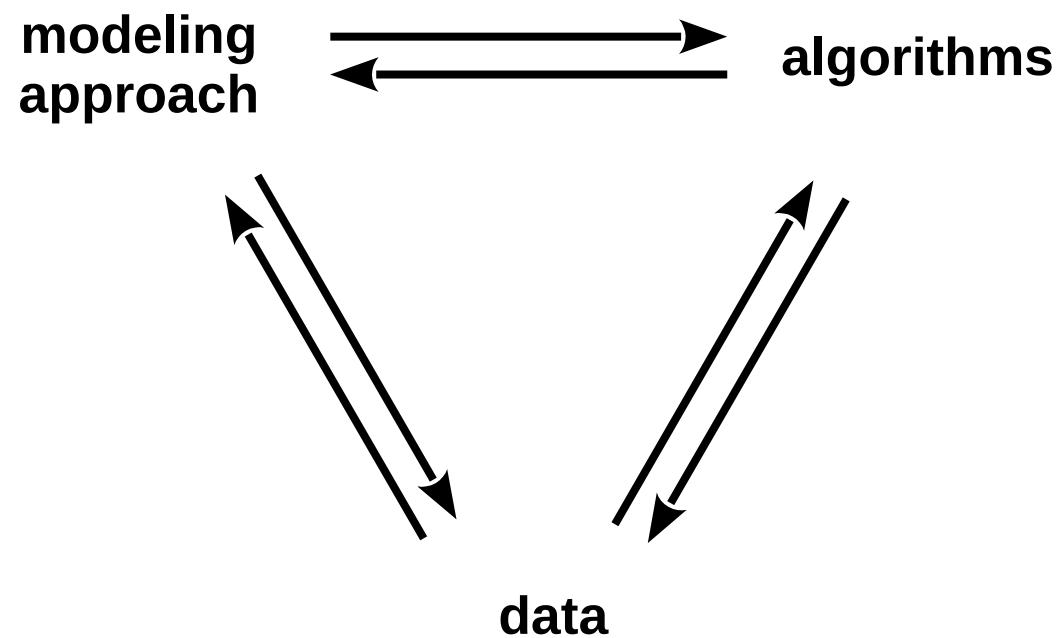
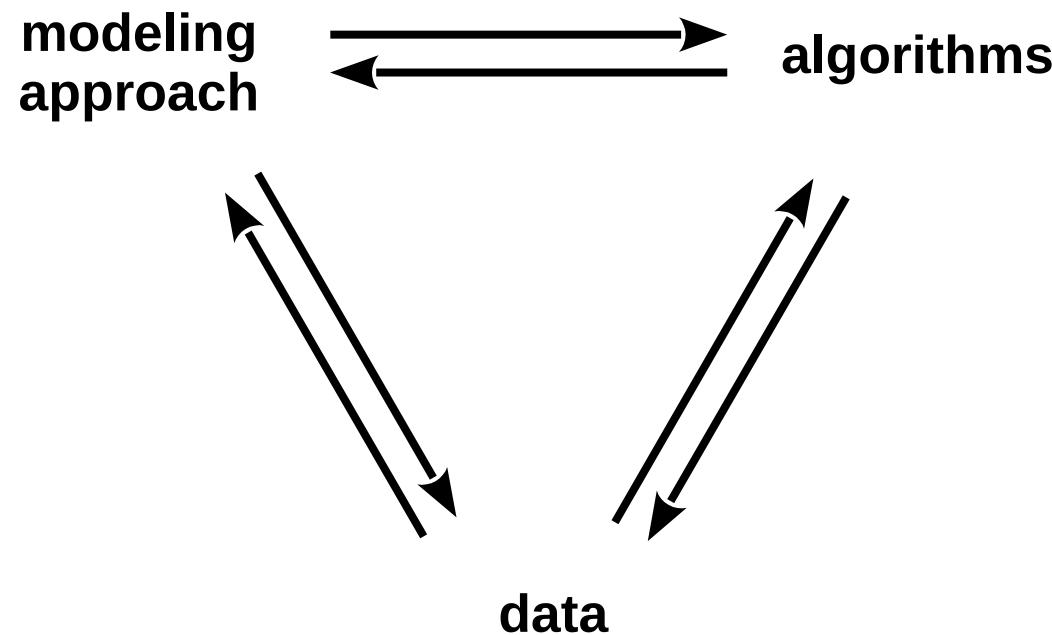


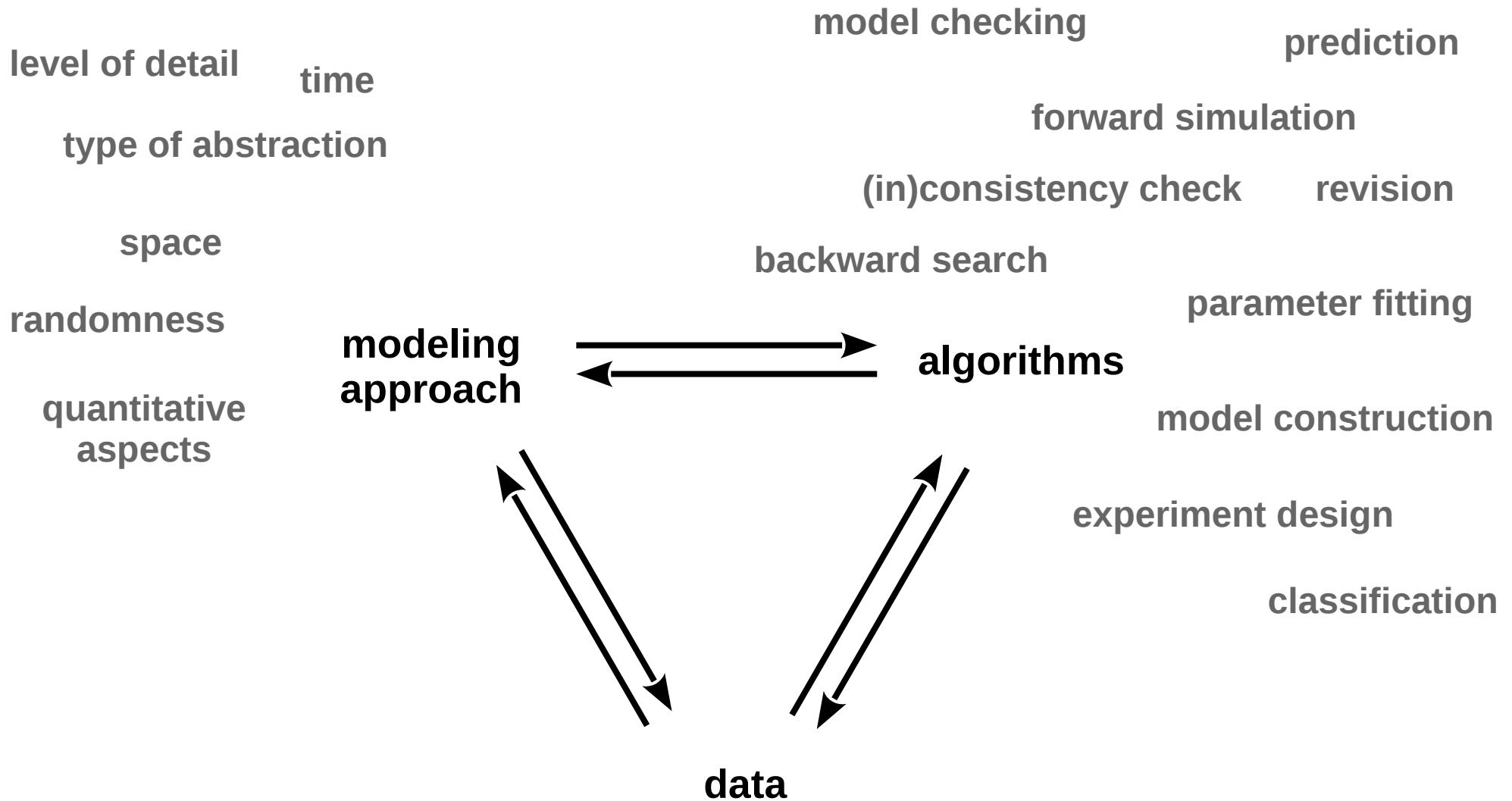
# The potential of Machine Learning in biology

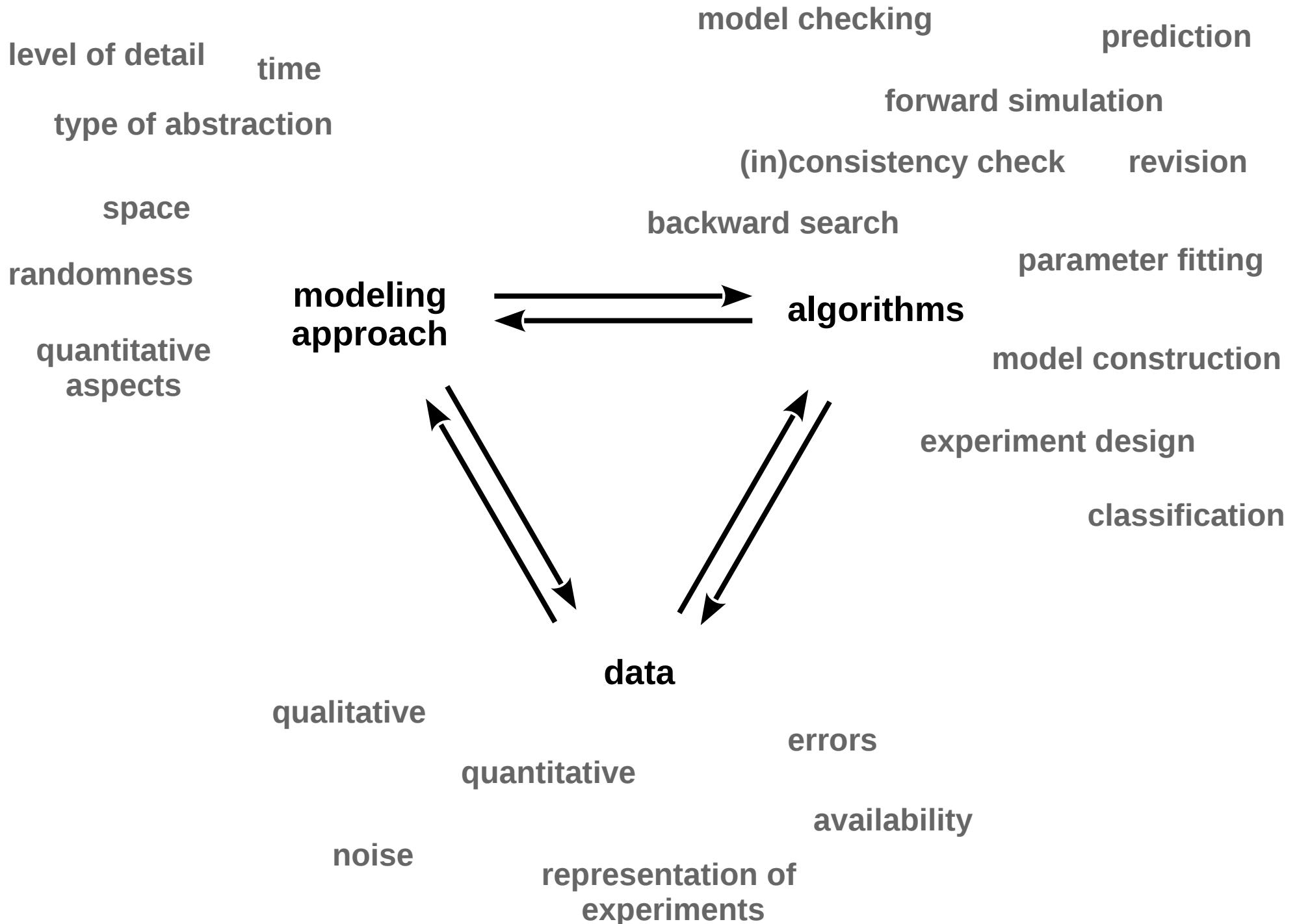
Robert Różański



level of detail      time  
type of abstraction  
  
space  
randomness  
quantitative aspects







# So what can be done?

- symbolic ML
- standard supervised ML
- standard unsupervised ML
- Deep Learning

# Symbolic ML

# Symbolic ML

- Modeling approach: symbolic models (Boolean Networks, Bayesian Networks, Petri Nets, Pathway Logic, ... (many more))

