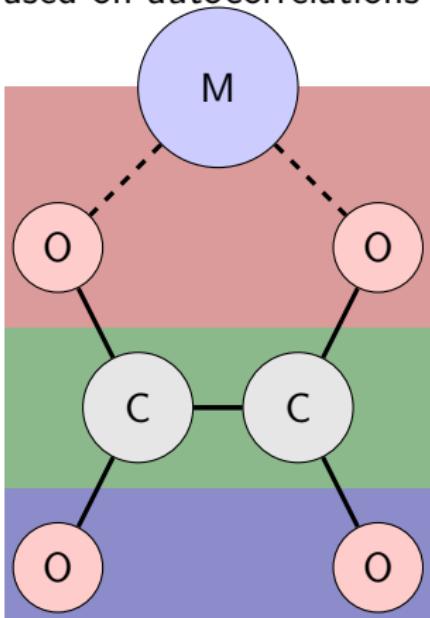
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$$(Z_i - Z_j)$$

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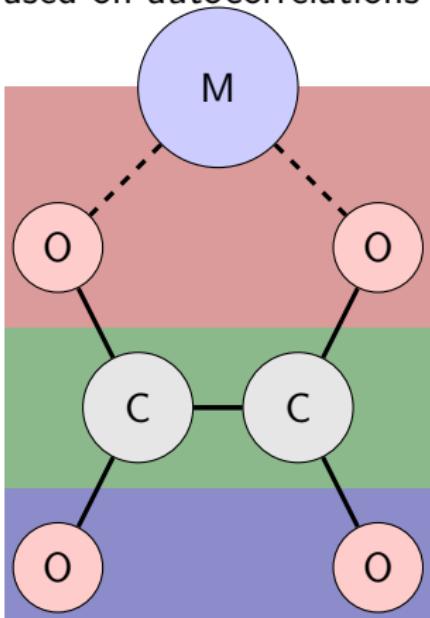
$$d_3 : \sum_{M,O} Z_M Z_O (Z_i - Z_j)$$

properties: T, χ, Z, I, S

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

~ 160 features in total

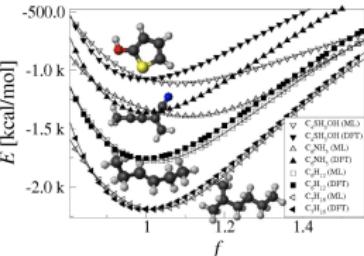
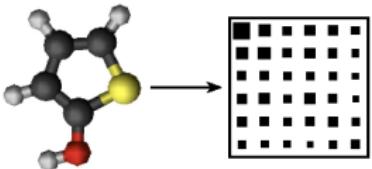
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Coulomb matrices

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

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

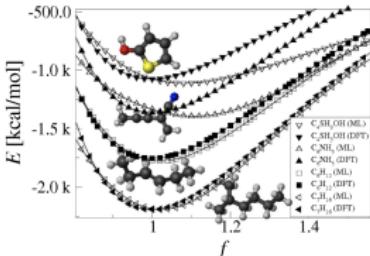
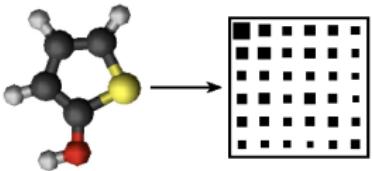


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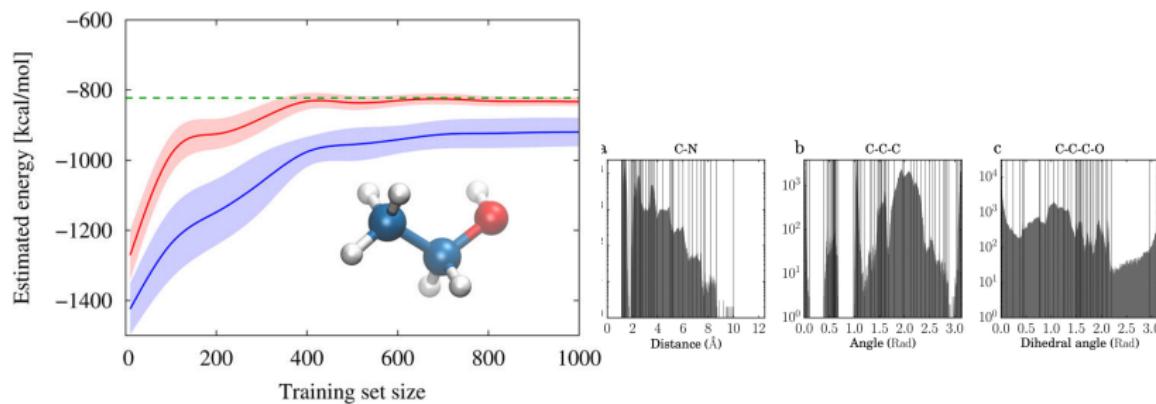


rotational and translational invariance

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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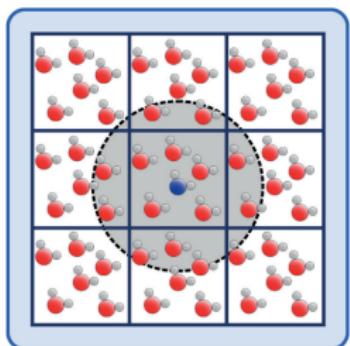
Basic idea is to create an atomic level representation that 'knows' about the neighborhood:

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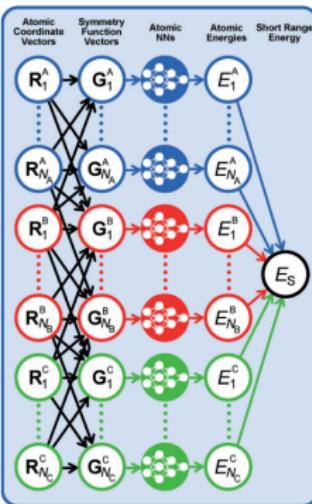
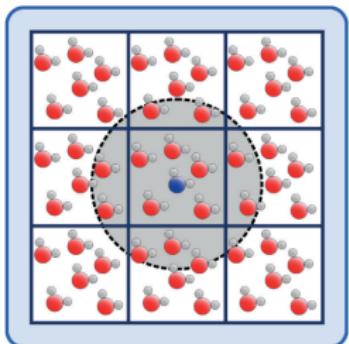
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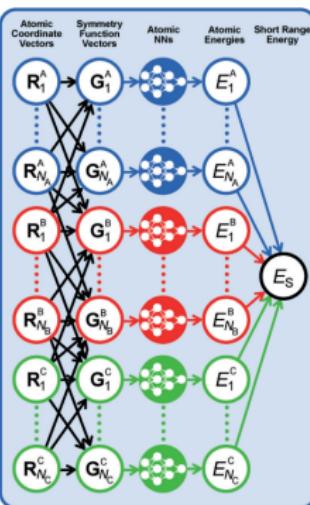
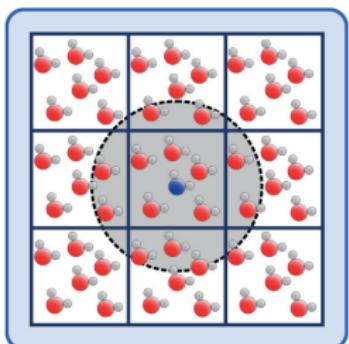
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J. Behler and M. Parrinello, Generalized Neural-Network Representation of High-Dimensional Potential-Energy Surfaces, *Phys. Rev. Lett.*, 98, 146401, 2007

Learning representations

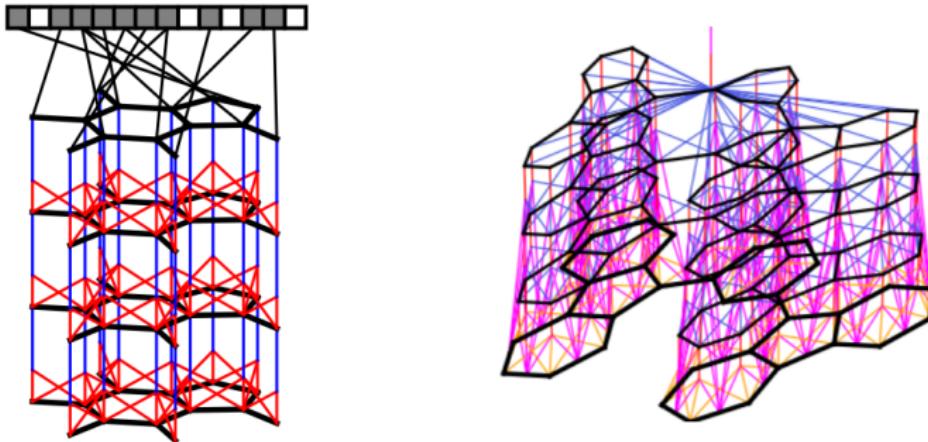
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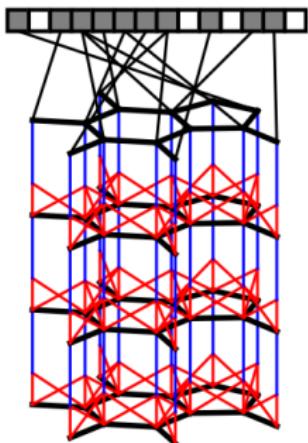
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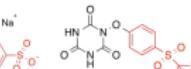
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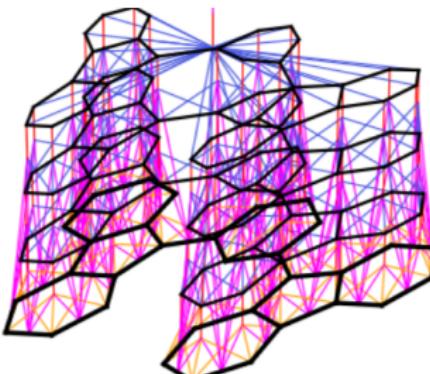
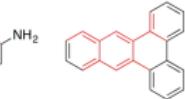
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Fragments most activated by toxicity feature on SR-MMP dataset



Fragments most activated by toxicity feature on NR-AHR dataset



Conclusions

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

Multiple linear regression



Multiple linear regression

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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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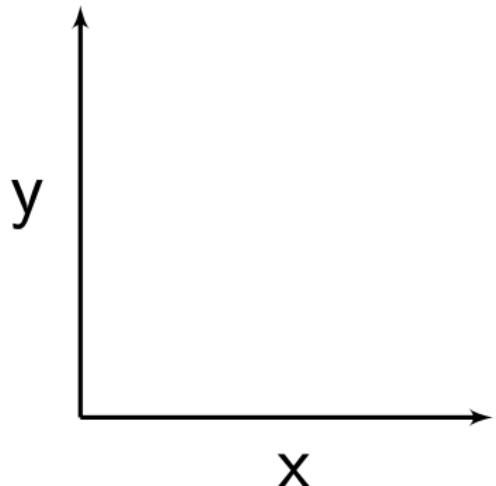
Notice how we handle the constant terms

Multiple linear regression II

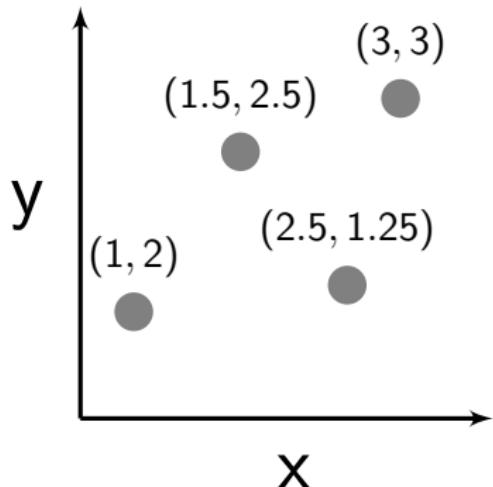
Let's solve our regularized least-squares problem:

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

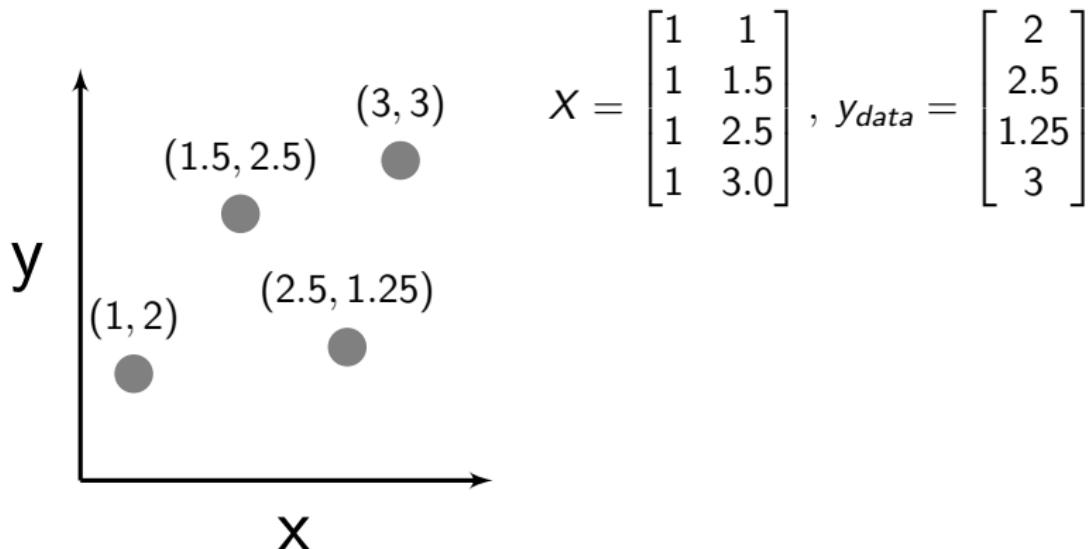
Simple example in 1D



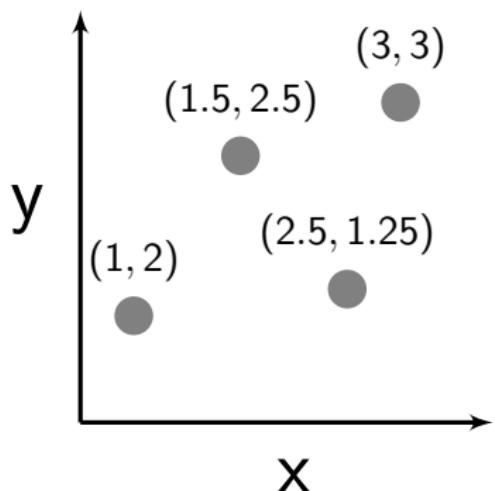
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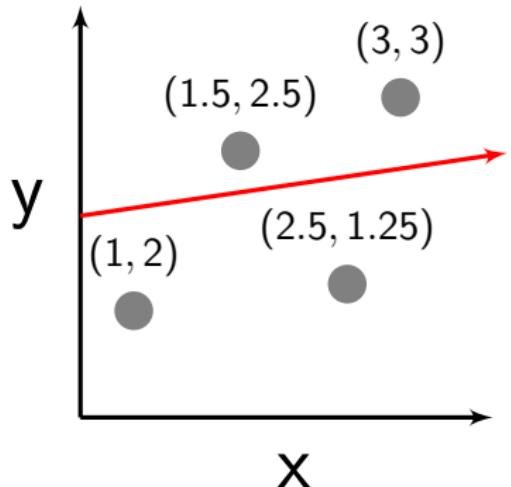
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$$X = \begin{bmatrix} 1 & 1 \\ 1 & 1.5 \\ 1 & 2.5 \\ 1 & 3.0 \end{bmatrix}, y_{data} = \begin{bmatrix} 2 \\ 2.5 \\ 1.25 \\ 3 \end{bmatrix}$$