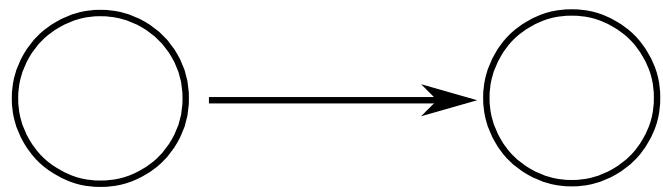
# Symbolic ML

- Modeling approach: symbolic models (Boolean Networks, Bayesian Networks, Petri Nets, Pathway Logic, ... (many more))
- quantitative/spatial/temporal aspects abstracted away to some degree (models can have some discrete states and transition between them)

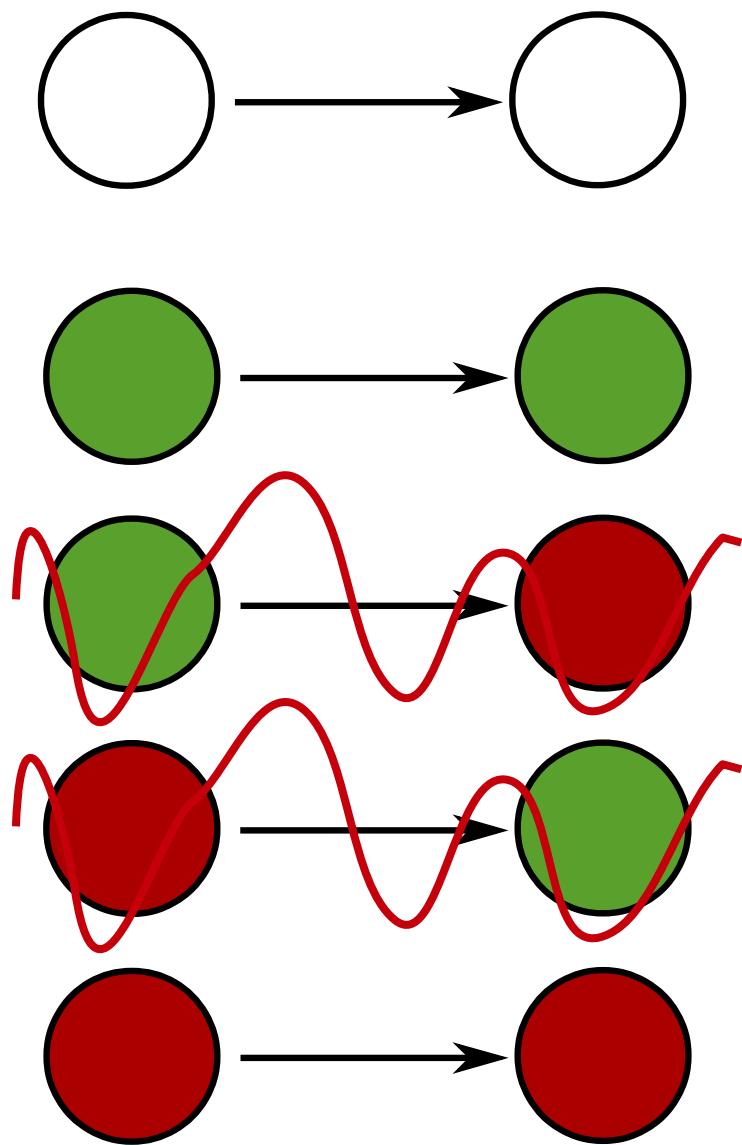
# Symbolic ML

- Modeling approach: symbolic models (Boolean Networks, Bayesian Networks, Petri Nets, Pathway Logic, ... (many more))
- quantitative/spatial/temporal aspects abstracted away to some degree (models can have some discrete states and transition between them)
- many algorithms exist - the simpler the formalism, the better (simulation, model checking, construction, revision, exp. design, ...)

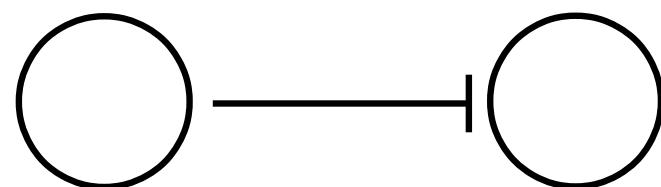
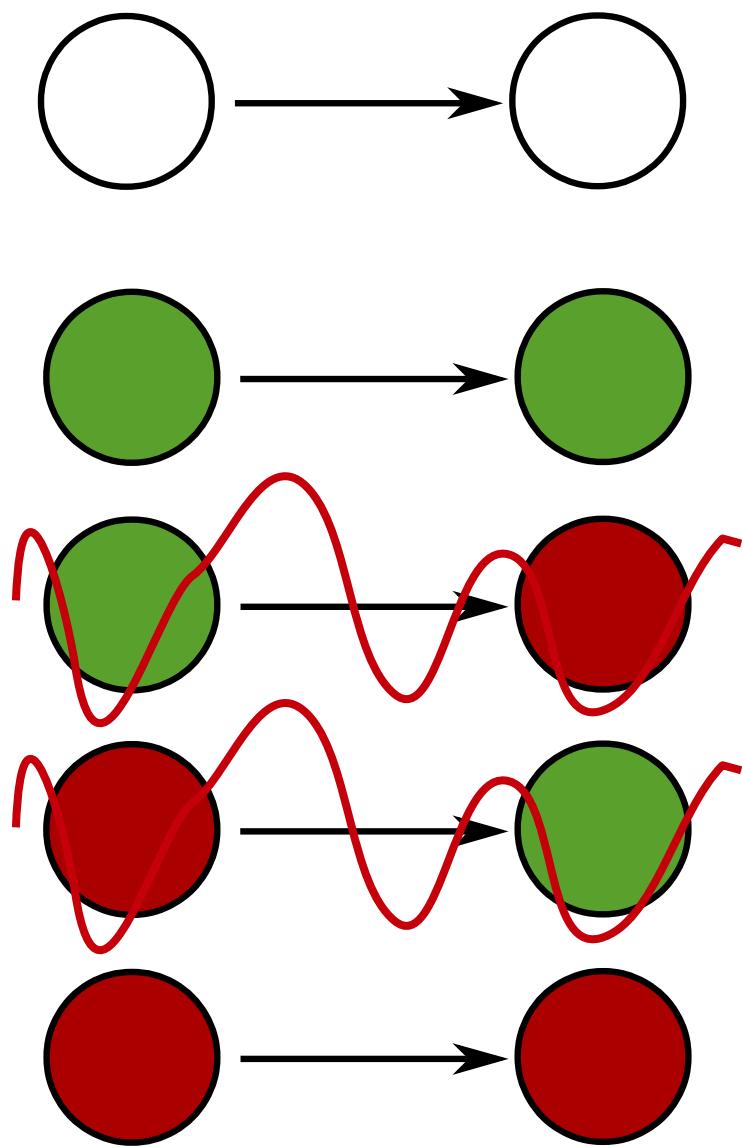
# Symbolic ML - example 1



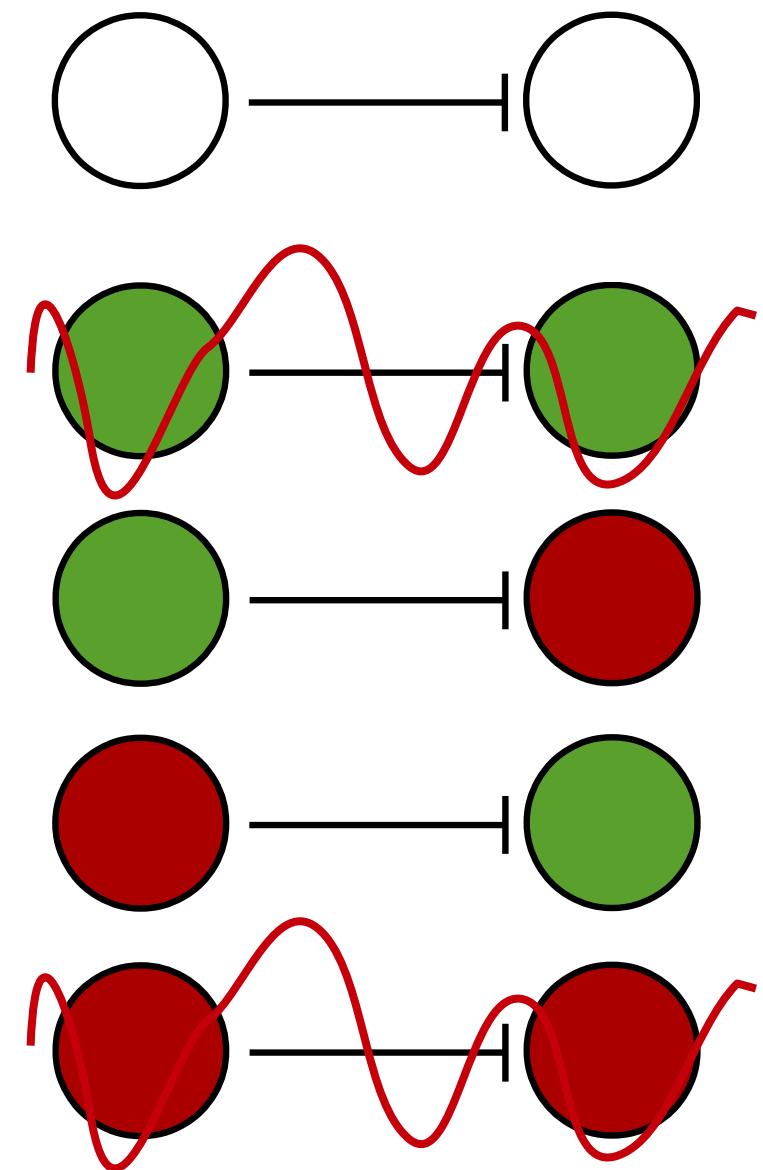
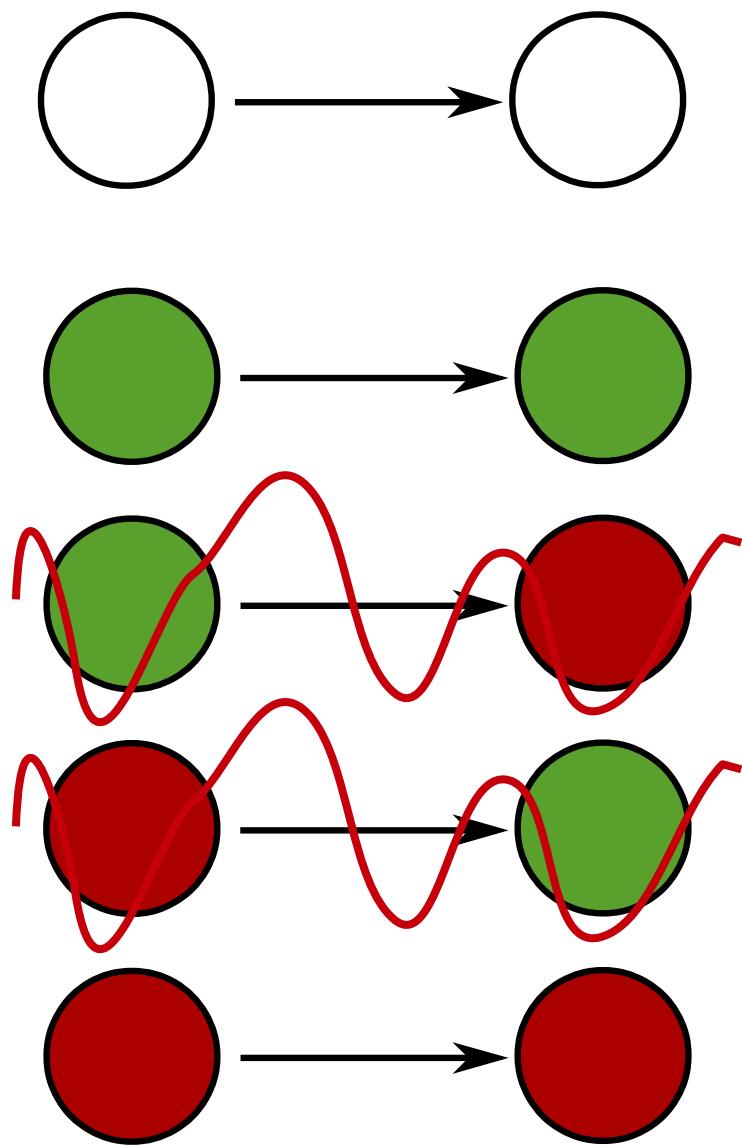
# Symbolic ML - example 1