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

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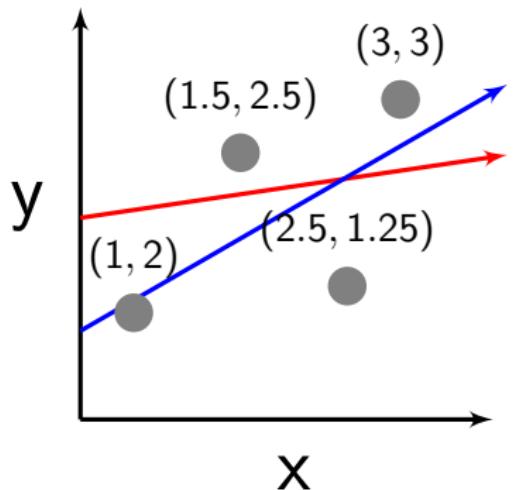


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$$= \begin{bmatrix} 1.9 \\ 0.15 \end{bmatrix} (\lambda = 0.0)$$

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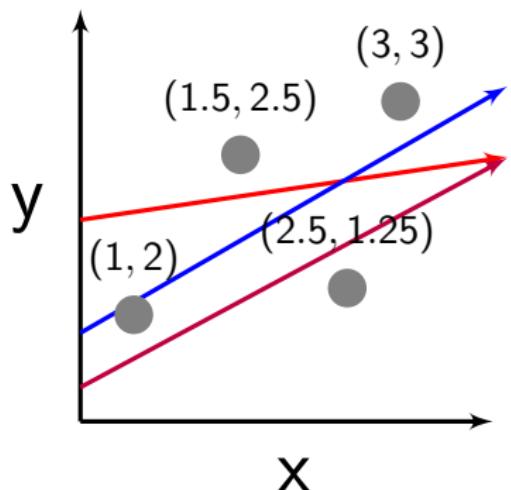


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$$= \begin{bmatrix} 0.82 \\ 0.58 \end{bmatrix} (\lambda = 1.0)$$

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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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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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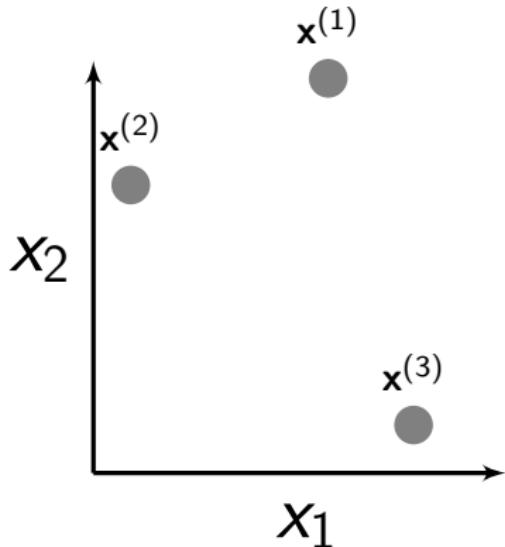
$$a = (K + I_n \lambda)^{-1} y$$

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

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

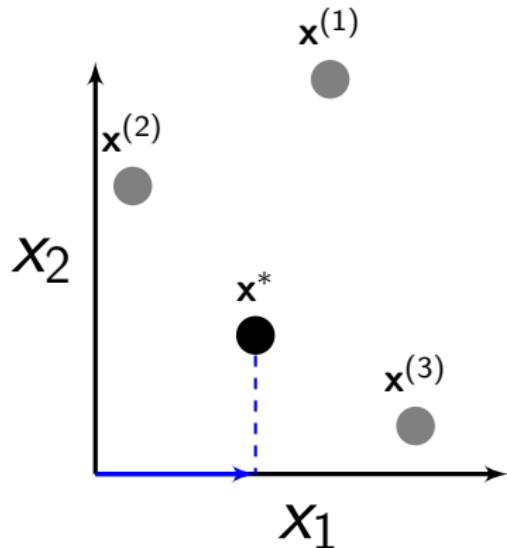
Linear kernel geometric picture

$$y(x^*) = w_1 x_1^* + w_2 x_2^*$$



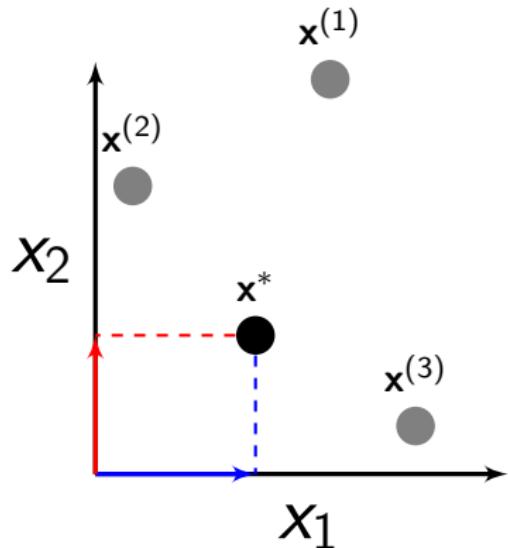
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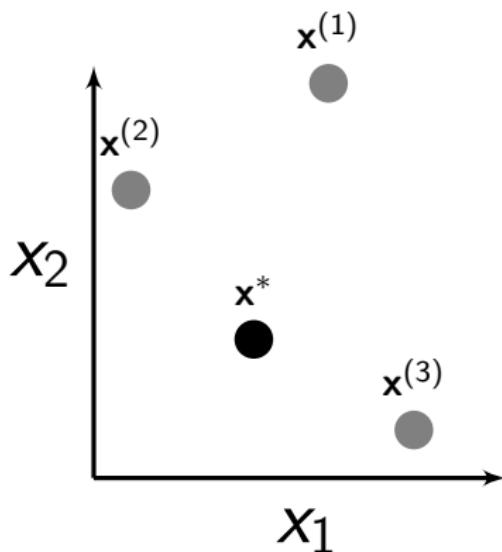
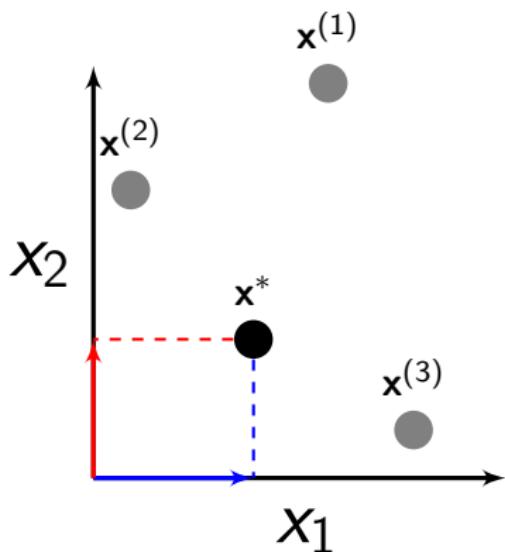
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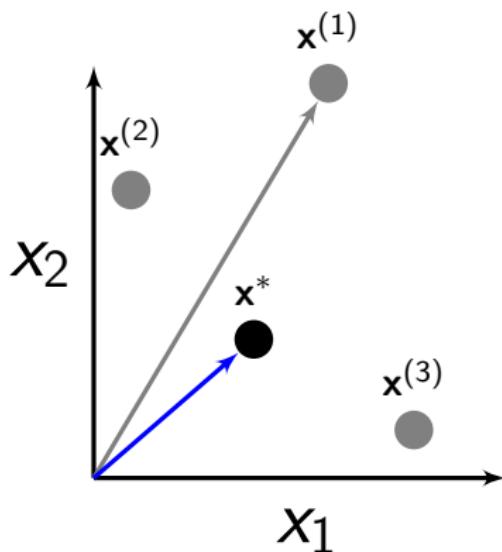
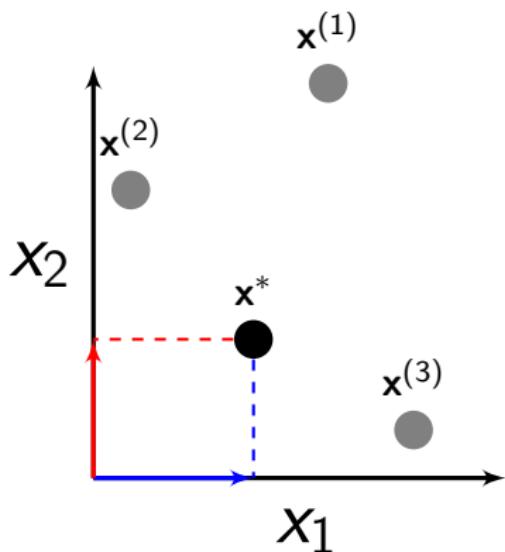
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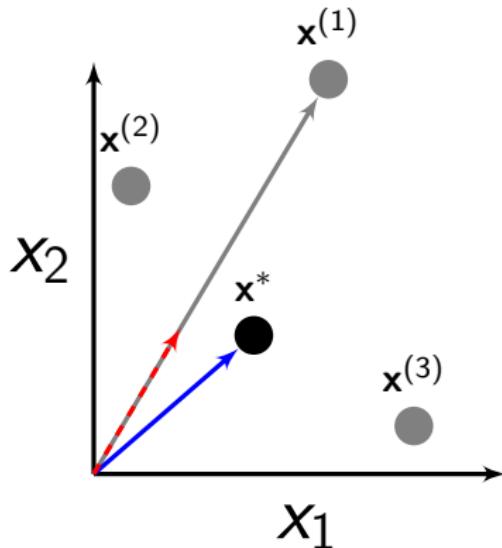
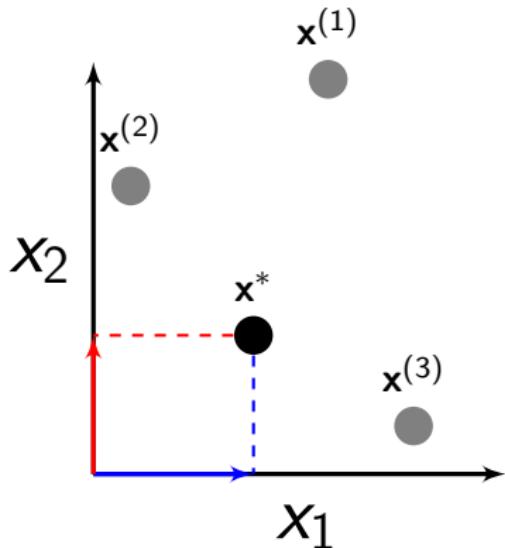
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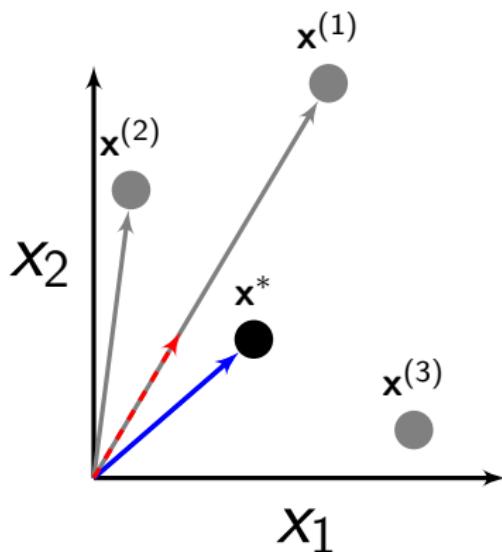
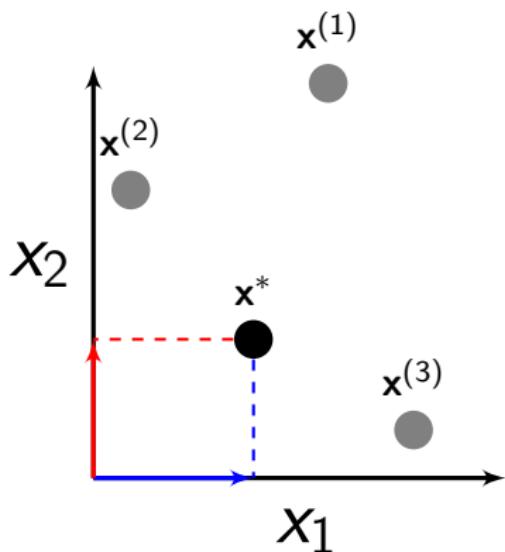
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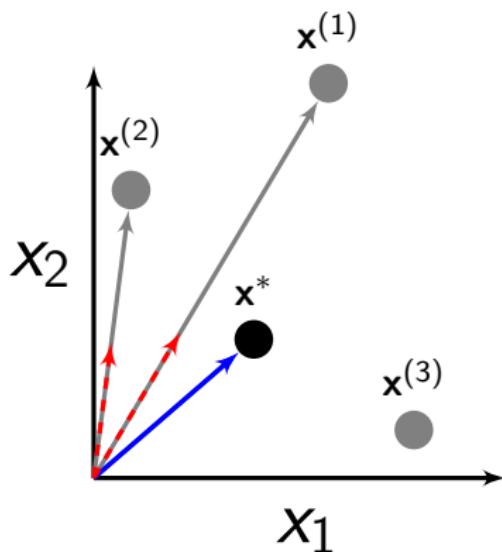
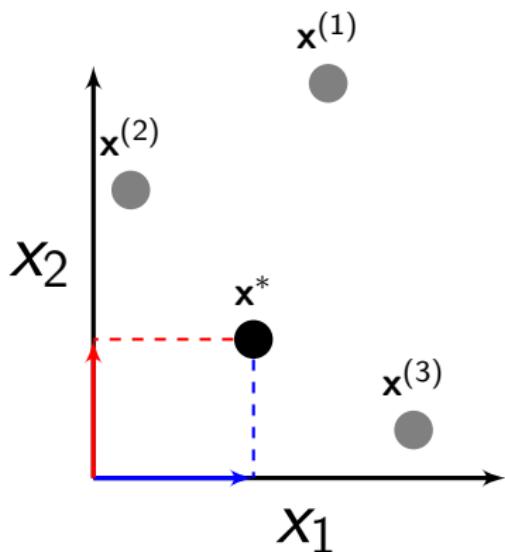
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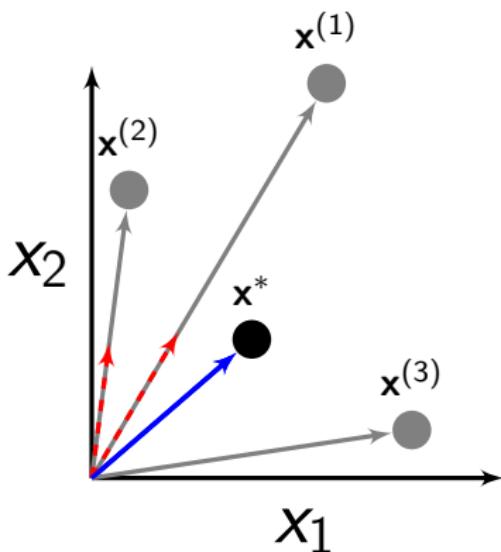
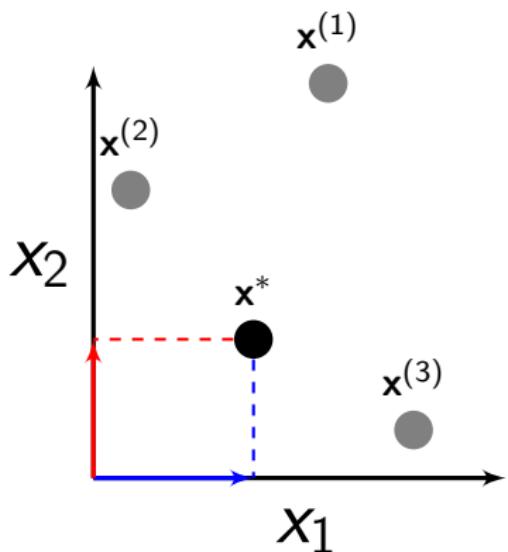
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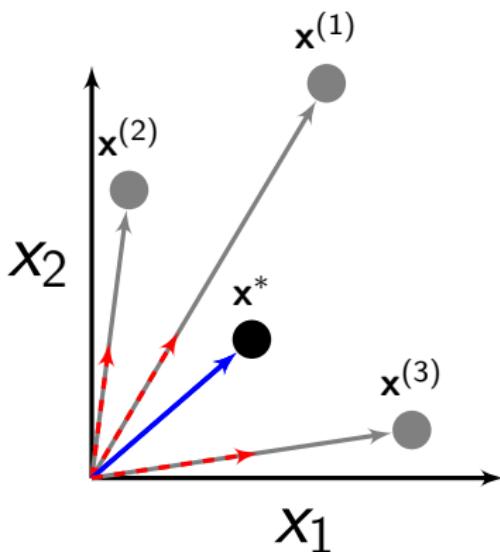
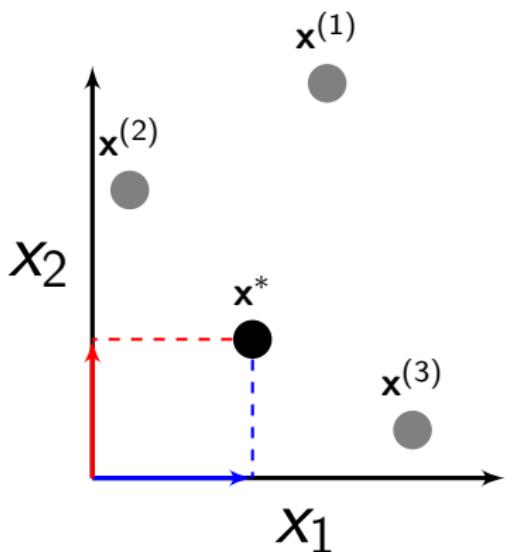
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Nonlinear regression