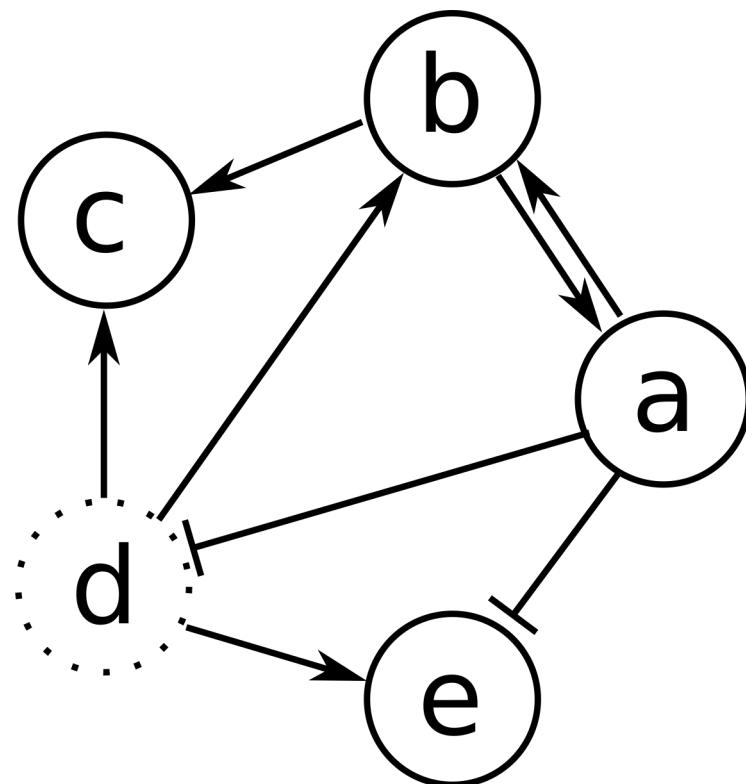
# Symbolic ML - example 1



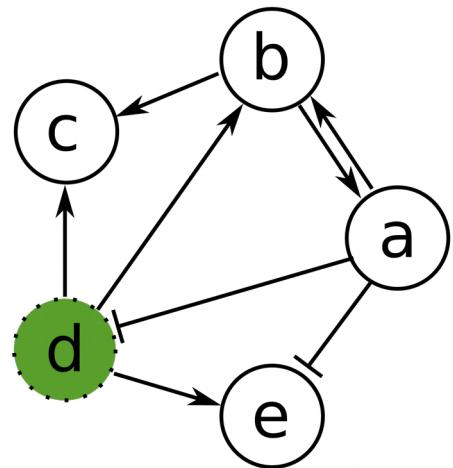
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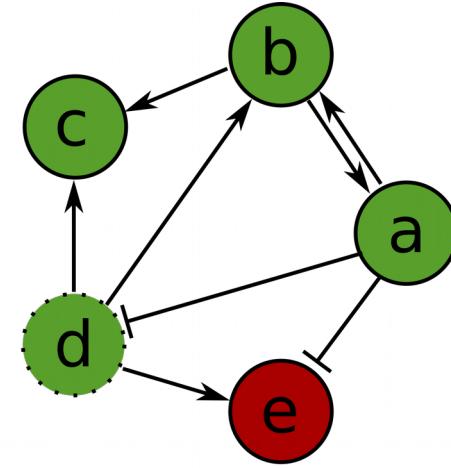
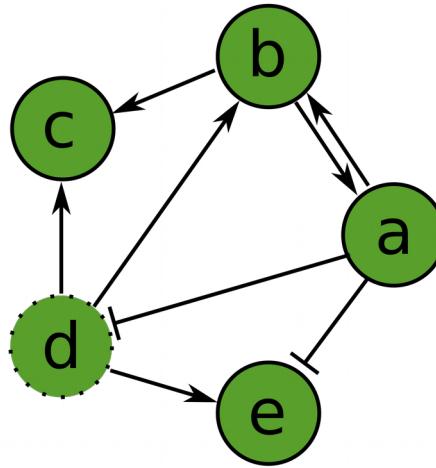
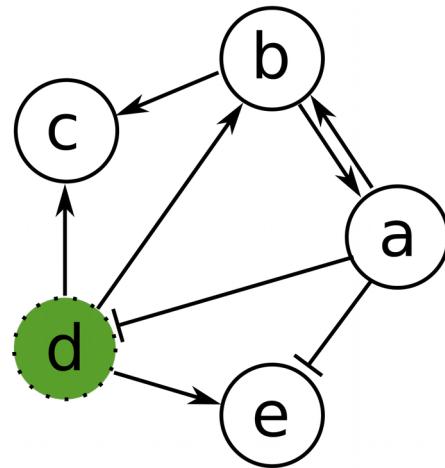
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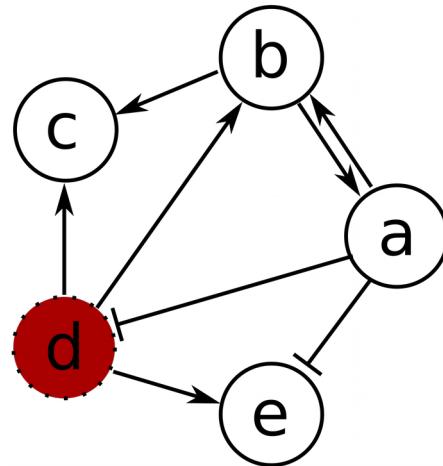
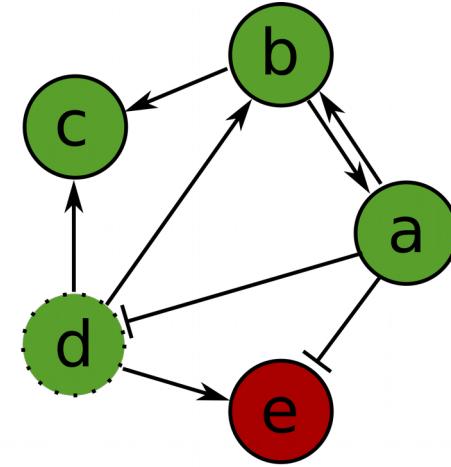
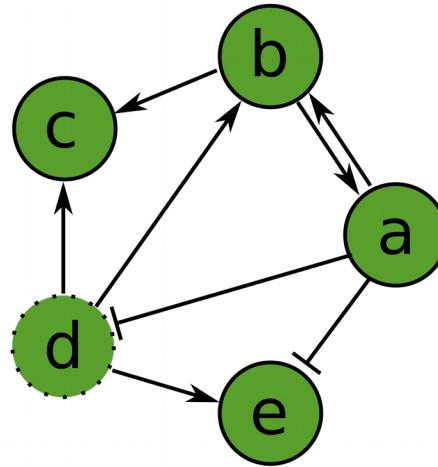
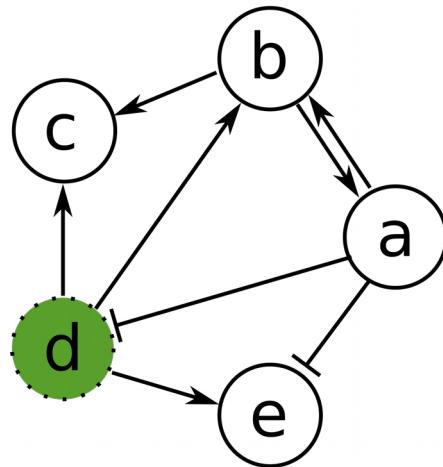
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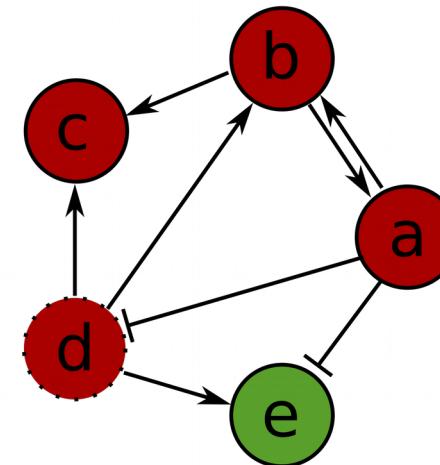
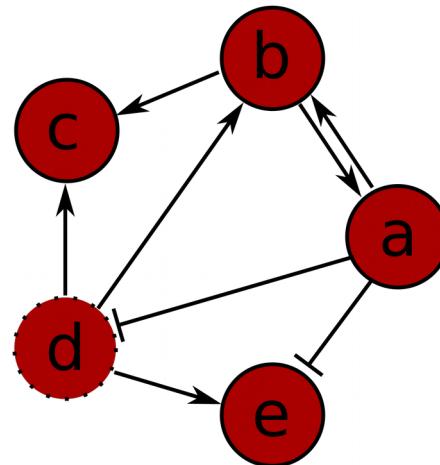
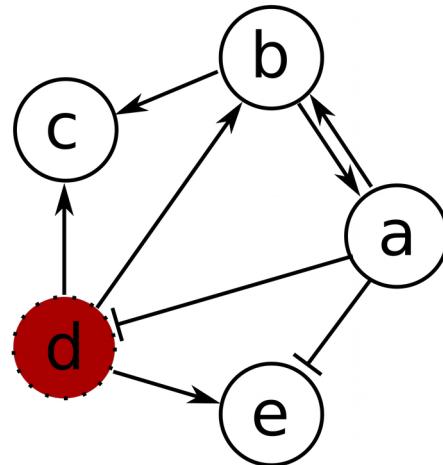
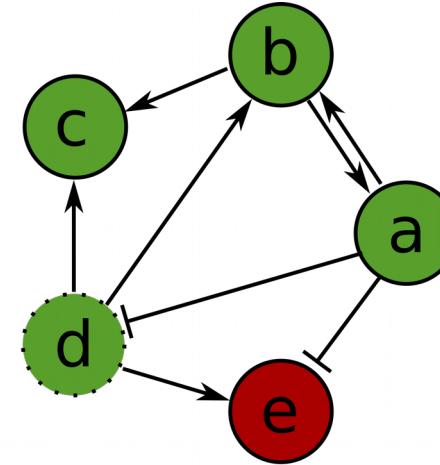
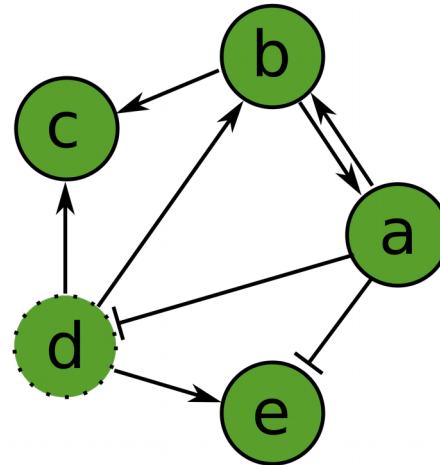
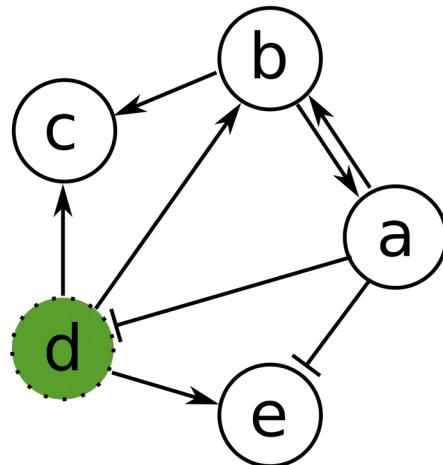
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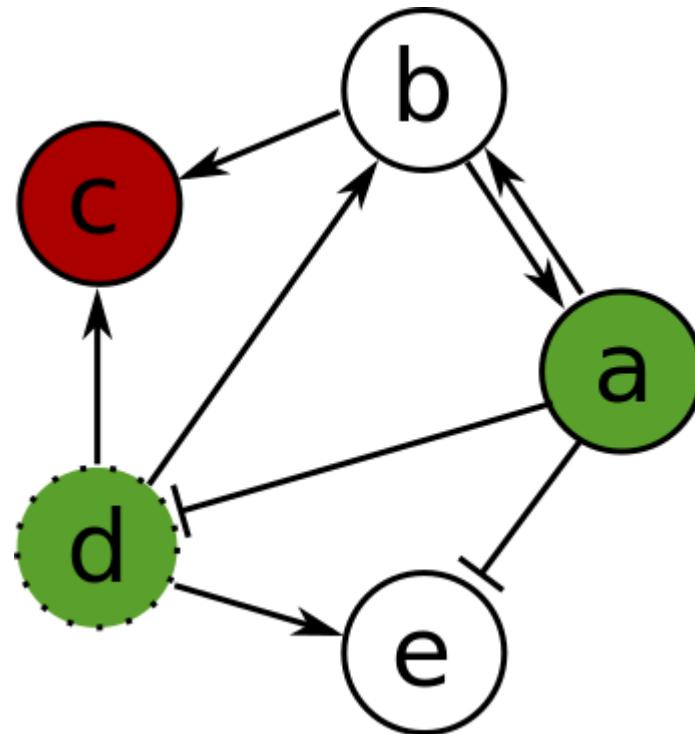
# Symbolic ML - example 1