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$$y_{QUAD}(x) = w_1 + w_2x_1 + w_3x_2 + w_4x_1x_2 + w_5x_1^2 + w_6x_2^2$$

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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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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:

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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 φ is.

The Gaussian kernel and KRR

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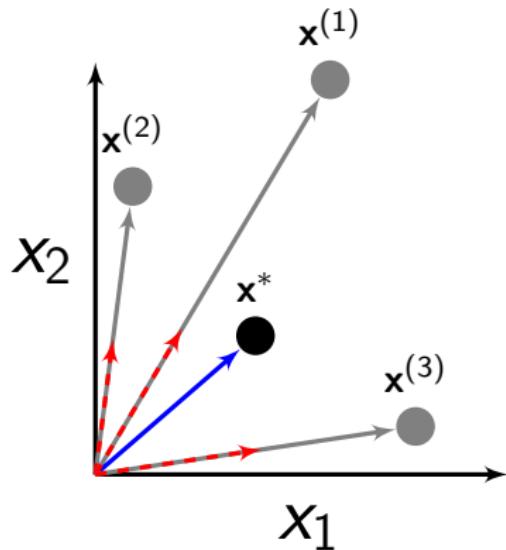
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Depends on σ to control non-locality.

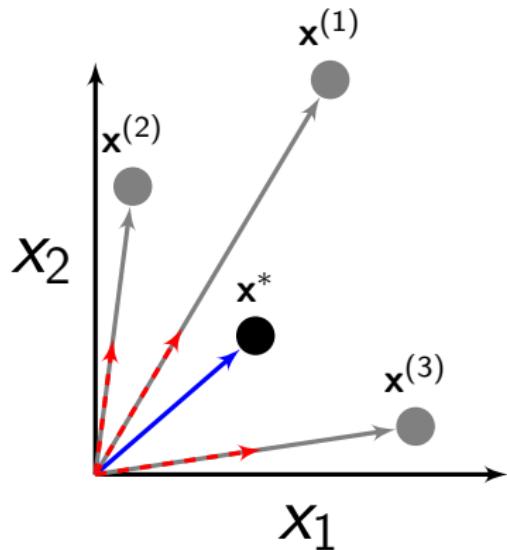
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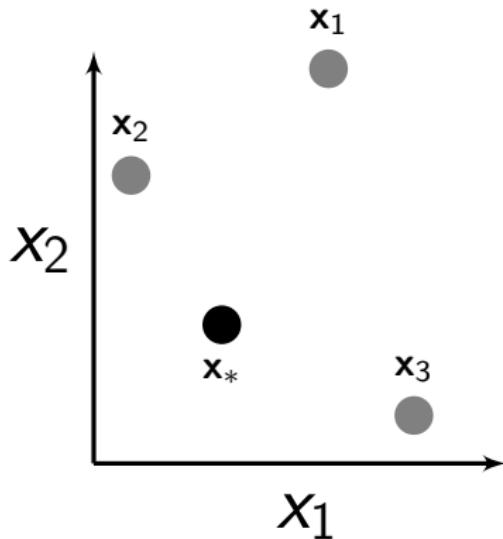


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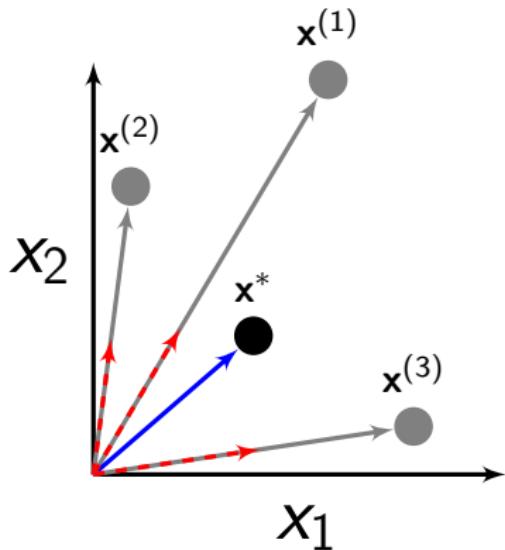
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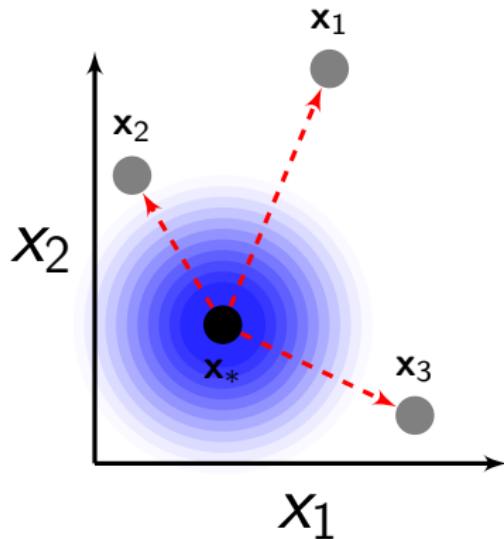
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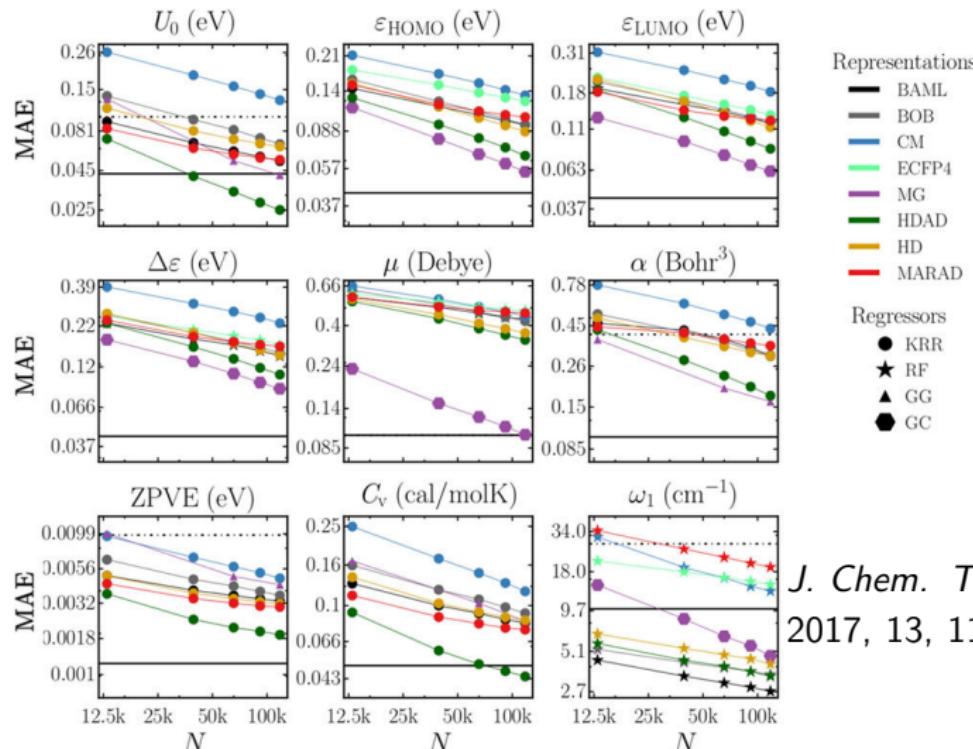
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- 4 check using cross-validation to choose σ and λ

KRR is widely used in chemistry



J. Chem. Theory Comput.
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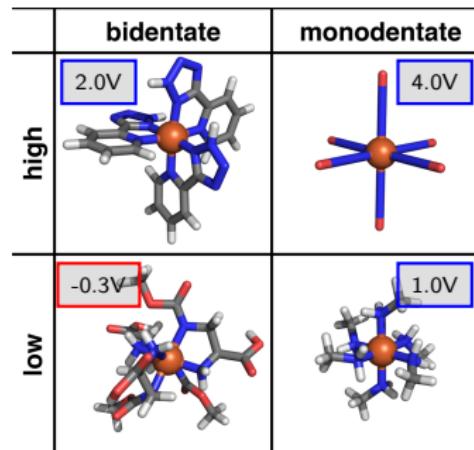
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KRR example

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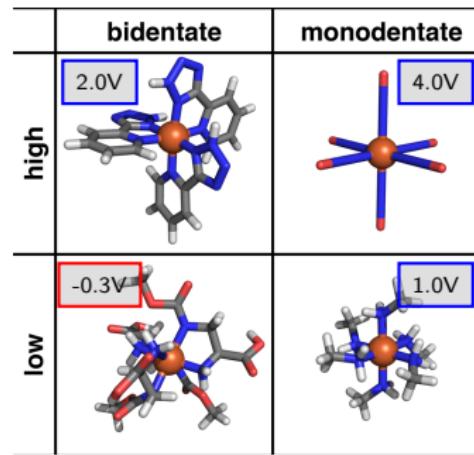
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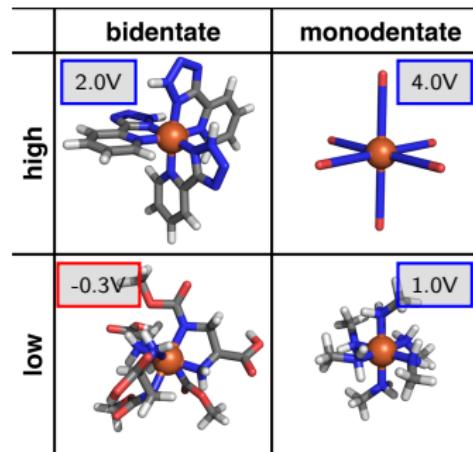
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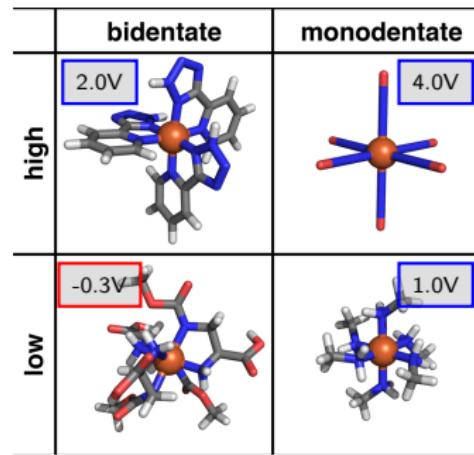


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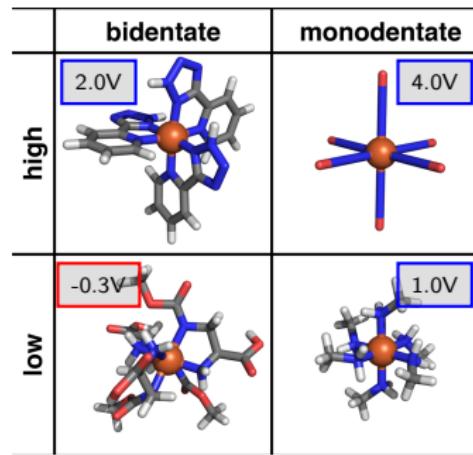
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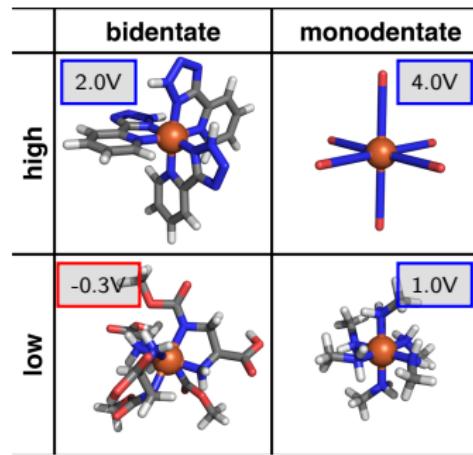
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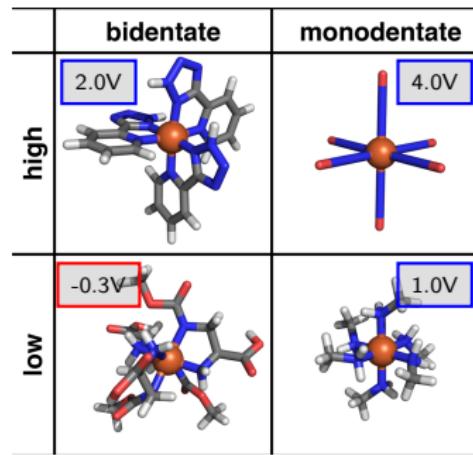
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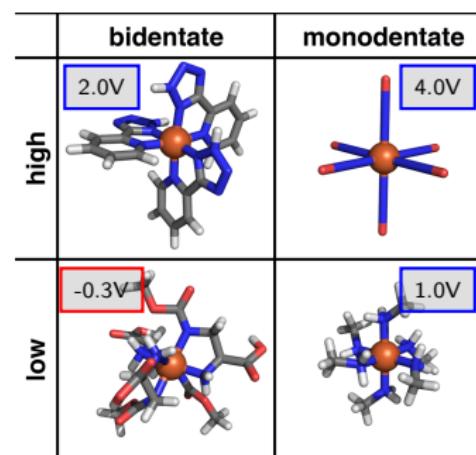
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$$\eta_{i,0} = p_i p_i$$

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

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

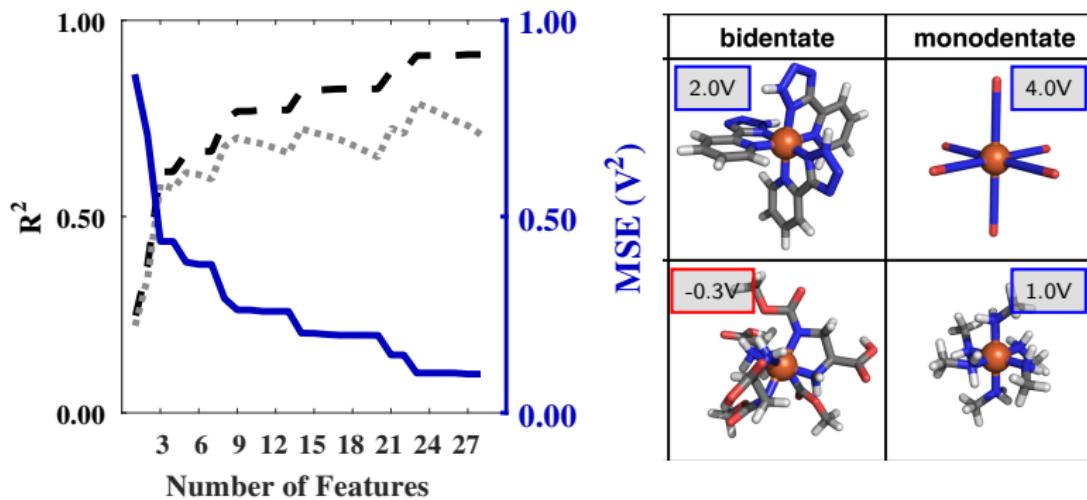
4 properties, $k \in [0, 5]$
 \implies 28 variables.

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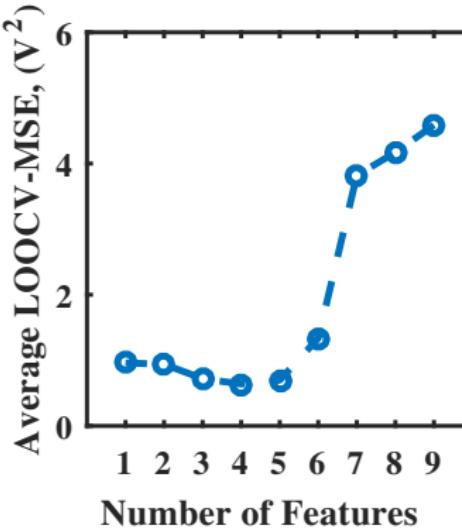
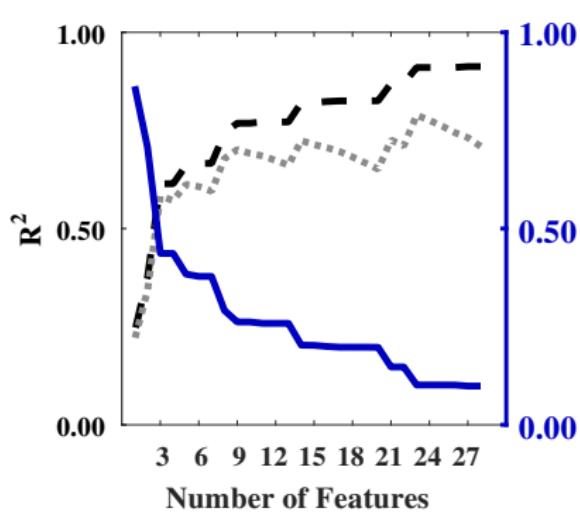
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How to pick important features?

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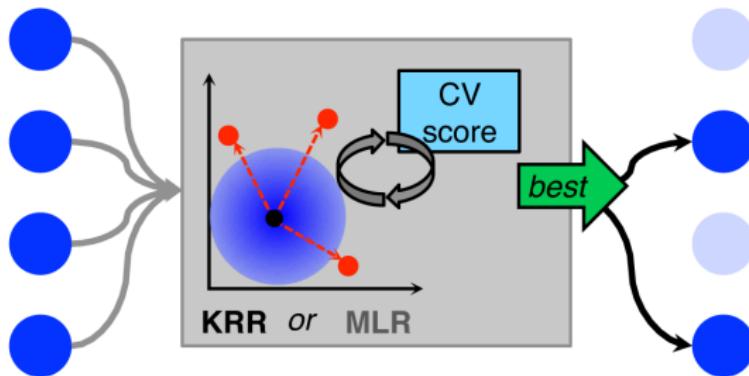
We don't know the optimal number upfront, and this is a combinatorial problem – possible for ≤ 30 dimensions or so, but rapidly becomes unfeasible.

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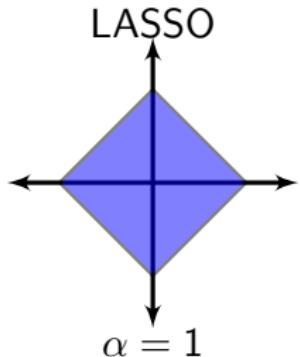
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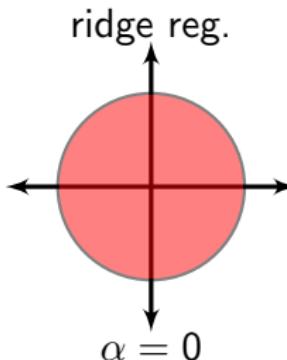
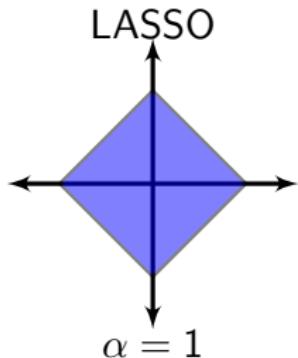
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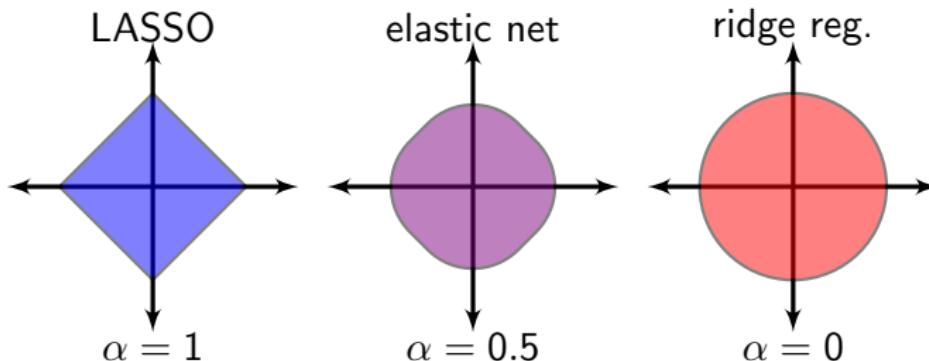
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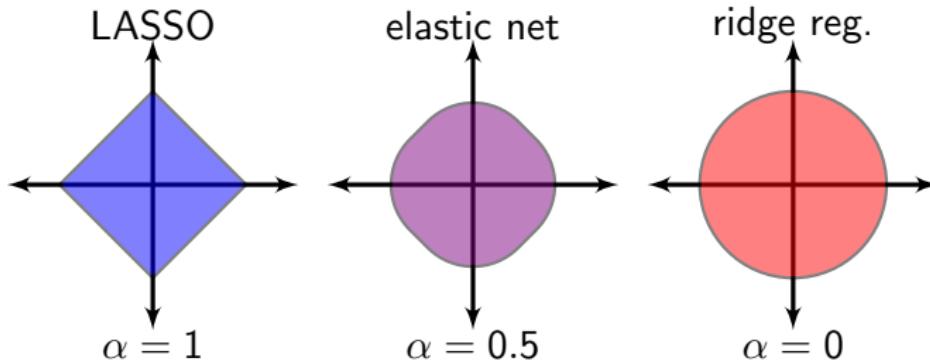
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Using even a small $\alpha > 0$ ensures the minimization is stable.

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Why not use even lower norms such as $\|w\|_0^{0.5}$? Convexity!

Conclusions

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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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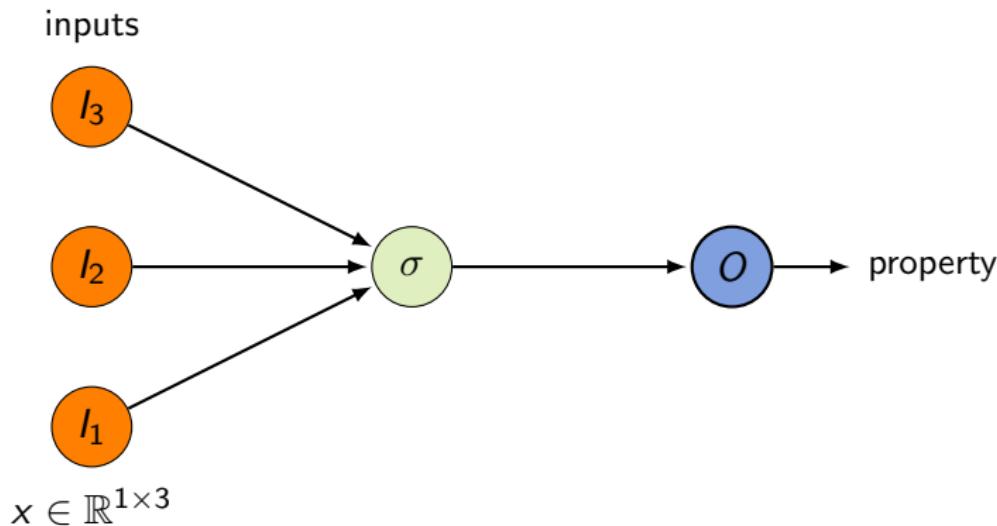
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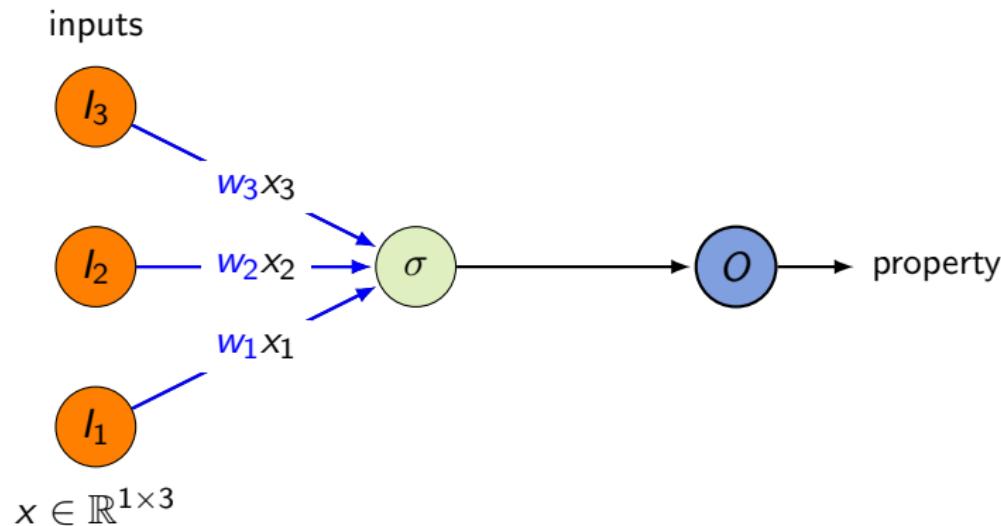
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- 5 easily scaled for different input structures.

The neuron

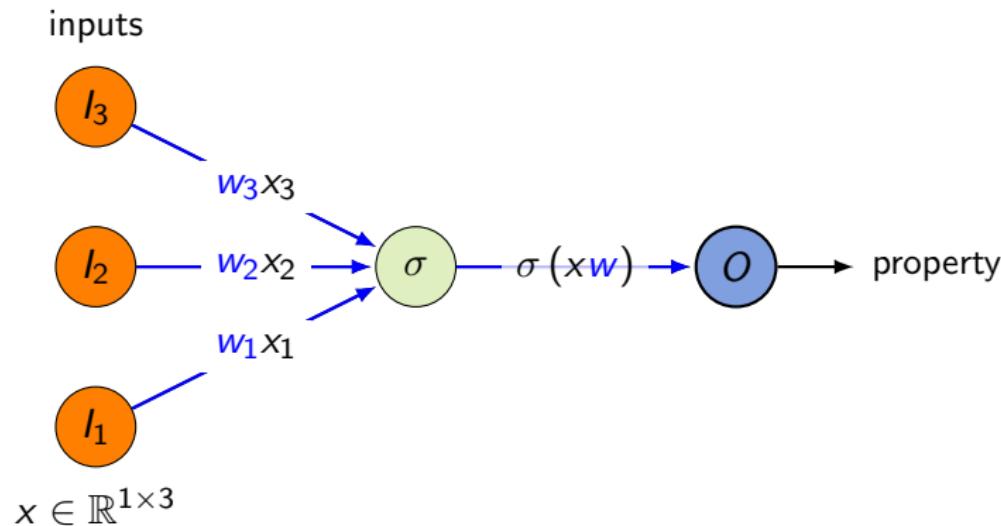
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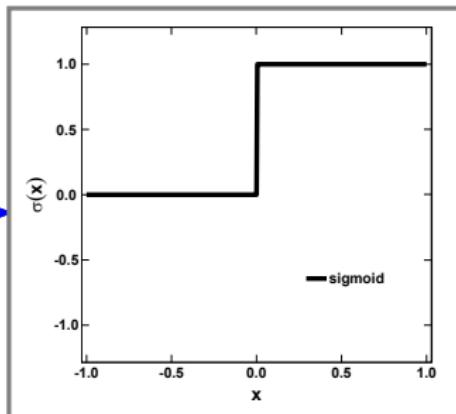
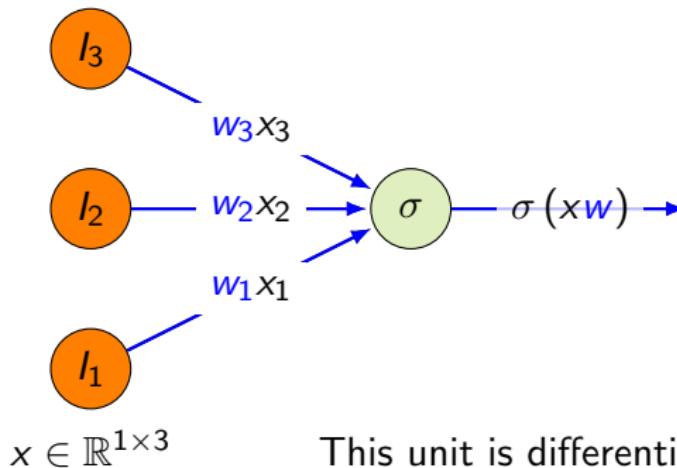