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# Symbolic ML - example 1



# Symbolic ML - example 1

- Gebser et al. “Repair and Prediction (Under Inconsistency) in Large Biological Networks with Answer Set Programming”

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- algorithms: Answer Set Programming (Clingo) to automate **consistency checks** and **model revision**
- initial model: *E. coli* (RegulonDB, 5150 interactions)
- data: Exponential-Stationary growth shift (Bradley et al. 2007) & Heatshock experiment (Allen et al. 2003)

# Symbolic ML - example 1

	data repair (sign)	model repair (interaction sign or input node)
Exp.-Stationary growth	40	42
Heatshock	34	94

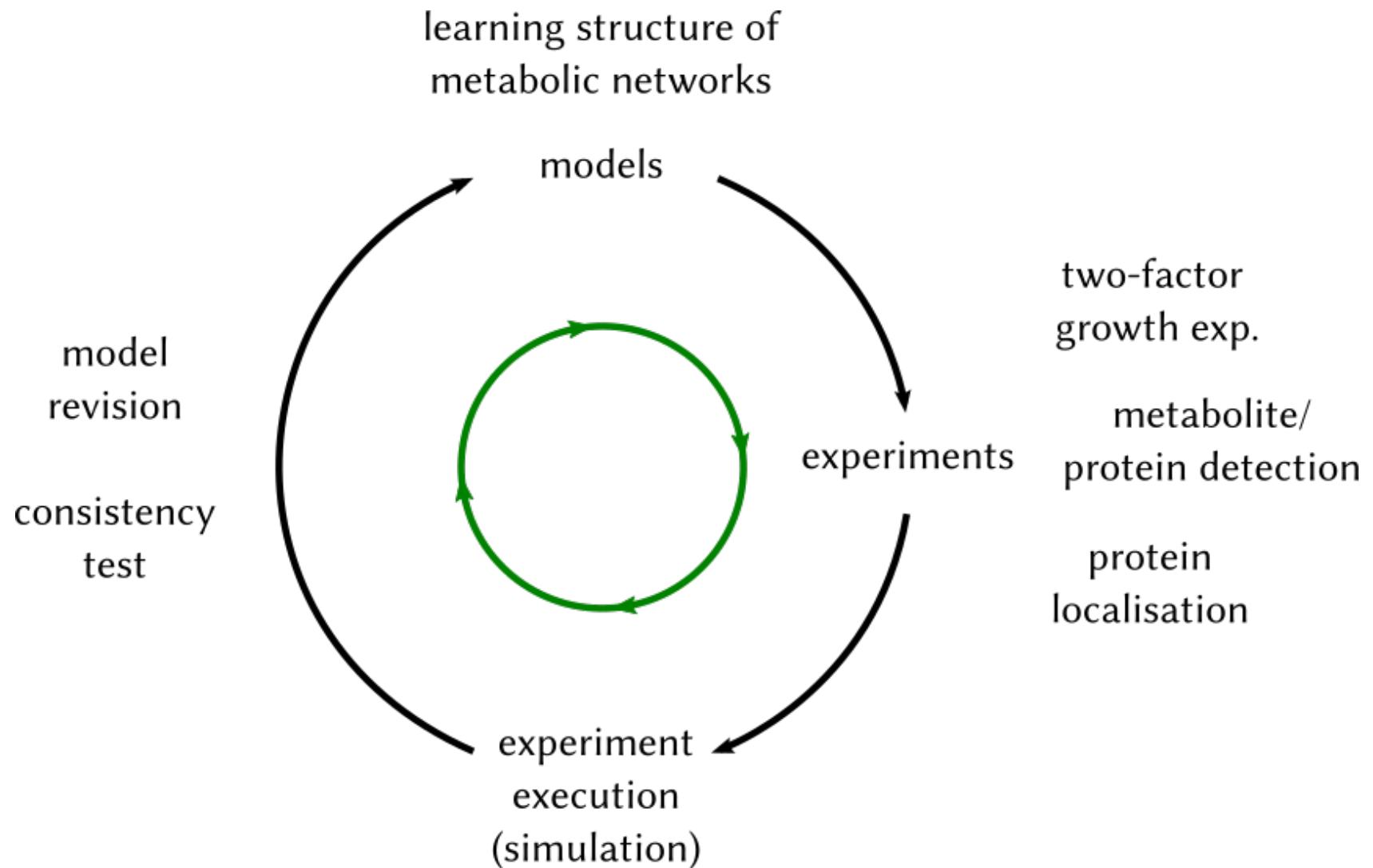
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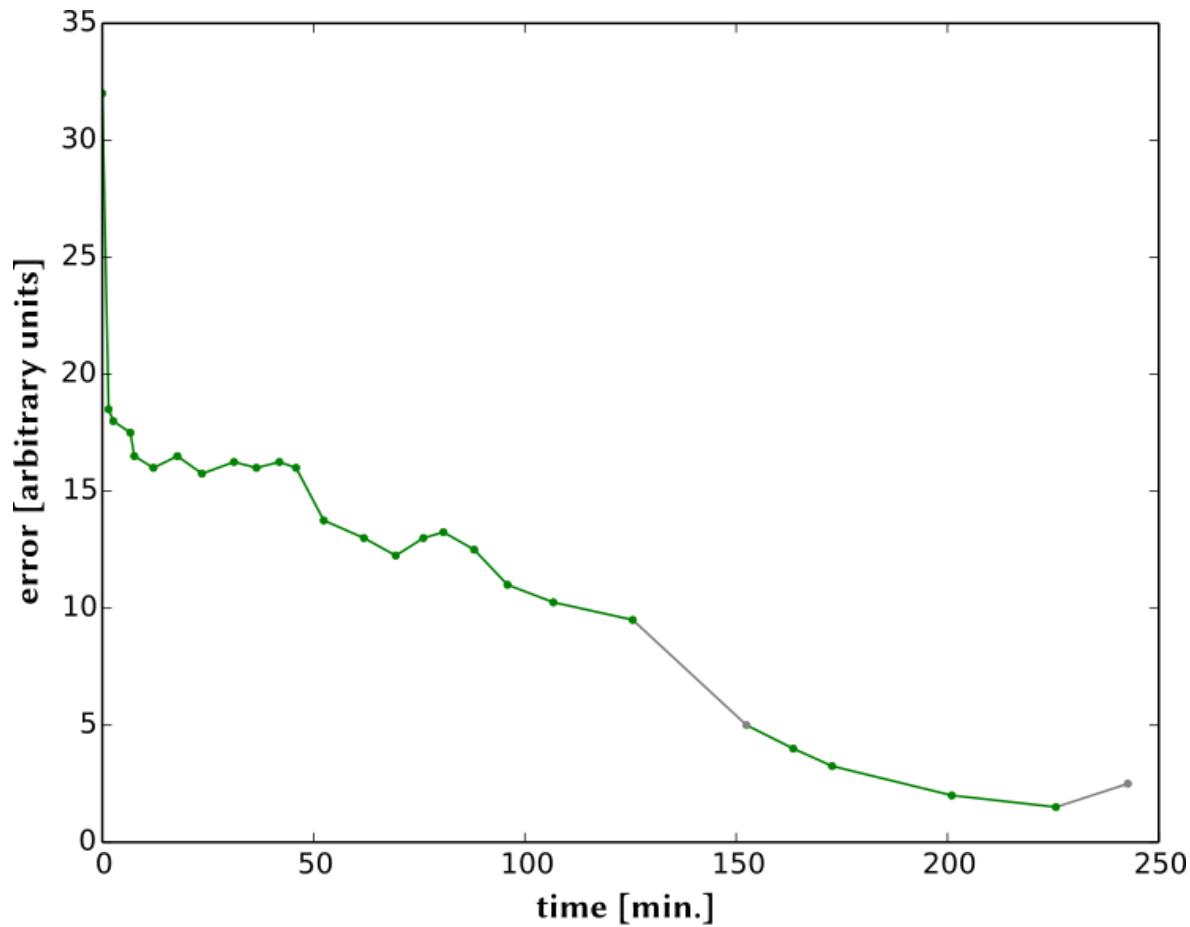
the method produces repairs of high quality:  
predictions from minimal repairs for unobserved  
nodes conform with test data (>90% accuracy  
rate)

# Symbolic ML - example 2

# Symbolic ML - example 2



# Symbolic ML - example 2

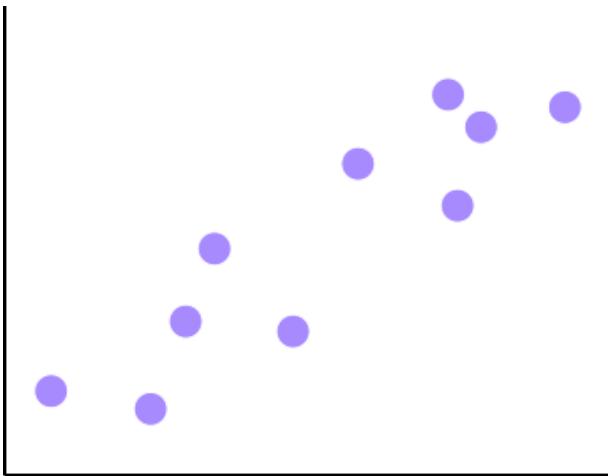


avg. error reduction: 76%

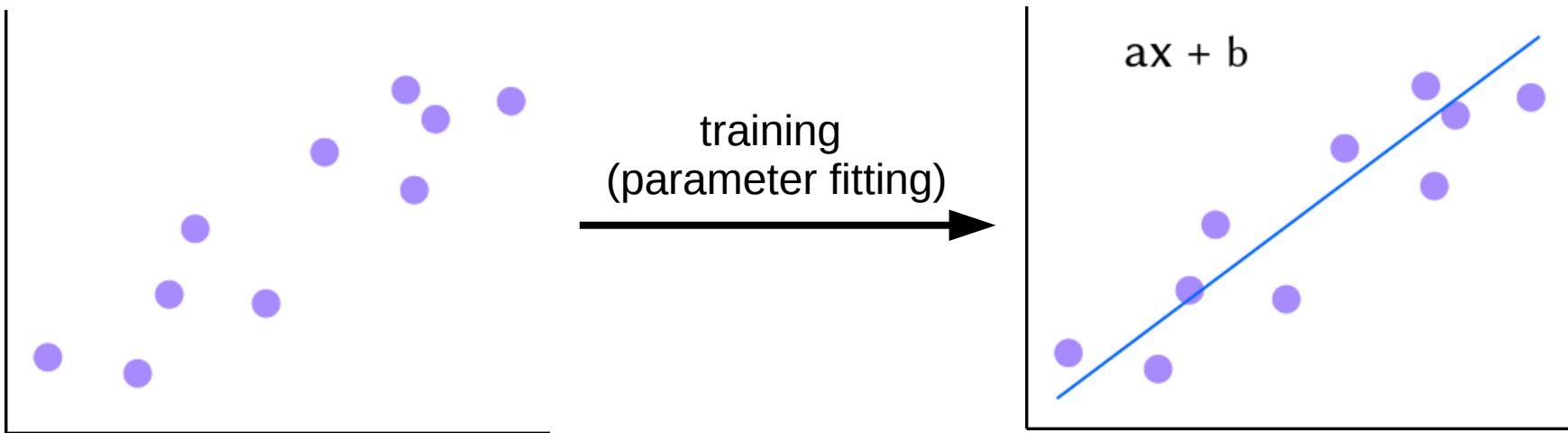
25-86 reactions

# Standard Supervised ML

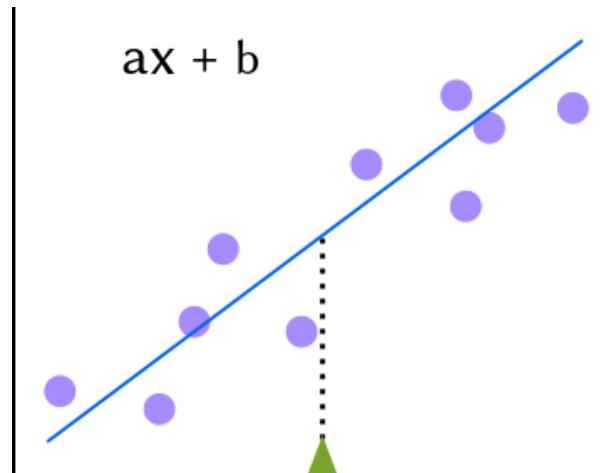
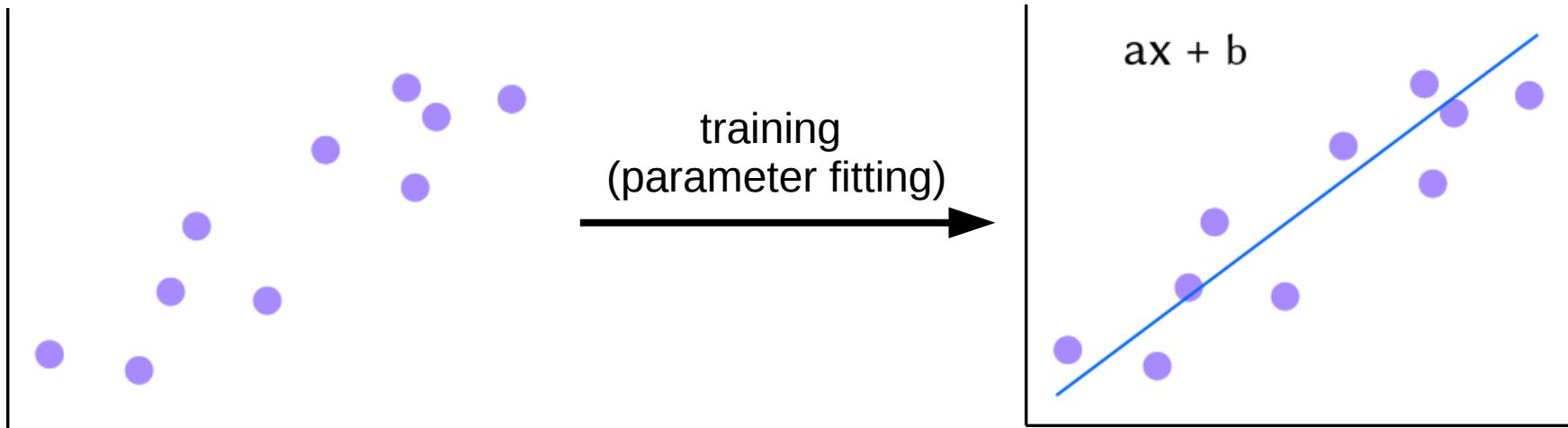
# Standard Supervised ML



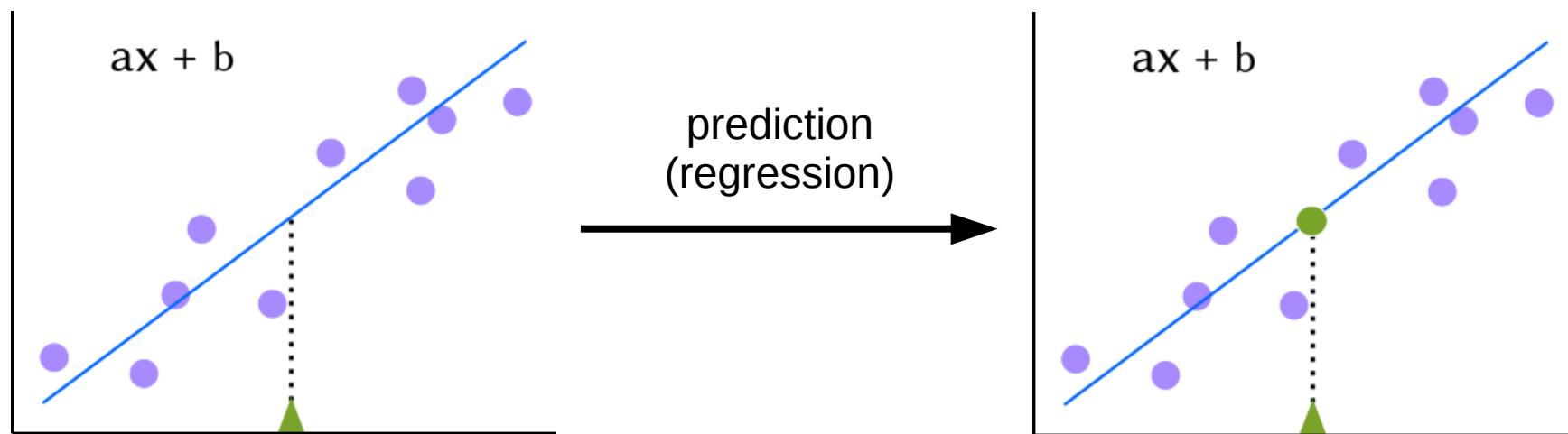
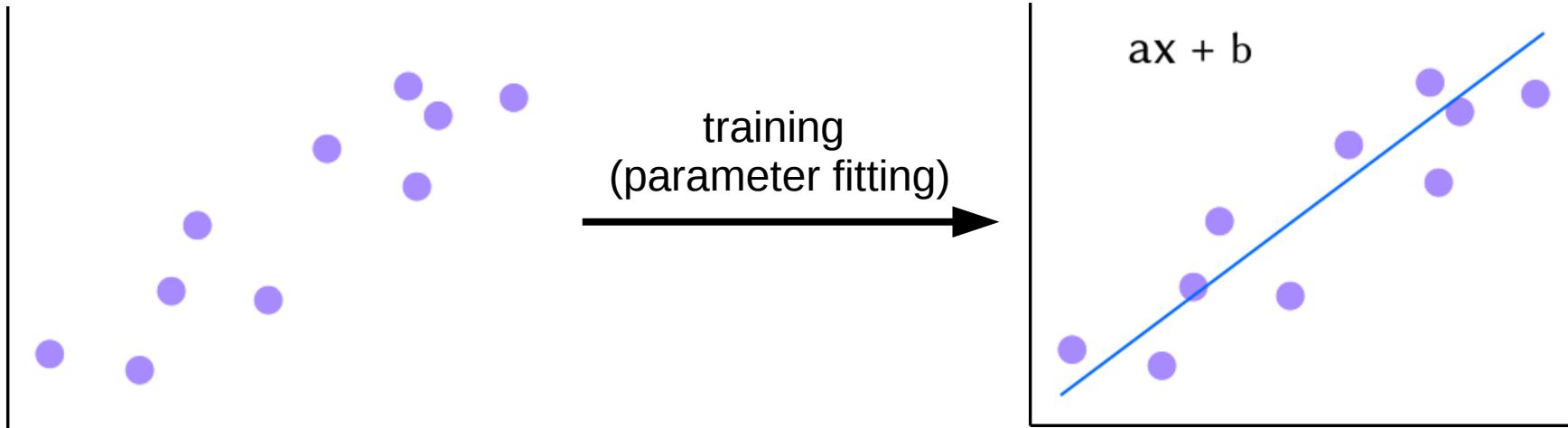
# Standard Supervised ML



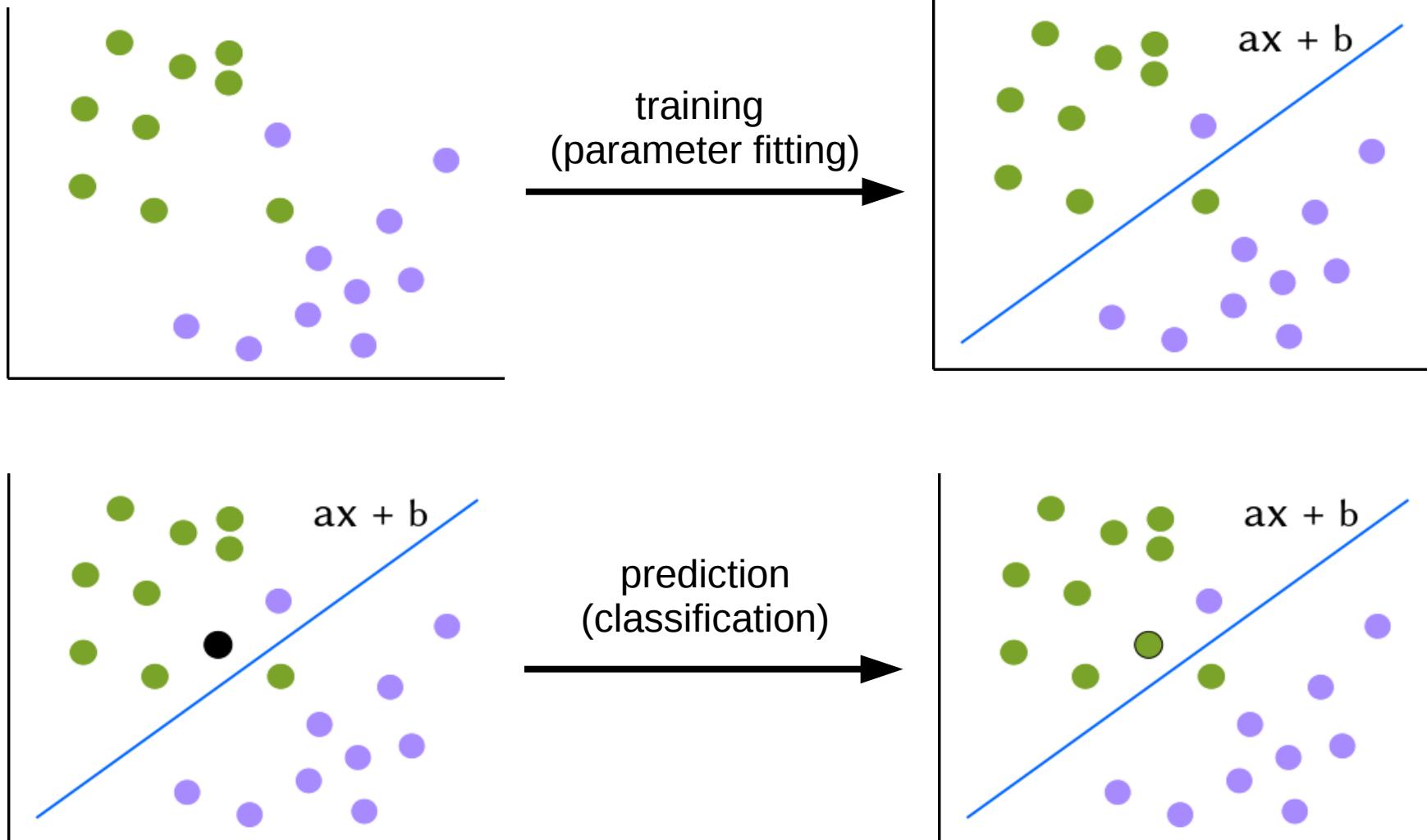
# Standard Supervised ML



# Standard Supervised ML



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# Standard Supervised ML

training data

labels            features

1.34 [0.33, 0.4, 0.67, -0.52]

3.56 [0.29, 0.73, 0.55, 0.12]

2.21 [0.36, 0.24, 0.47, 0.29]

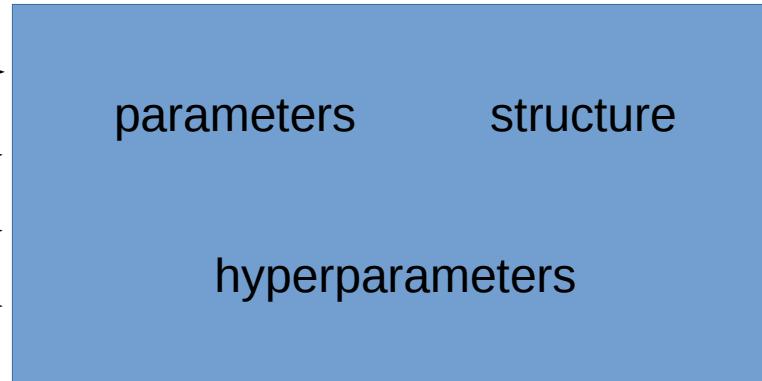
0.78 [0.85, 0.33, -0.7, 0.23]