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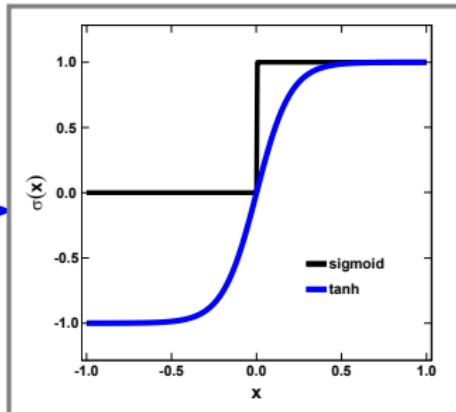
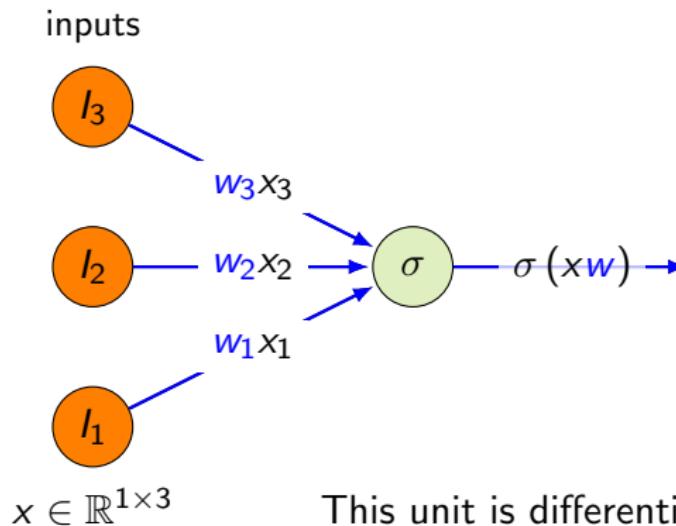
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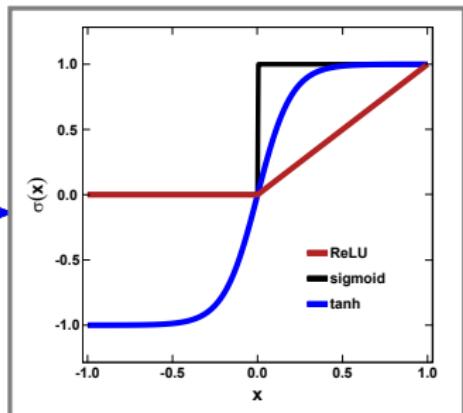
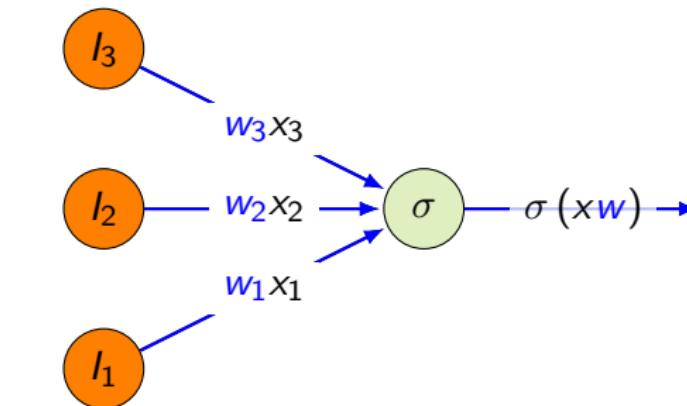
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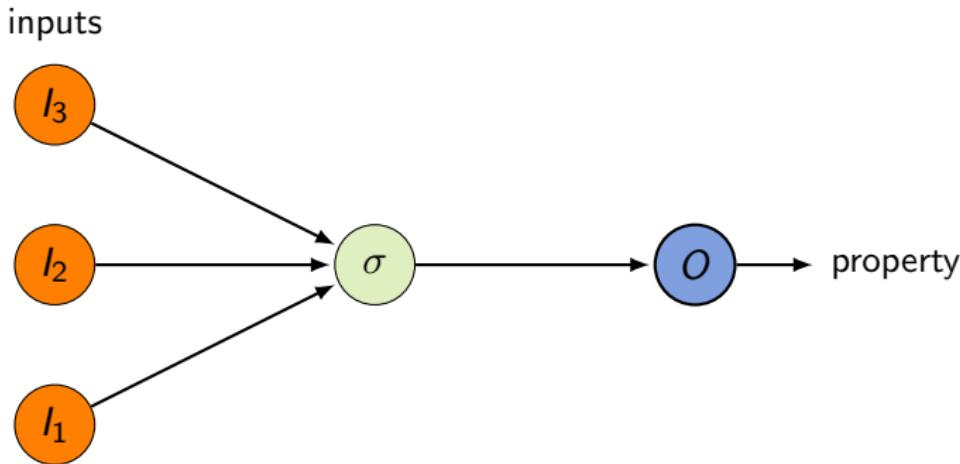


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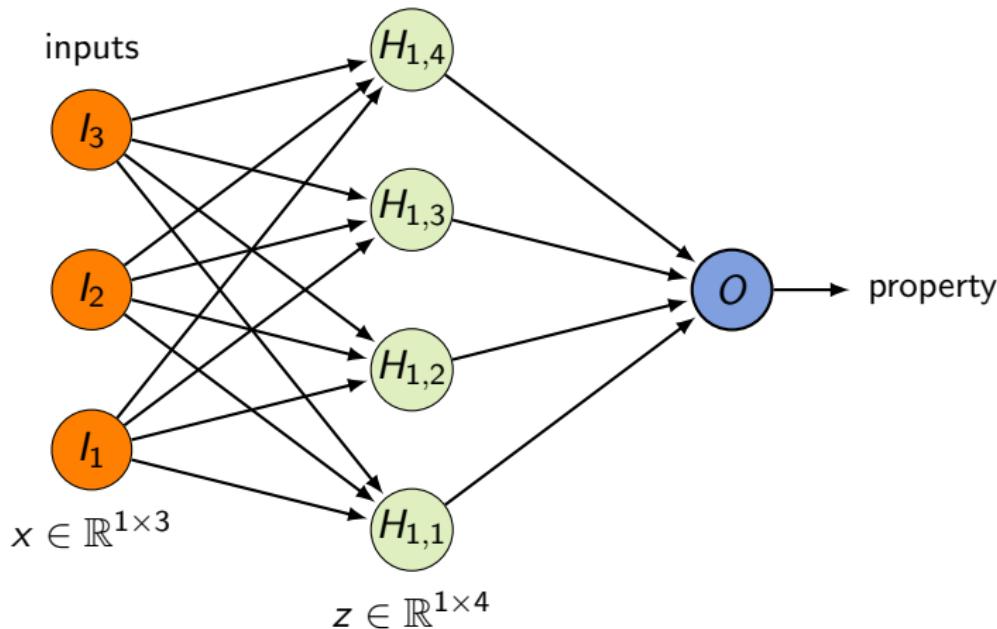
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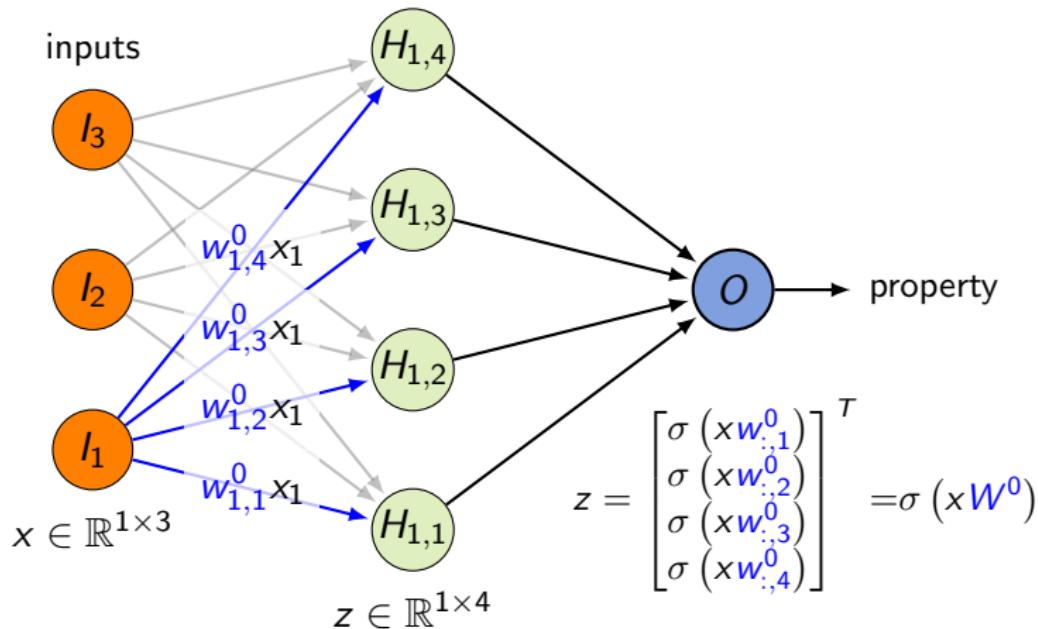
The perceptron