# Standard Supervised ML

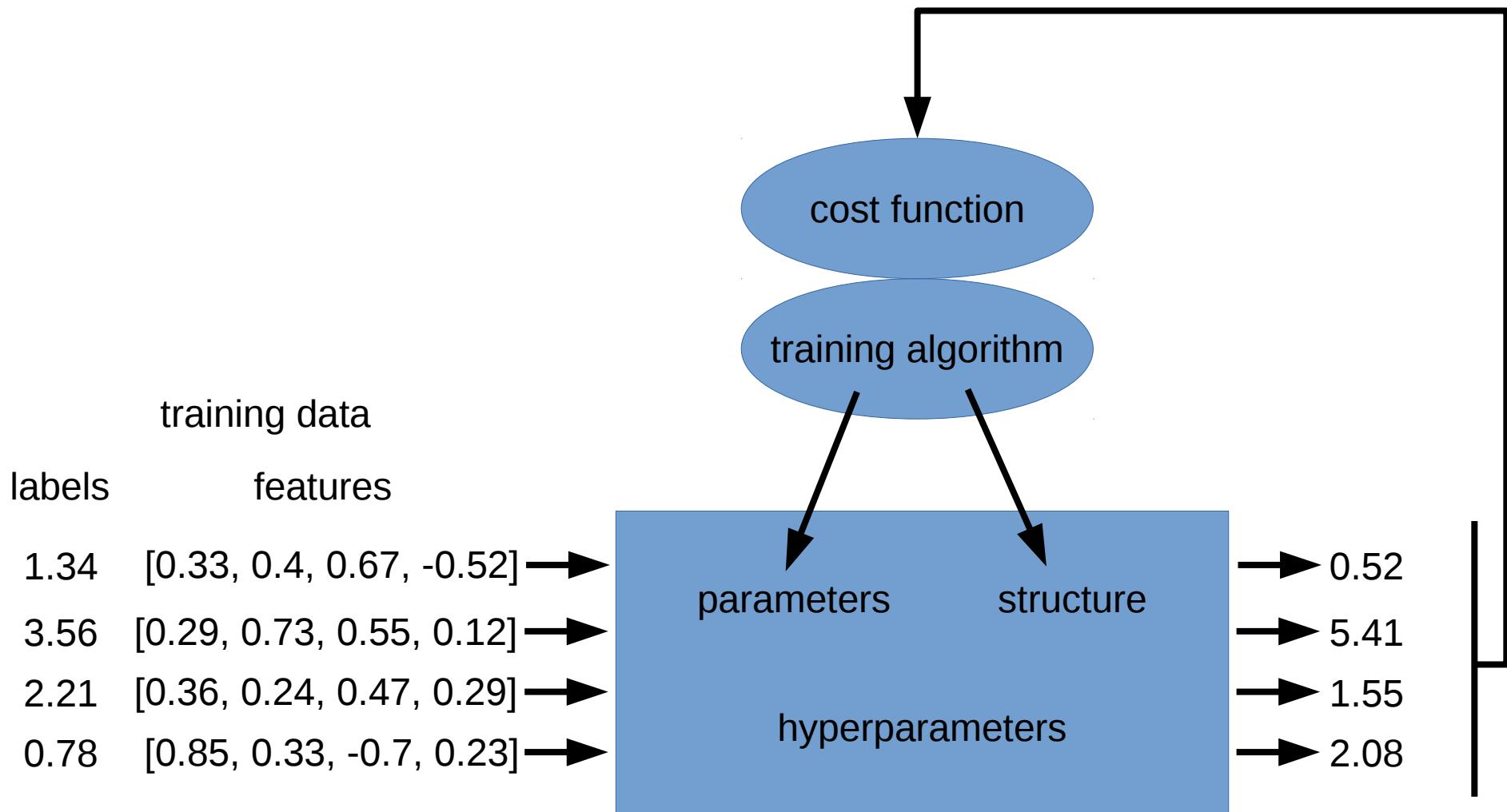
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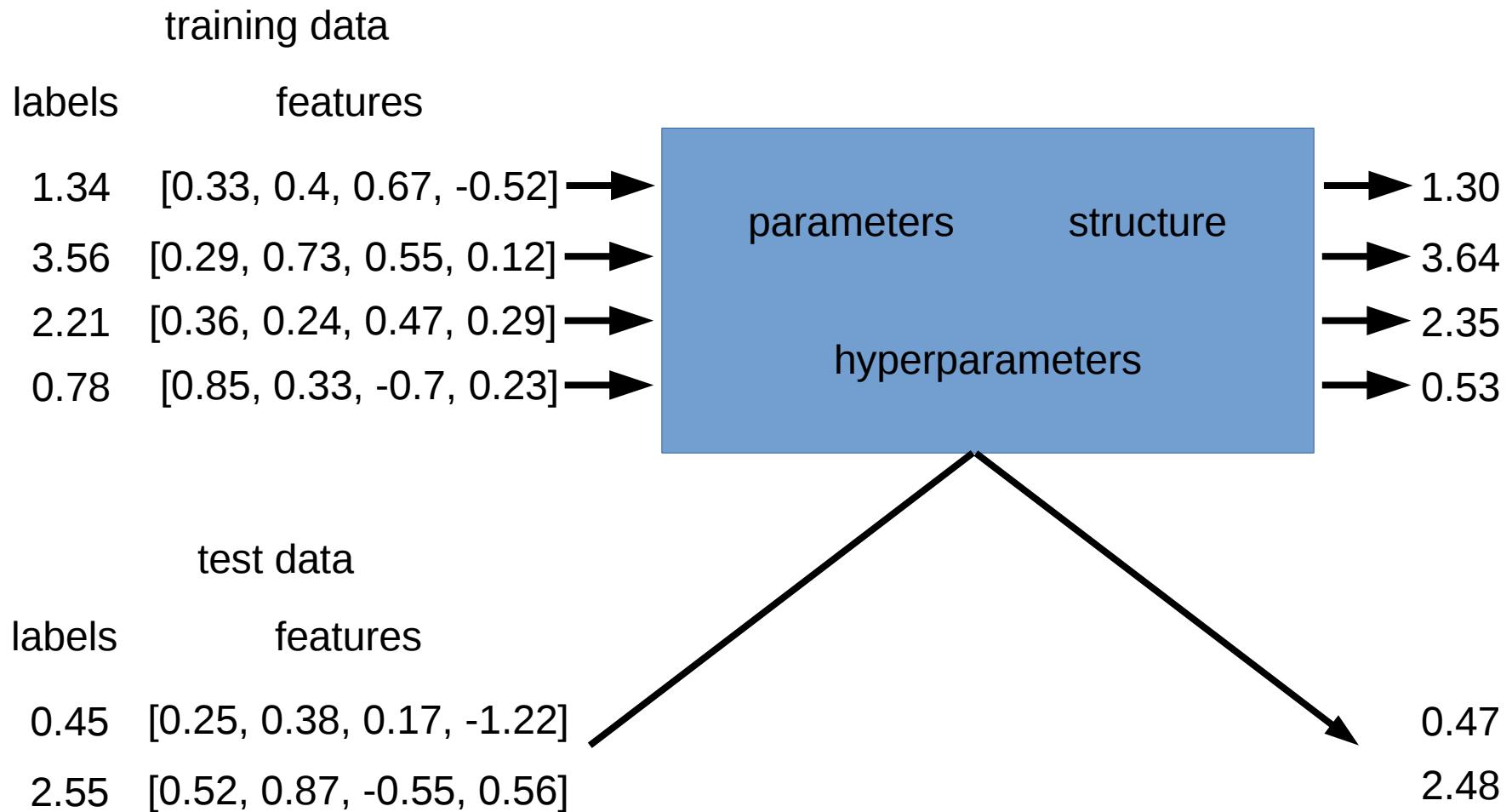
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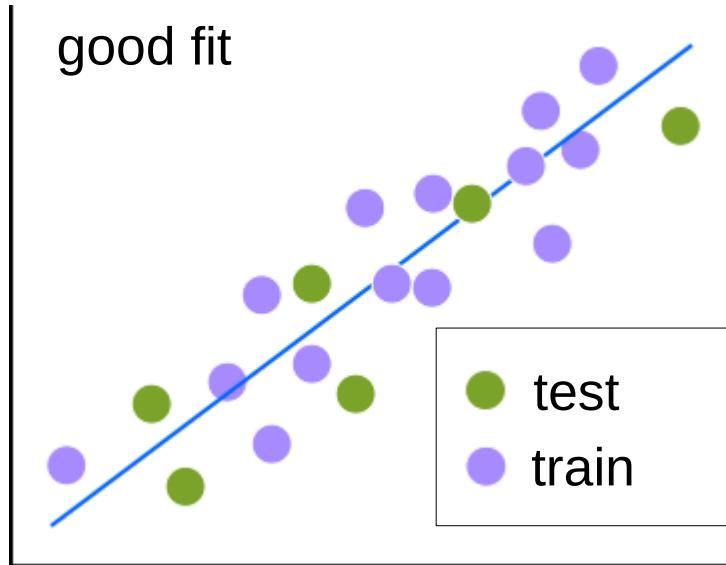
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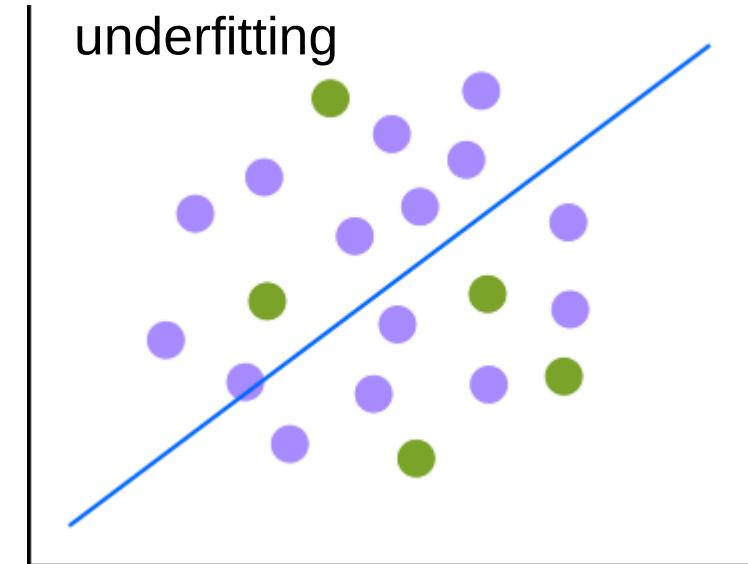
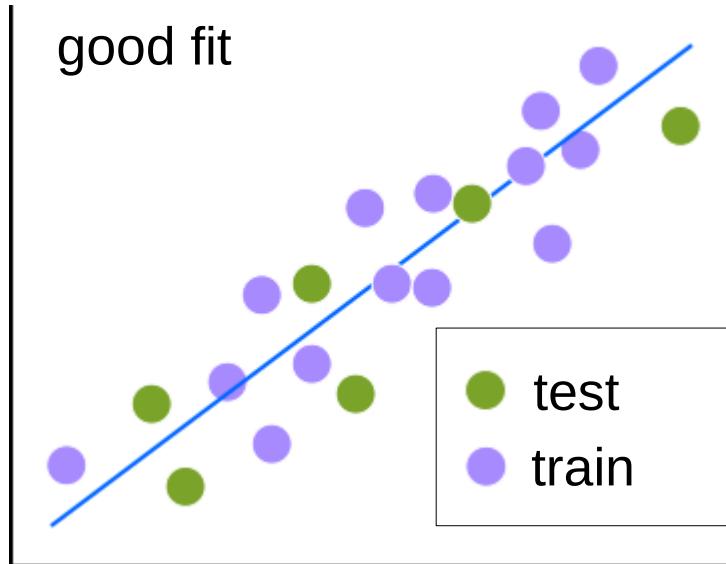
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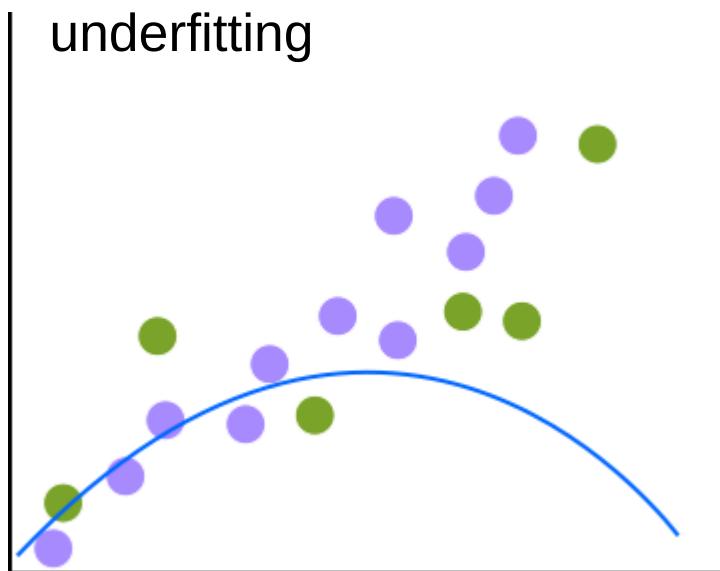
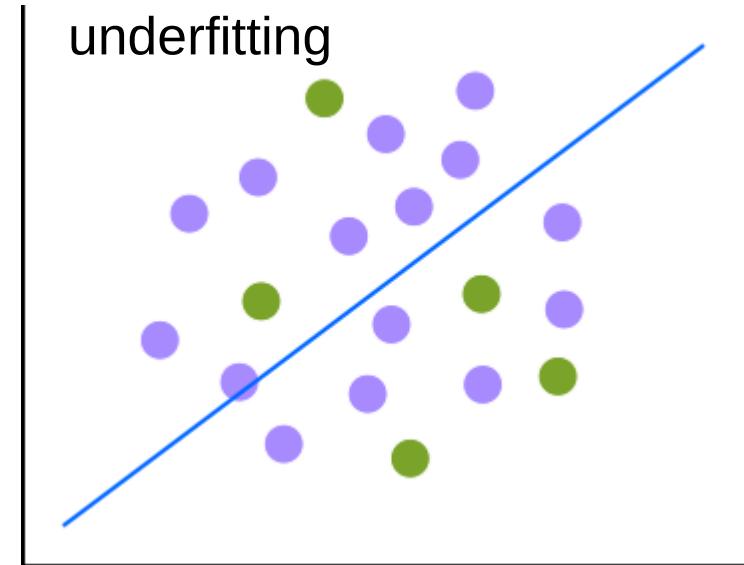
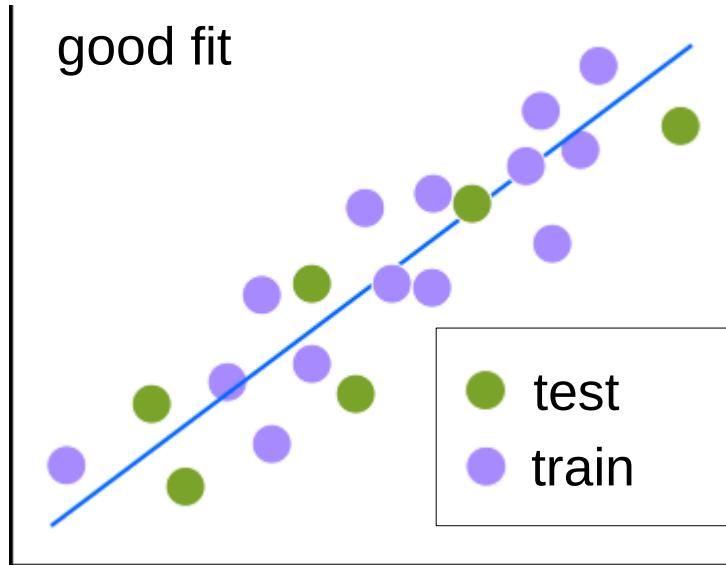
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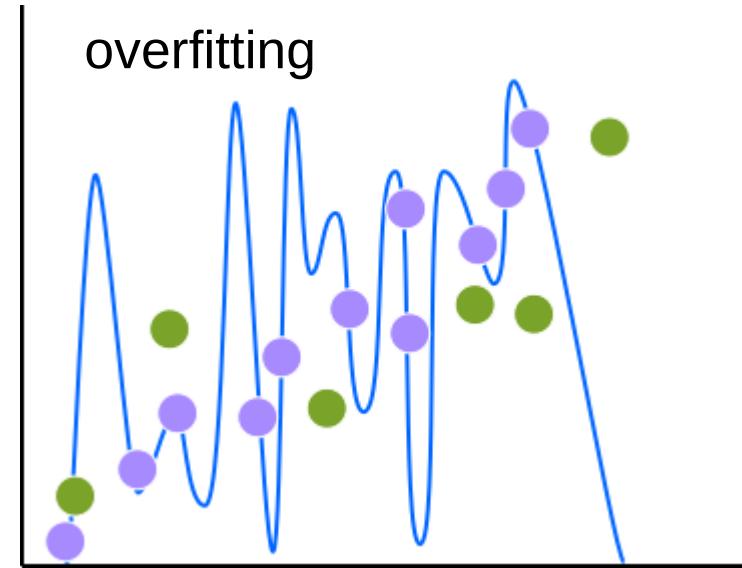
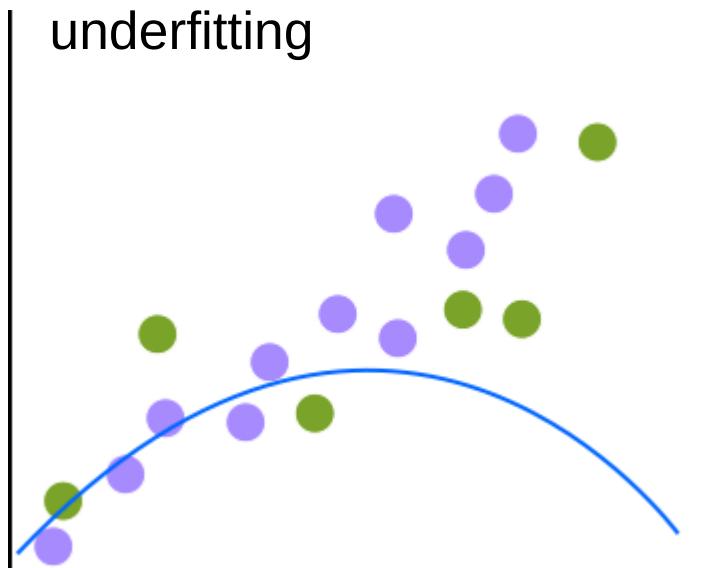
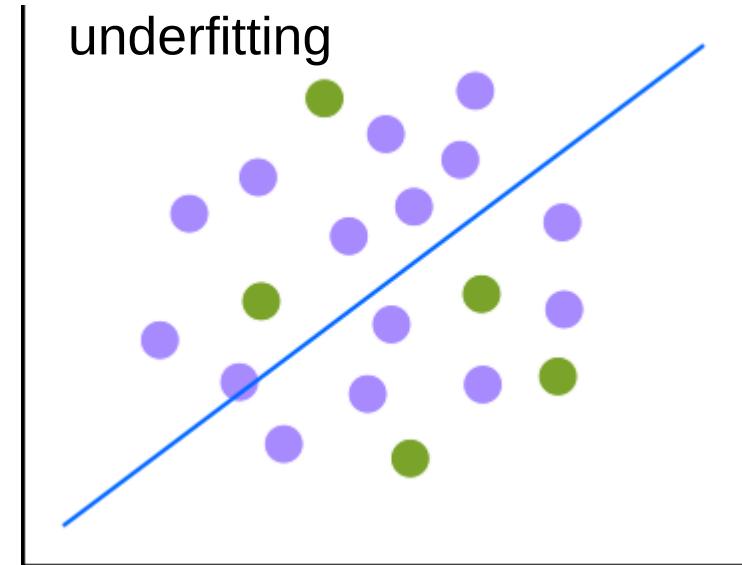
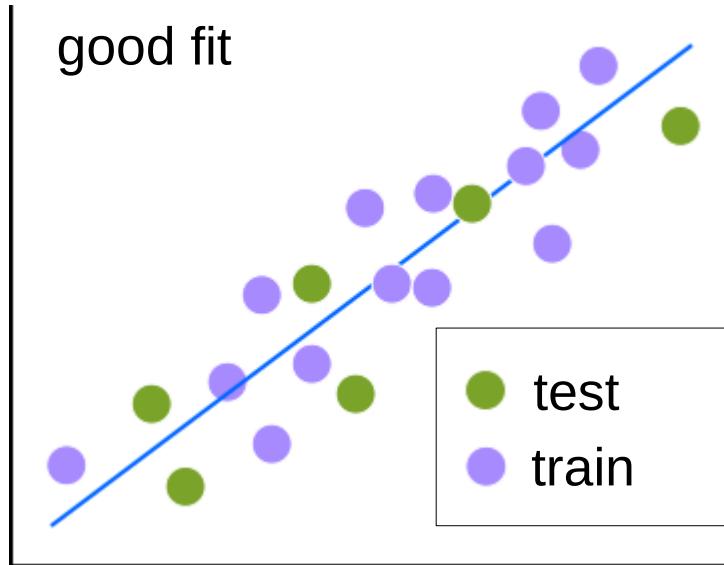
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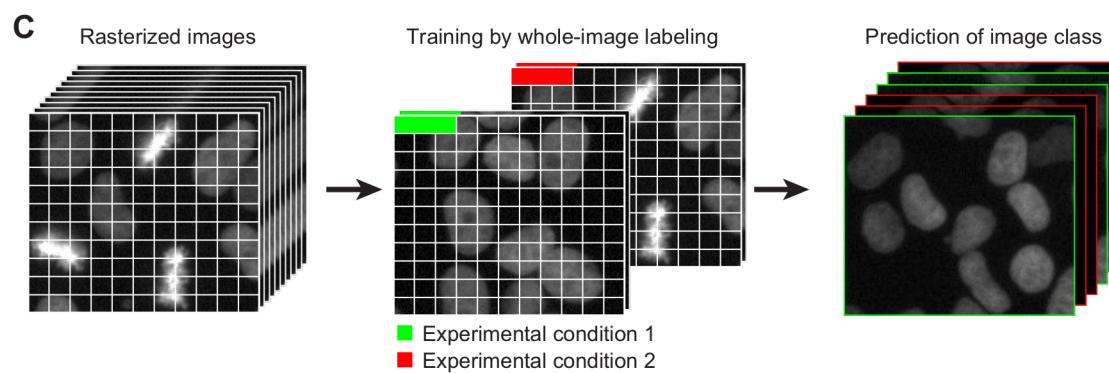
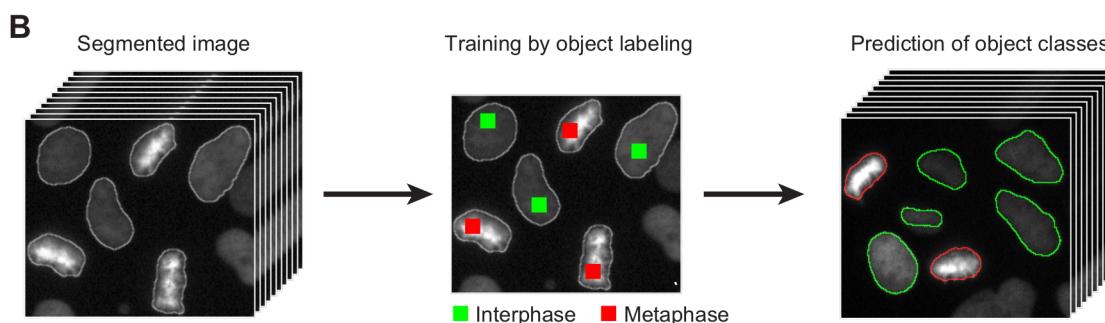
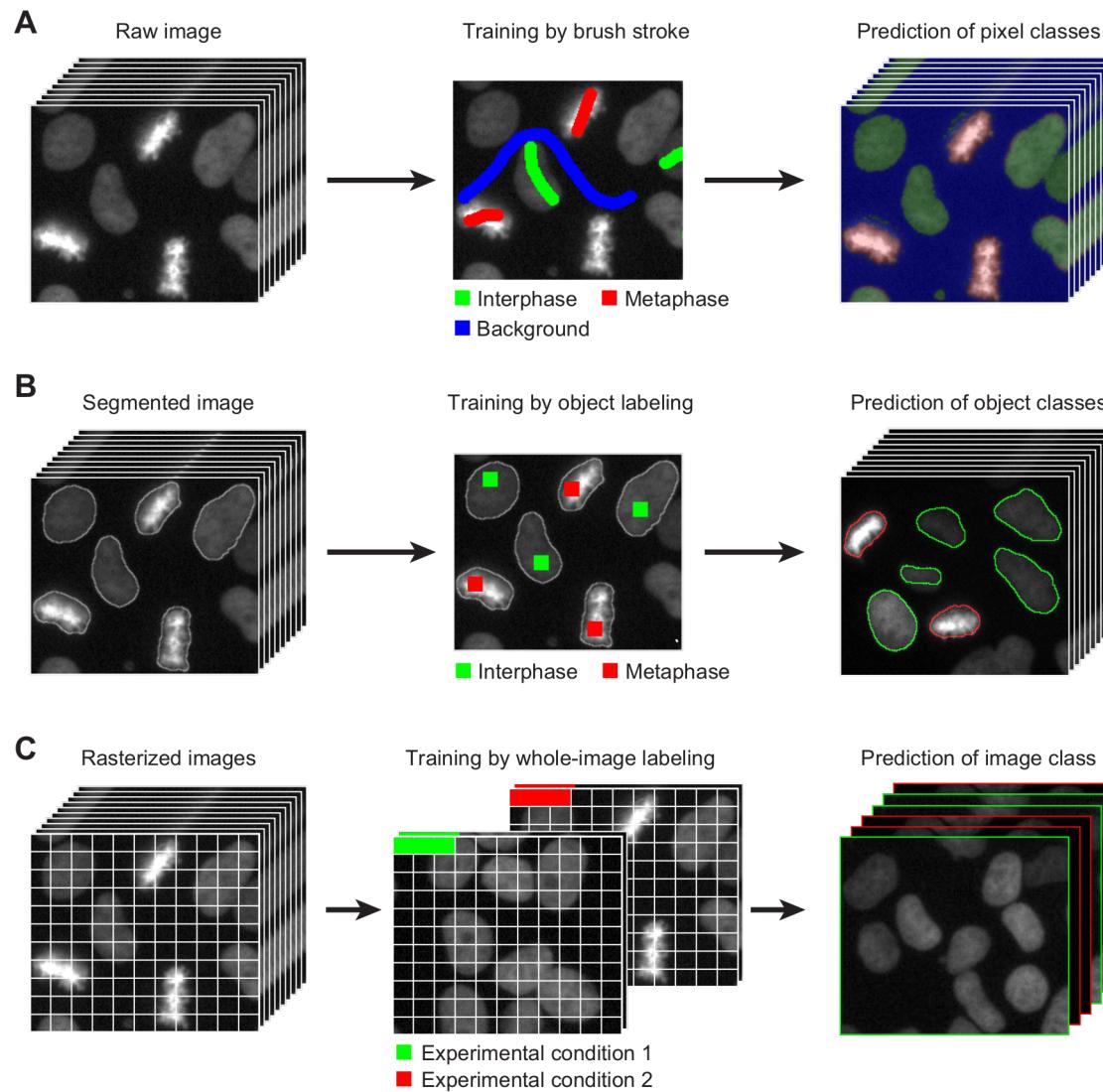
# Standard Supervised ML