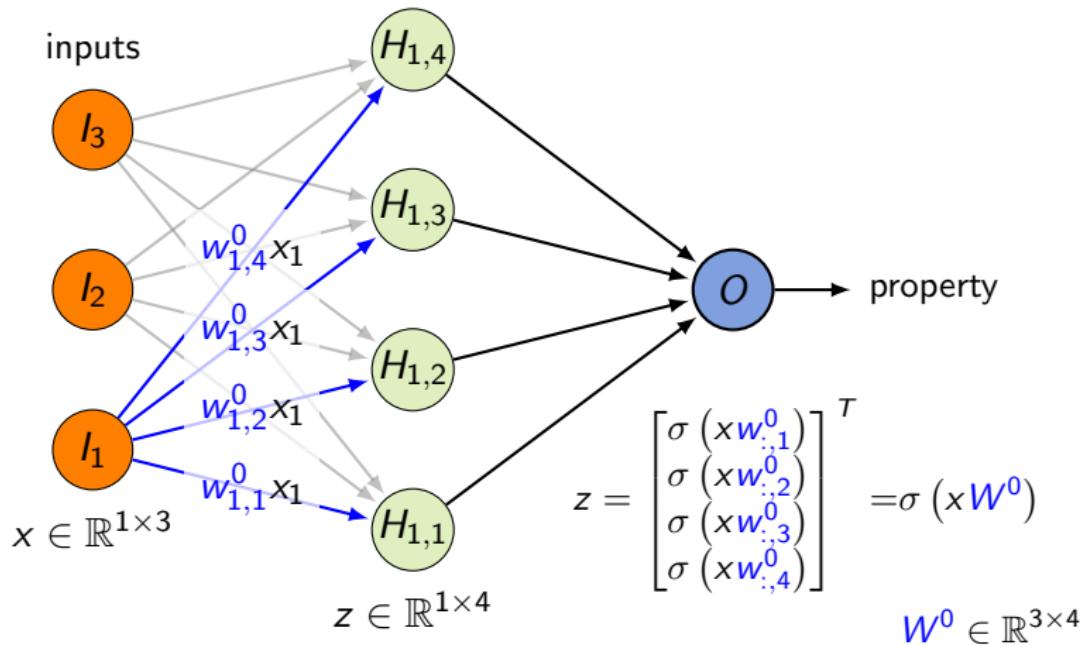
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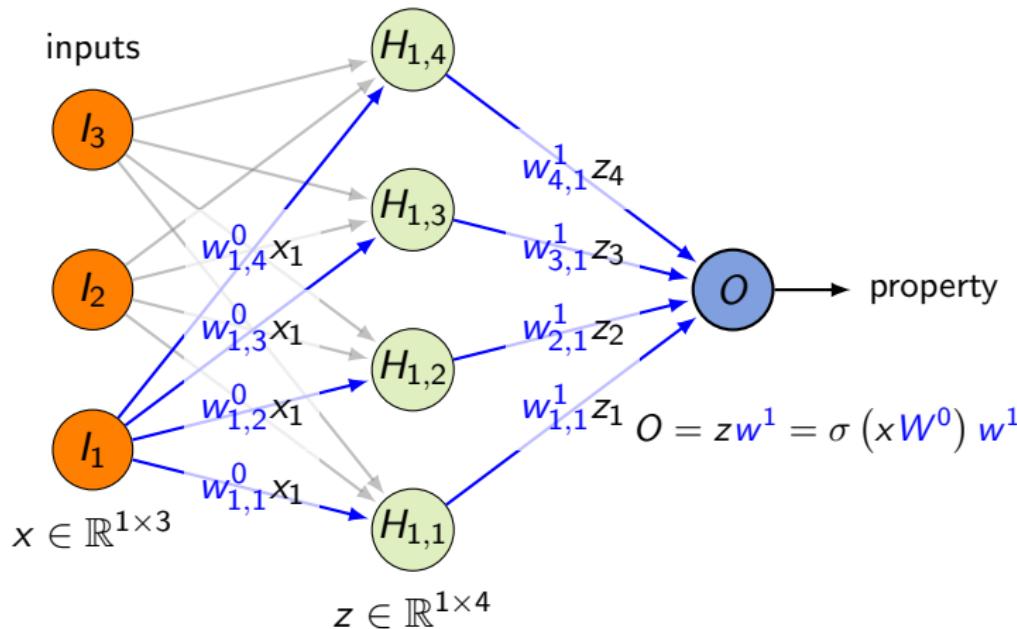
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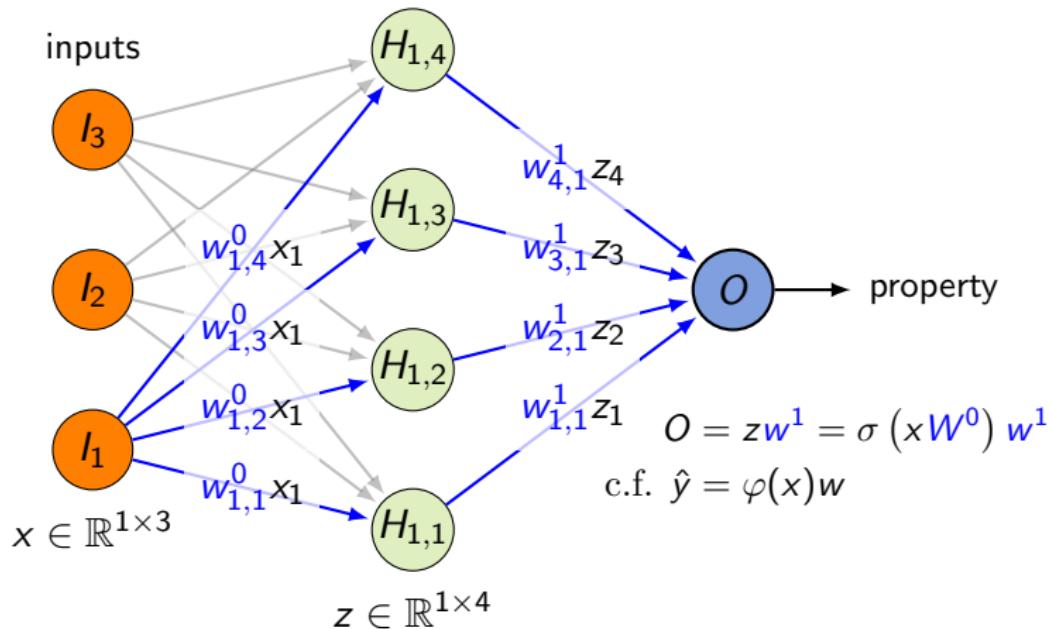
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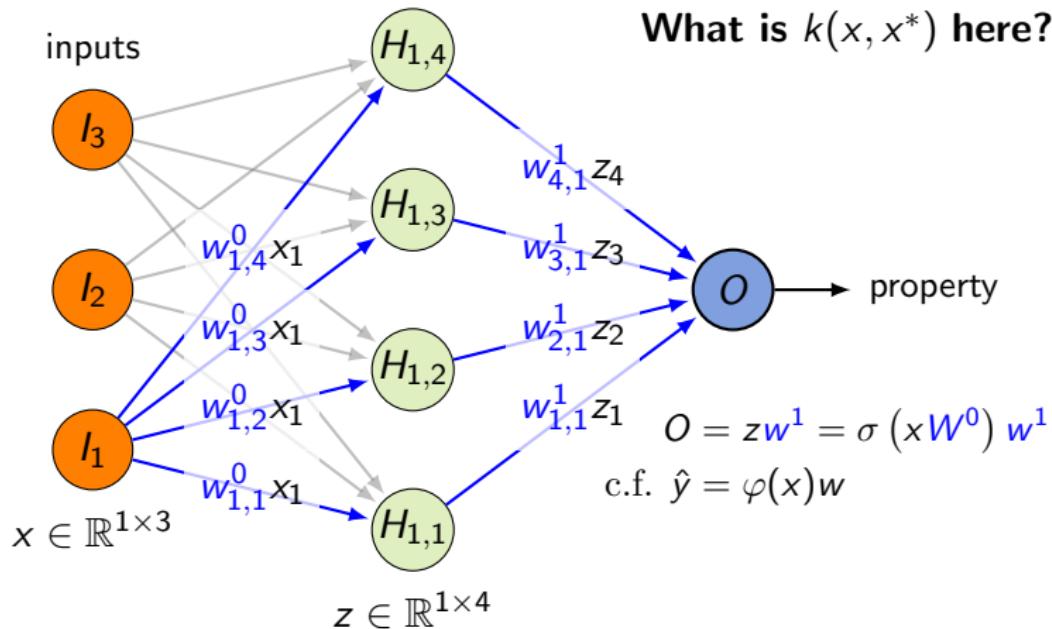
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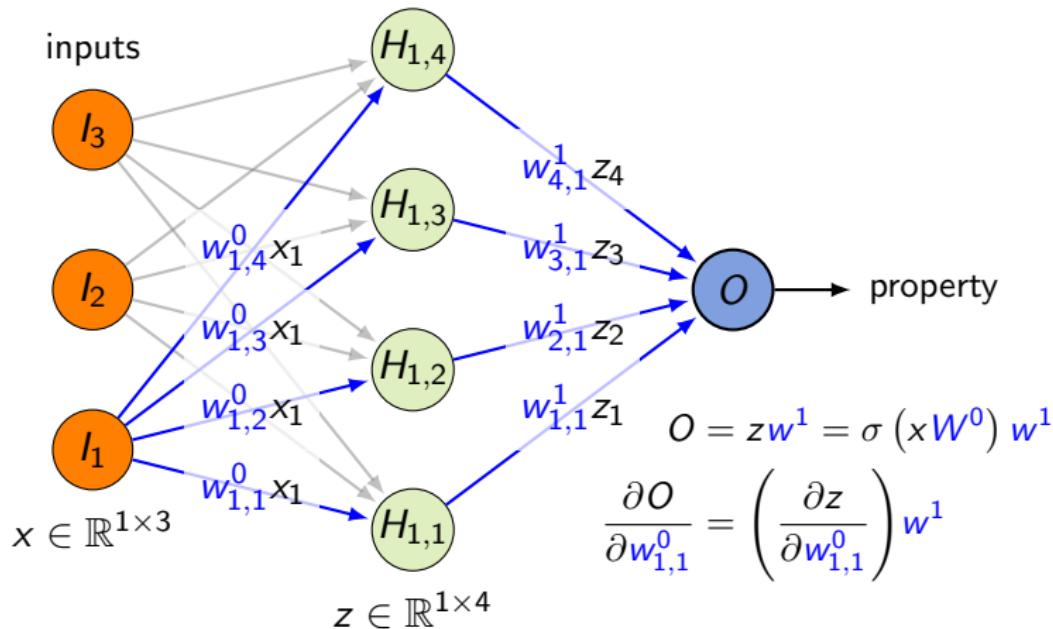
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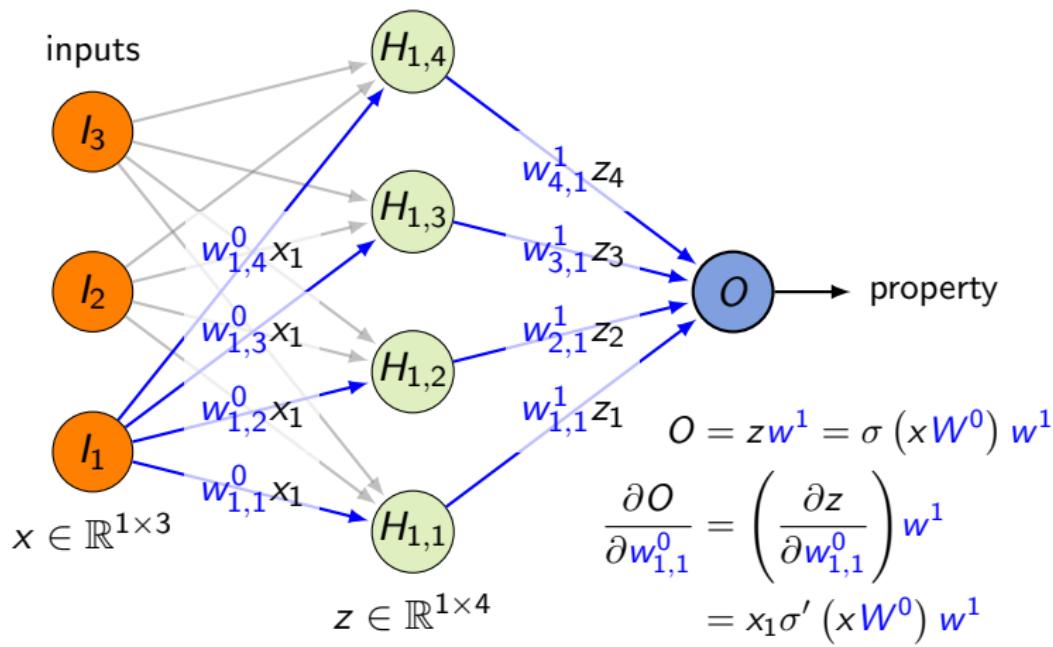
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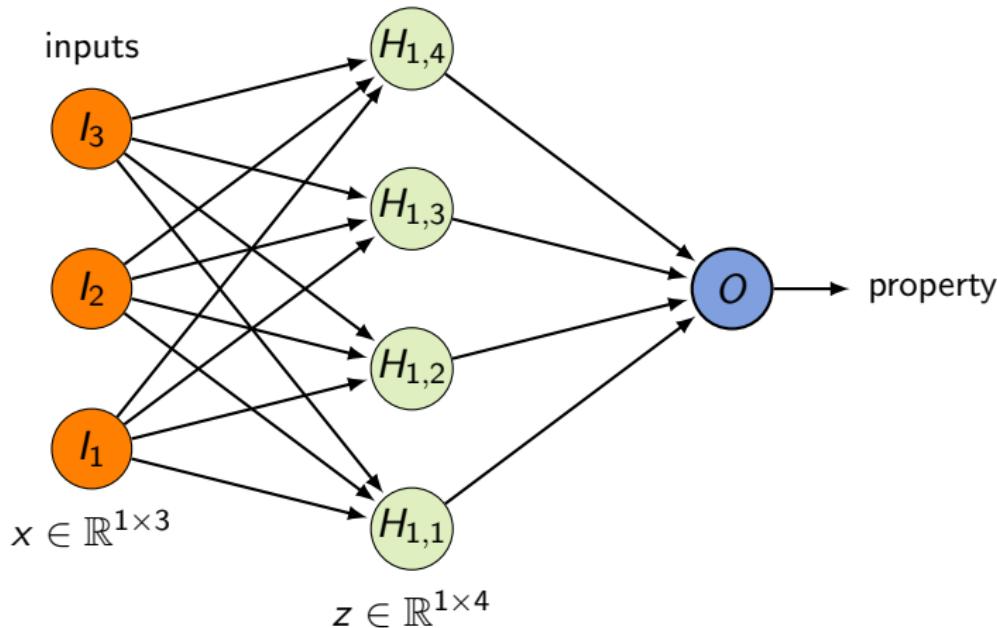
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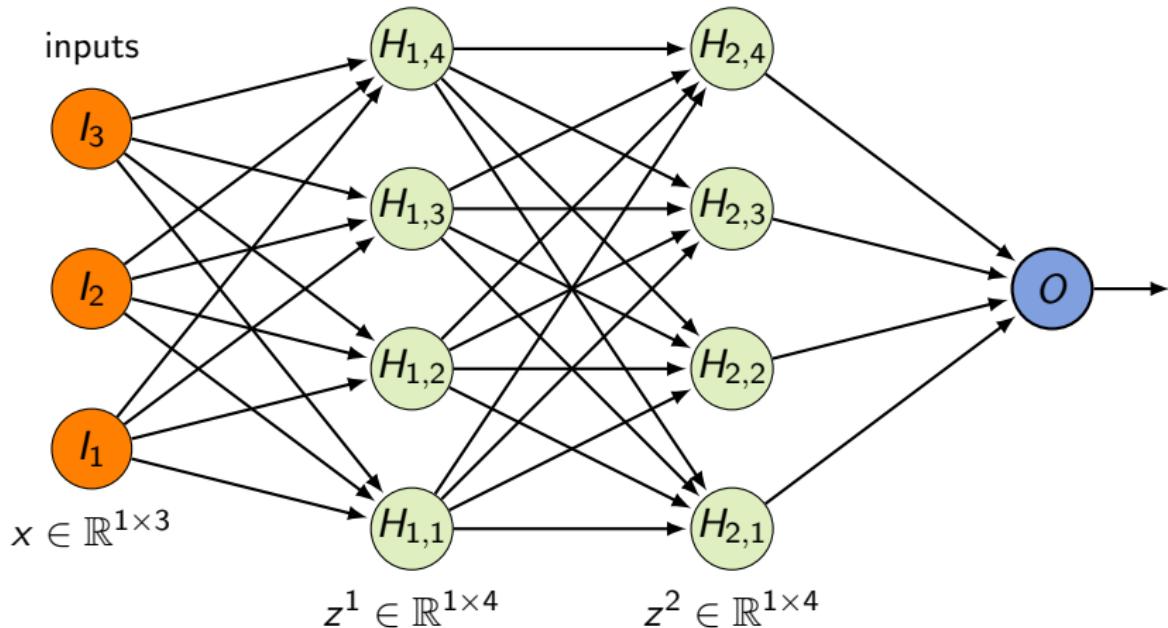
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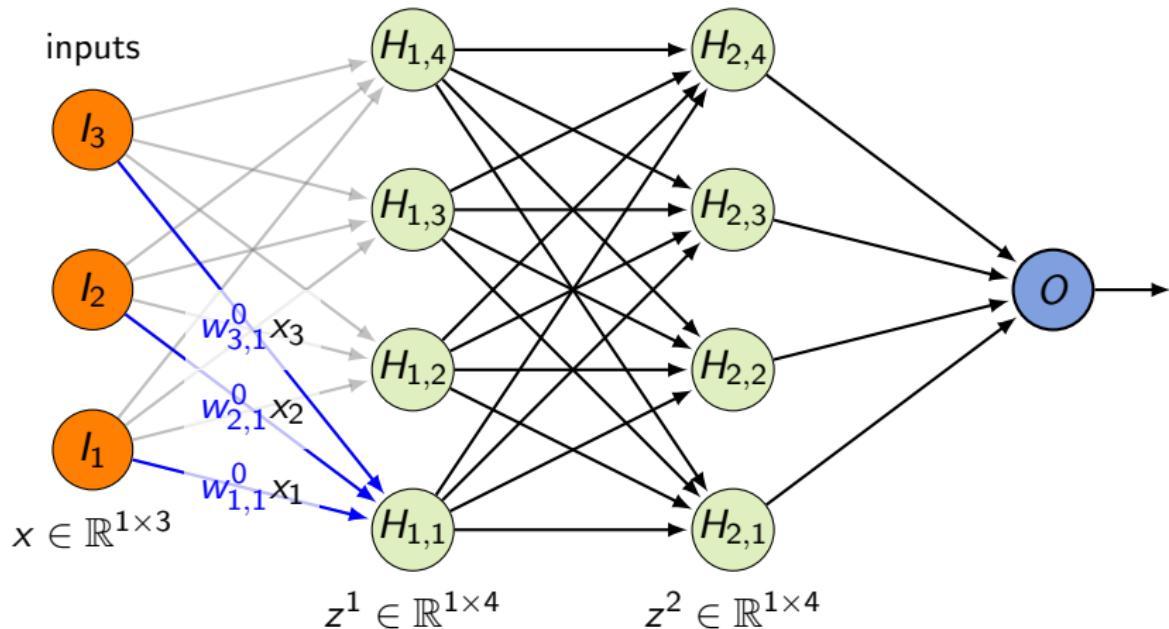
The *multilayer* perceptron



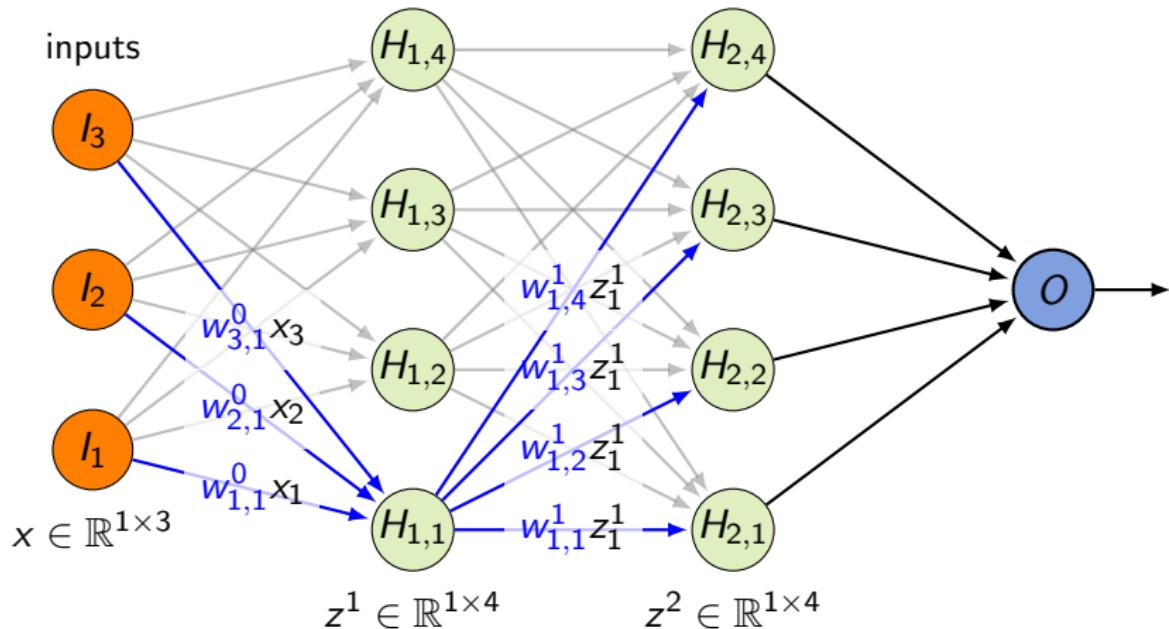
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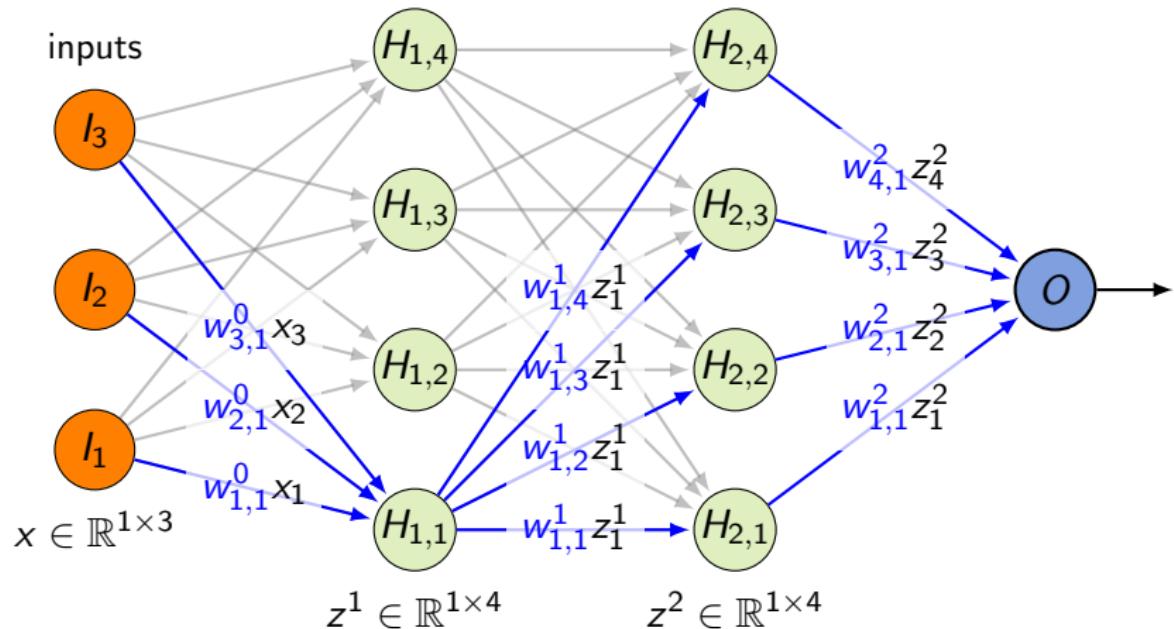
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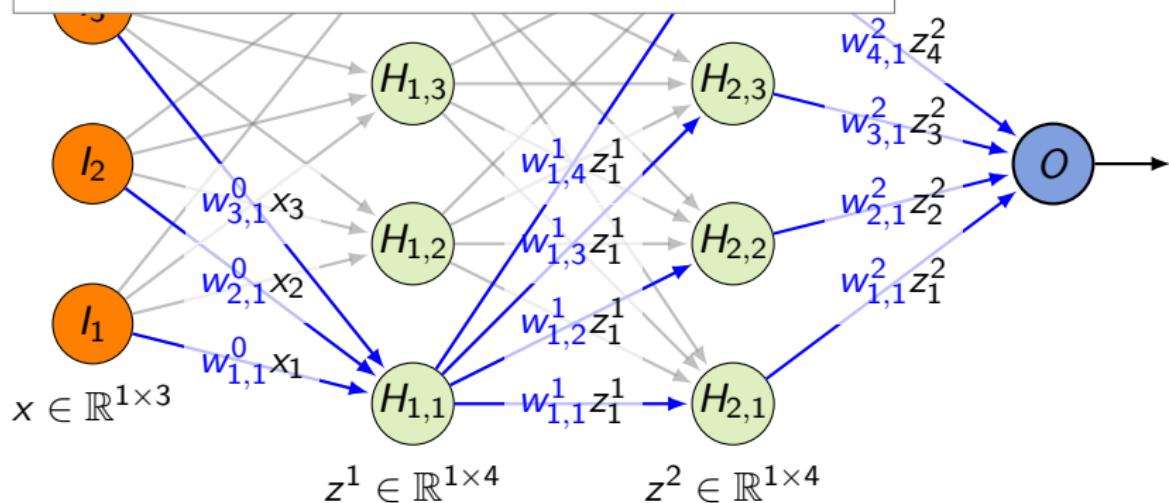


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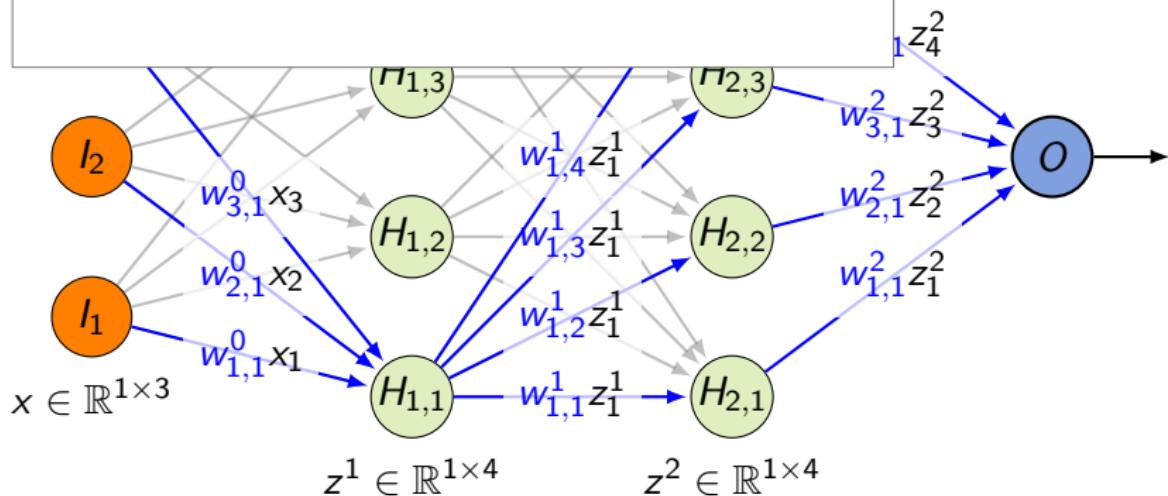
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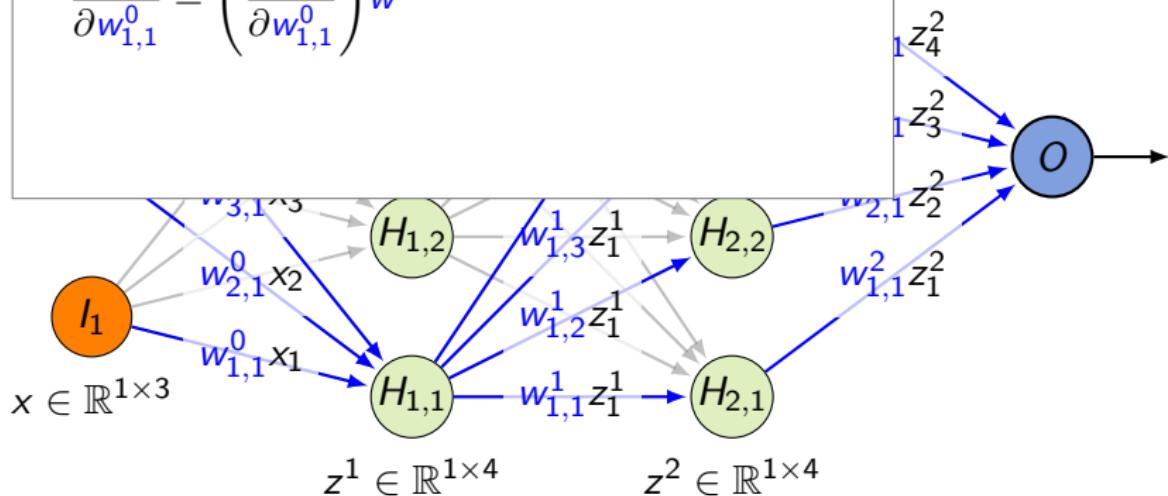
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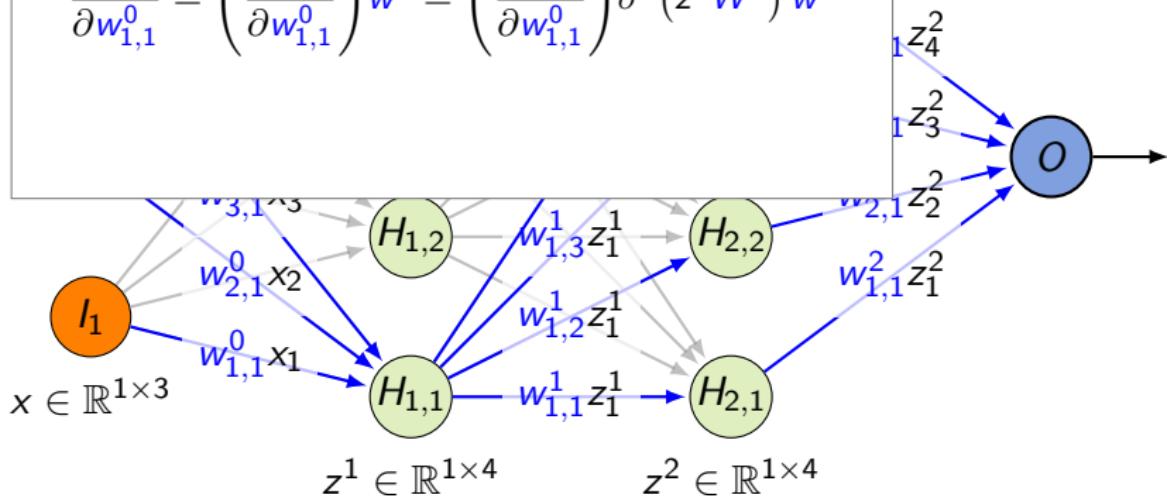
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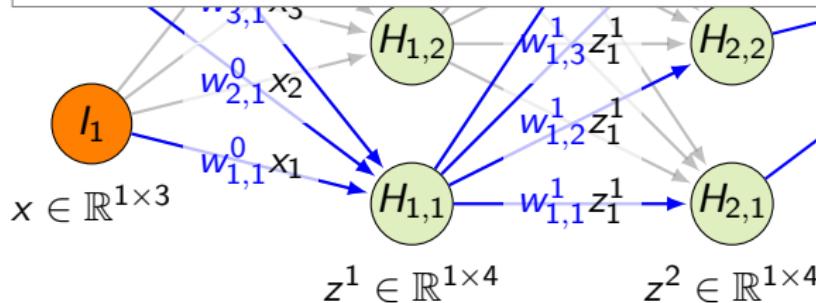
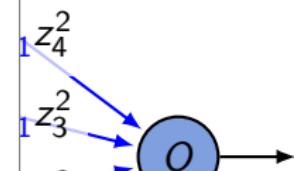


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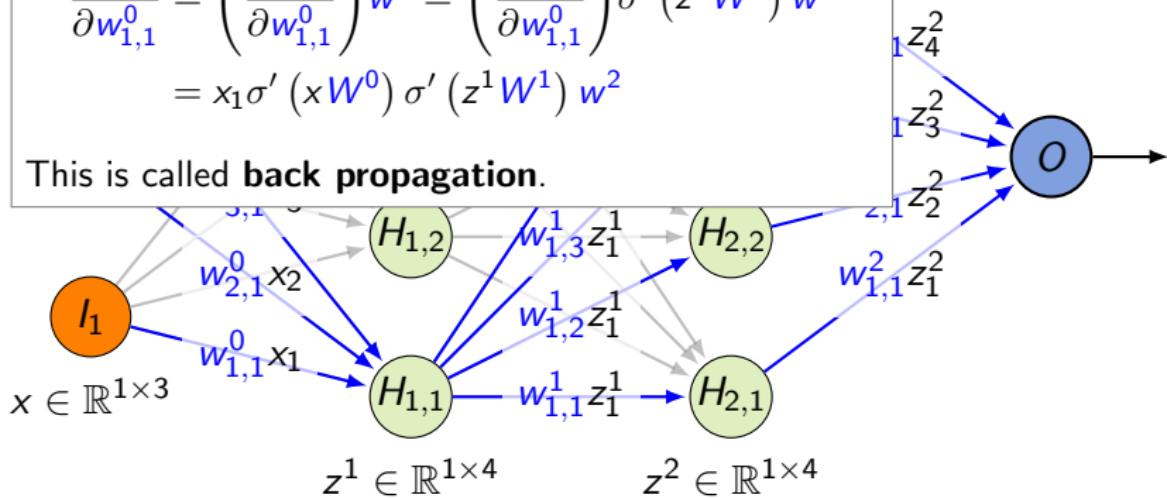
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This is called **back propagation**.

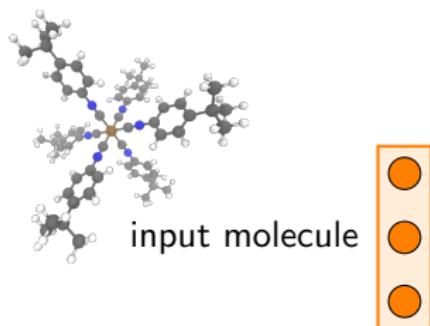


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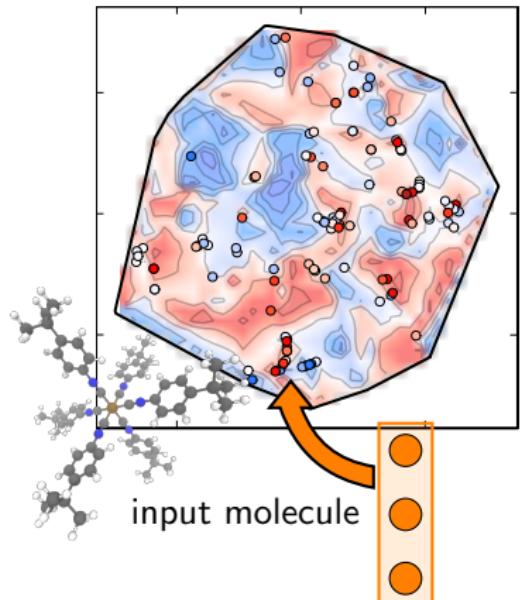
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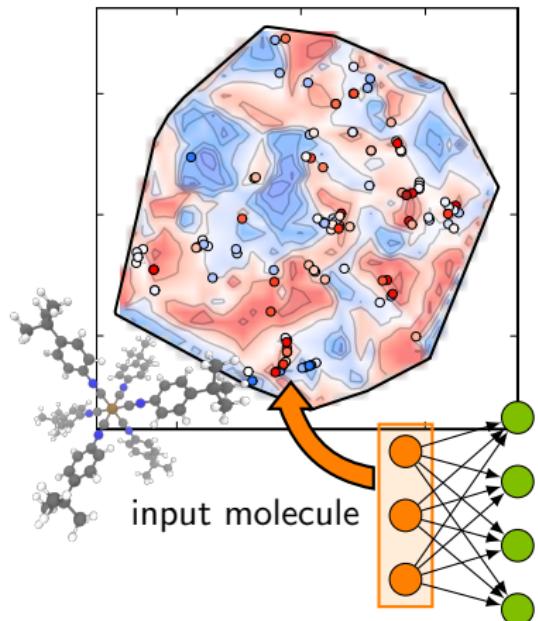
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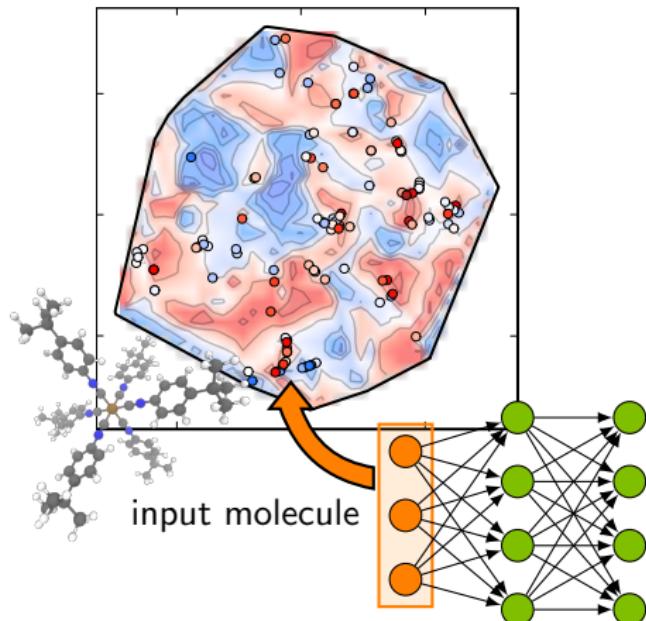
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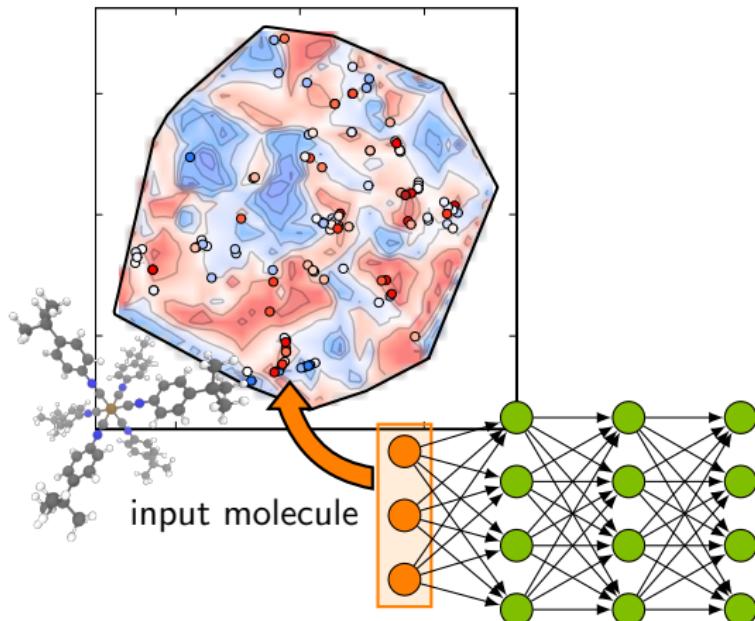
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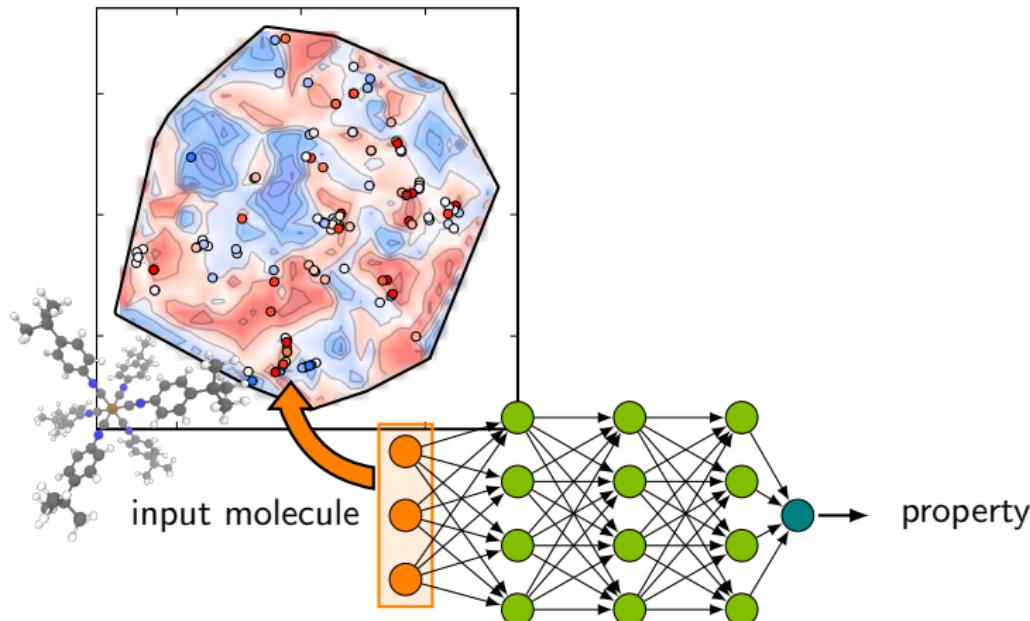
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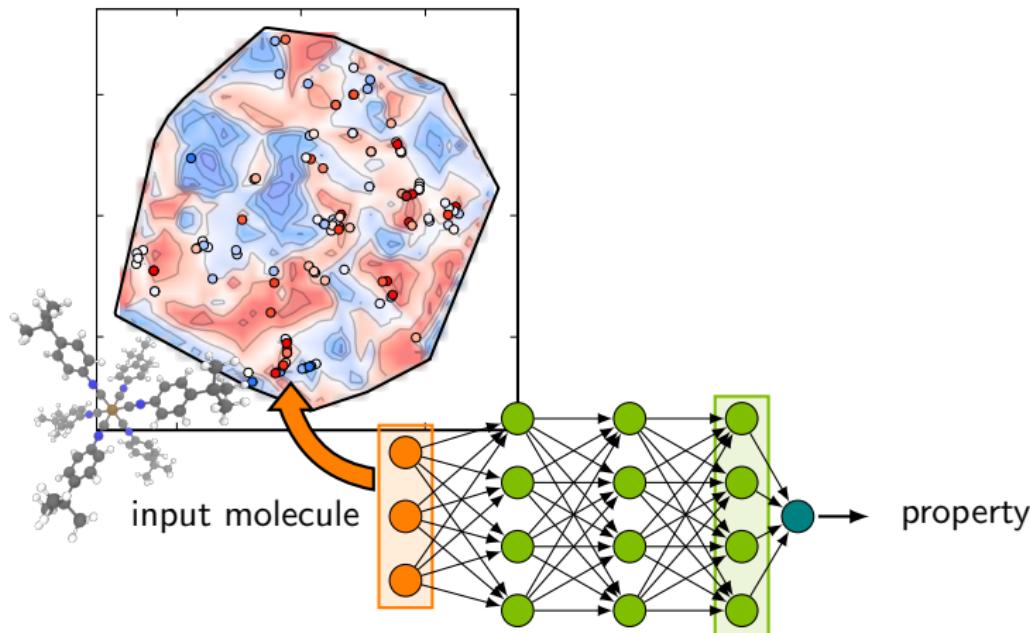
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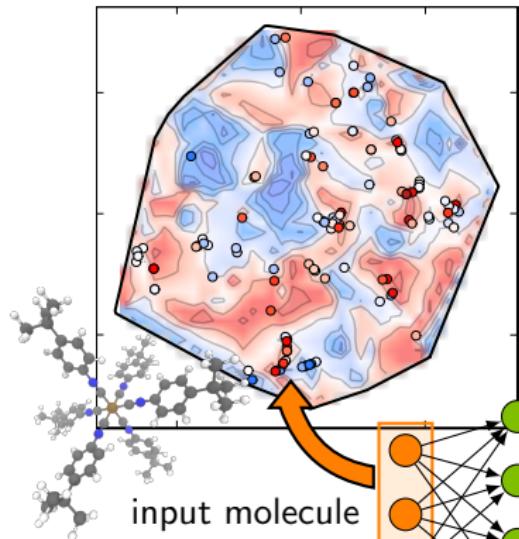
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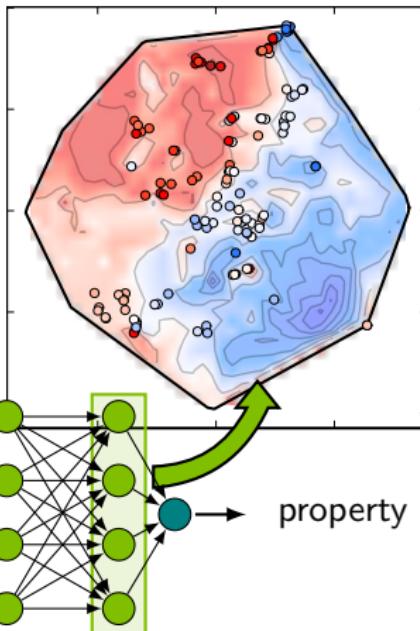
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latent space



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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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Convolutional → Layer used to extract information or “focus on” certain features. Use a sliding “feature detector” called a filter, which creates a map

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Dropout → zero out nodes to reduce specific node dependence

Output → Node right before result, linear for regression, sigmoid for classification. Maps latent space to final answer

Convolutional → Layer used to extract information or “focus on” certain features. Use a sliding “feature detector” called a filter, which creates a map

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

Interpretation as representation learning

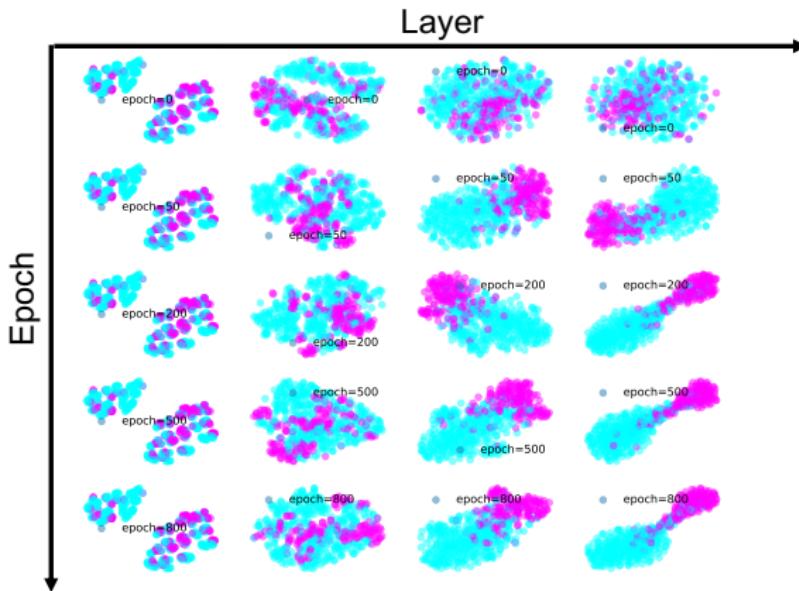
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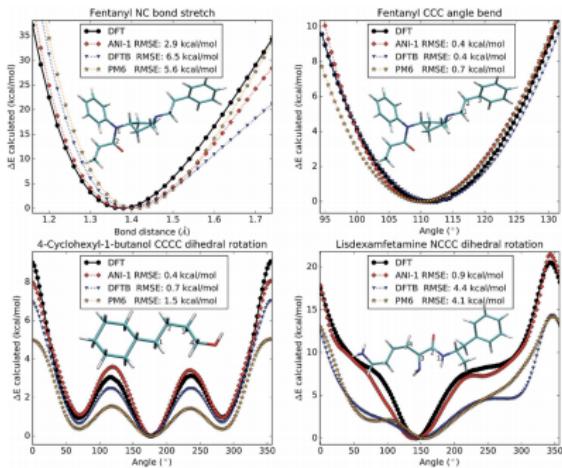
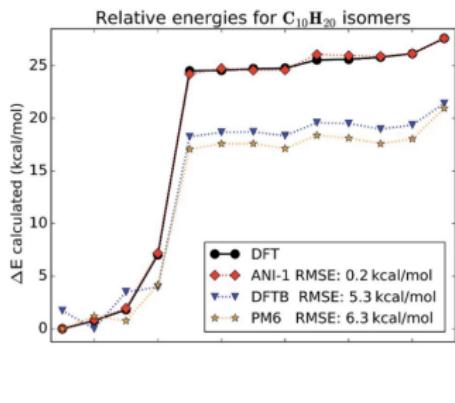
- 1 Neural network models provide model complexity ‘on tap’
- 2 Backpropagation allows easy access to derivatives
- 3 We can understand neural networks as automatic feature selection/transformation, followed by linear regression

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)

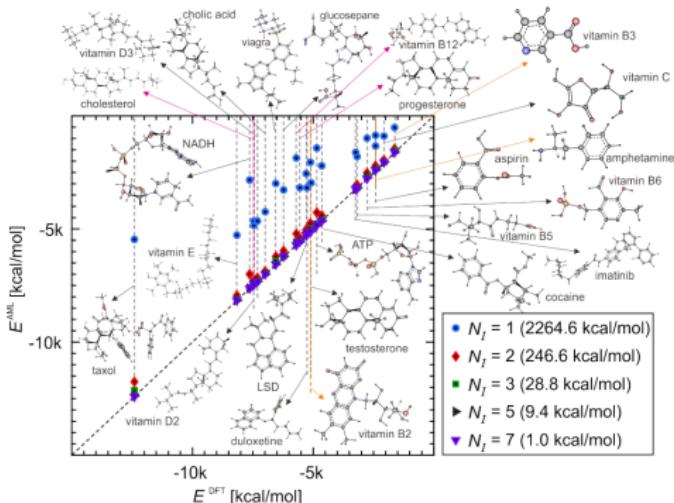
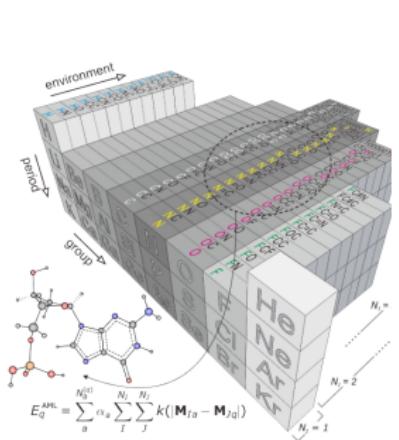
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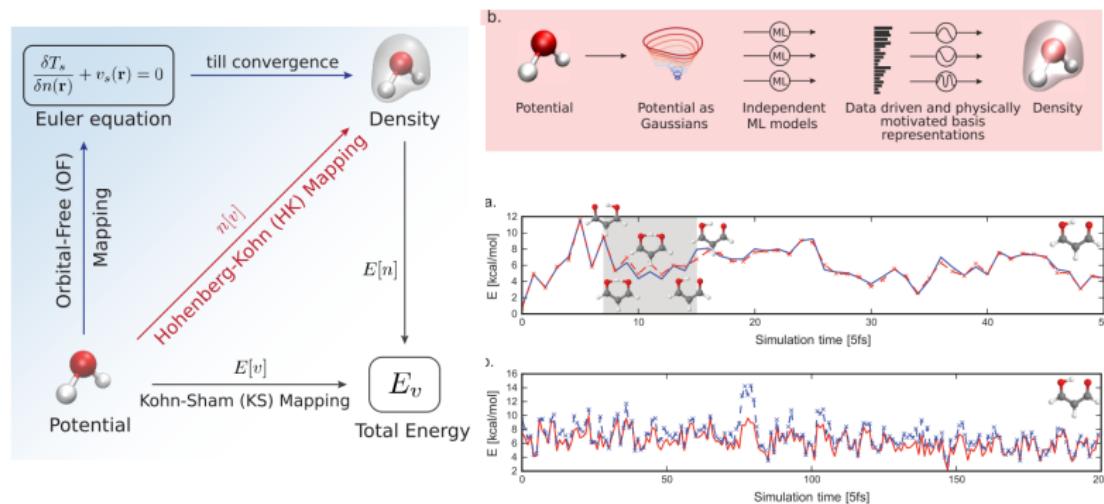
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Bogojeski, M. *et al.*, Burke, K. and Müller, K.R. *arXiv* 1811.06255, Efficient prediction of 3D electron densities using machine learning, 2018.



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Chenru Duan et. al. *ChemRxiv* .7616009, “Learning from Failure: Predicting Electronic Structure Calculation Outcomes with Machine Learning Models”, 2019.