# Standard Supervised ML



# Standard Supervised ML: example 1

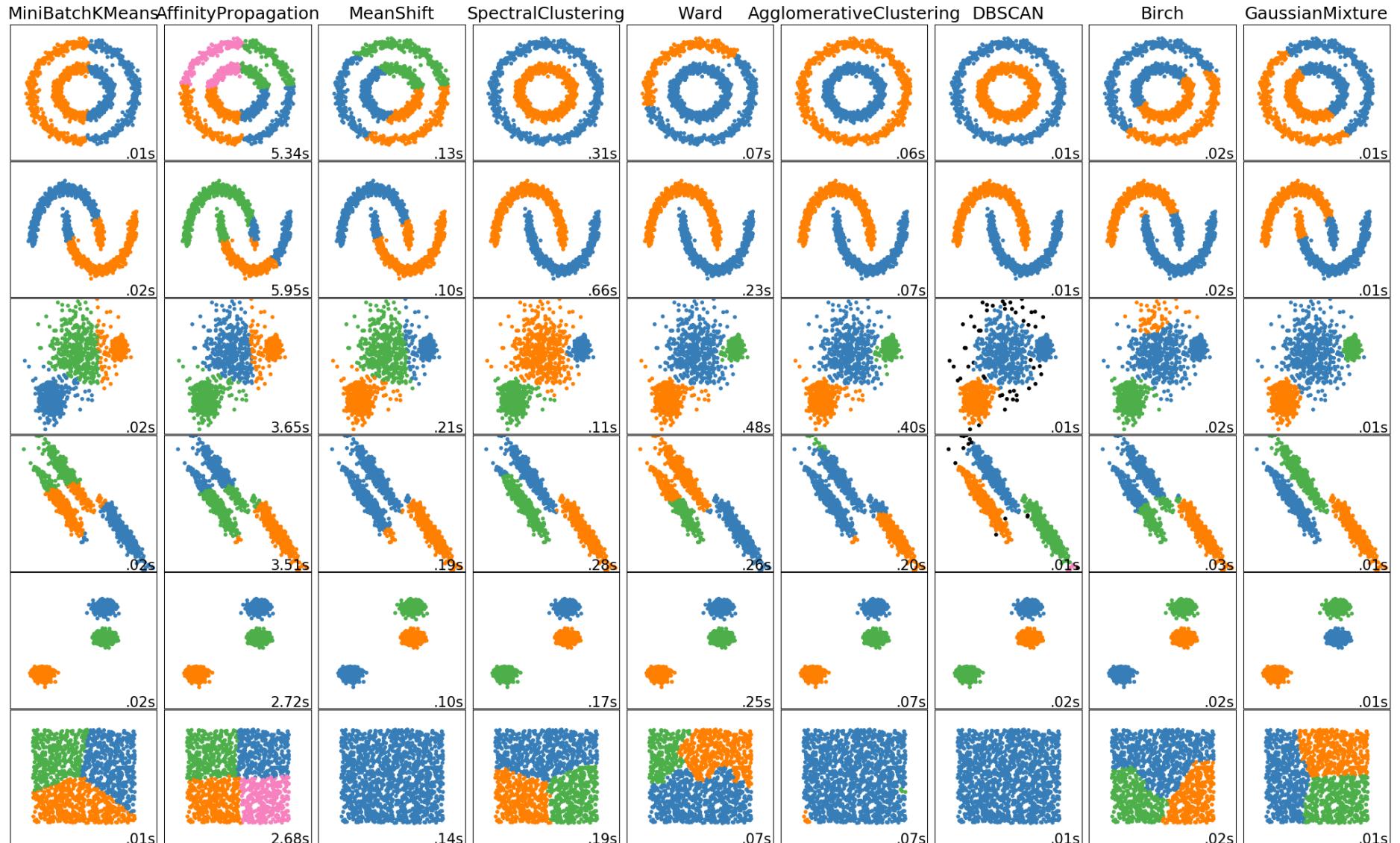


# Standard Supervised ML: example 2

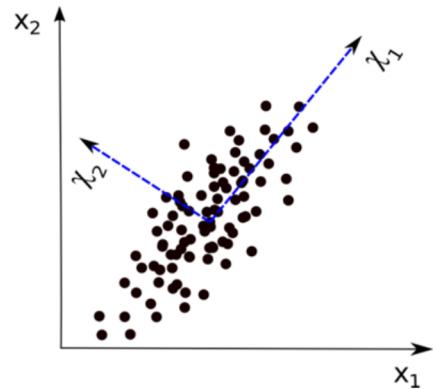
- Xu et al. A Gene Signature for Breast Cancer Prognosis Using Support Vector Machine (2012)
- 50 gene signature (microarray gene expression) used to predict metastasis using SVM (accuracy 0.97, sensitivity 0.99, specificity 0.93)
- improvement over 70 gene signature (Recursive Feature Elimination)

# Standard Unsupervised ML

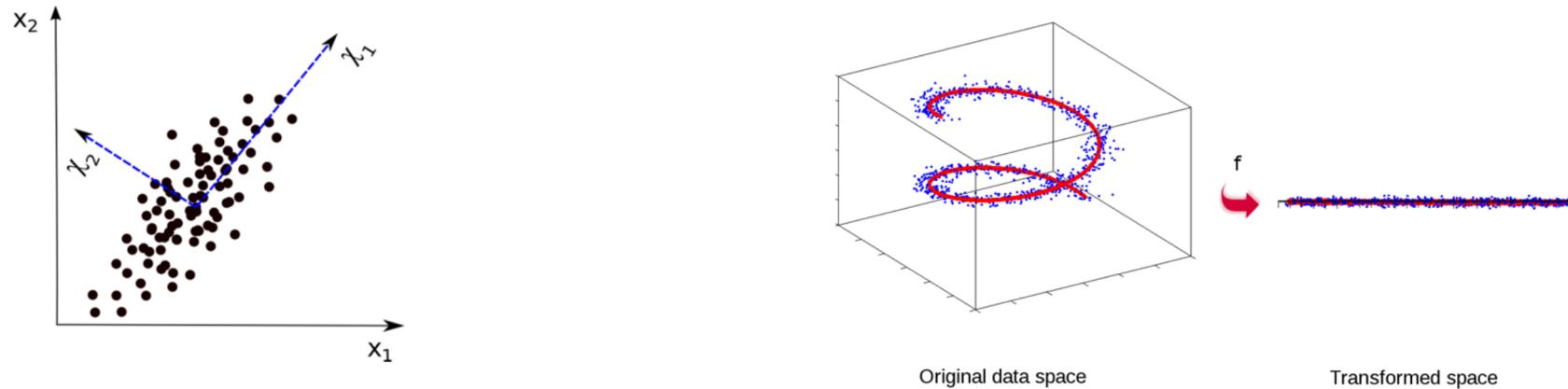
# Standard Unsupervised ML: clustering



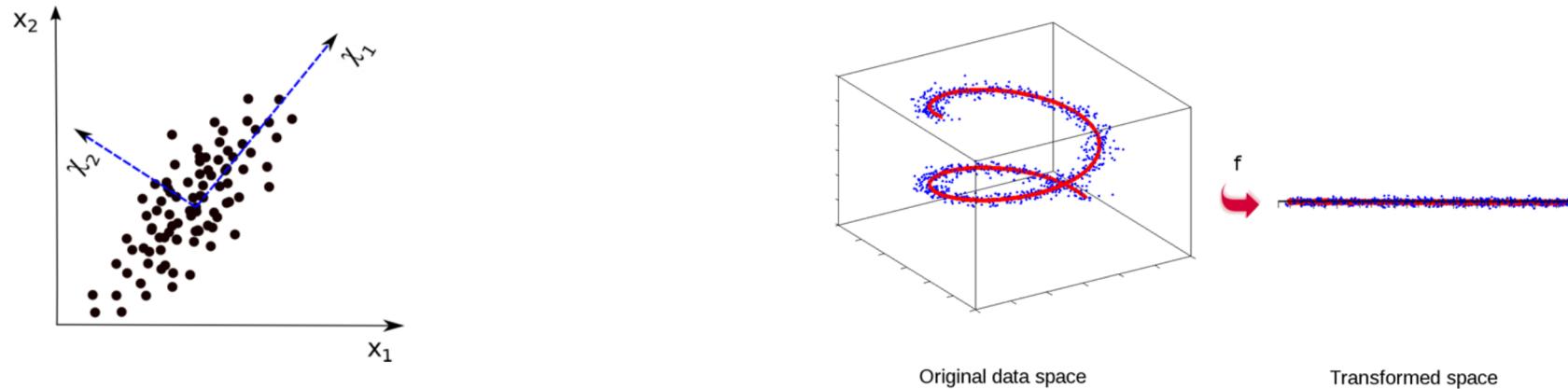
# Standard Unsupervised ML: dimensionality reduction



# Standard Unsupervised ML: dimensionality reduction

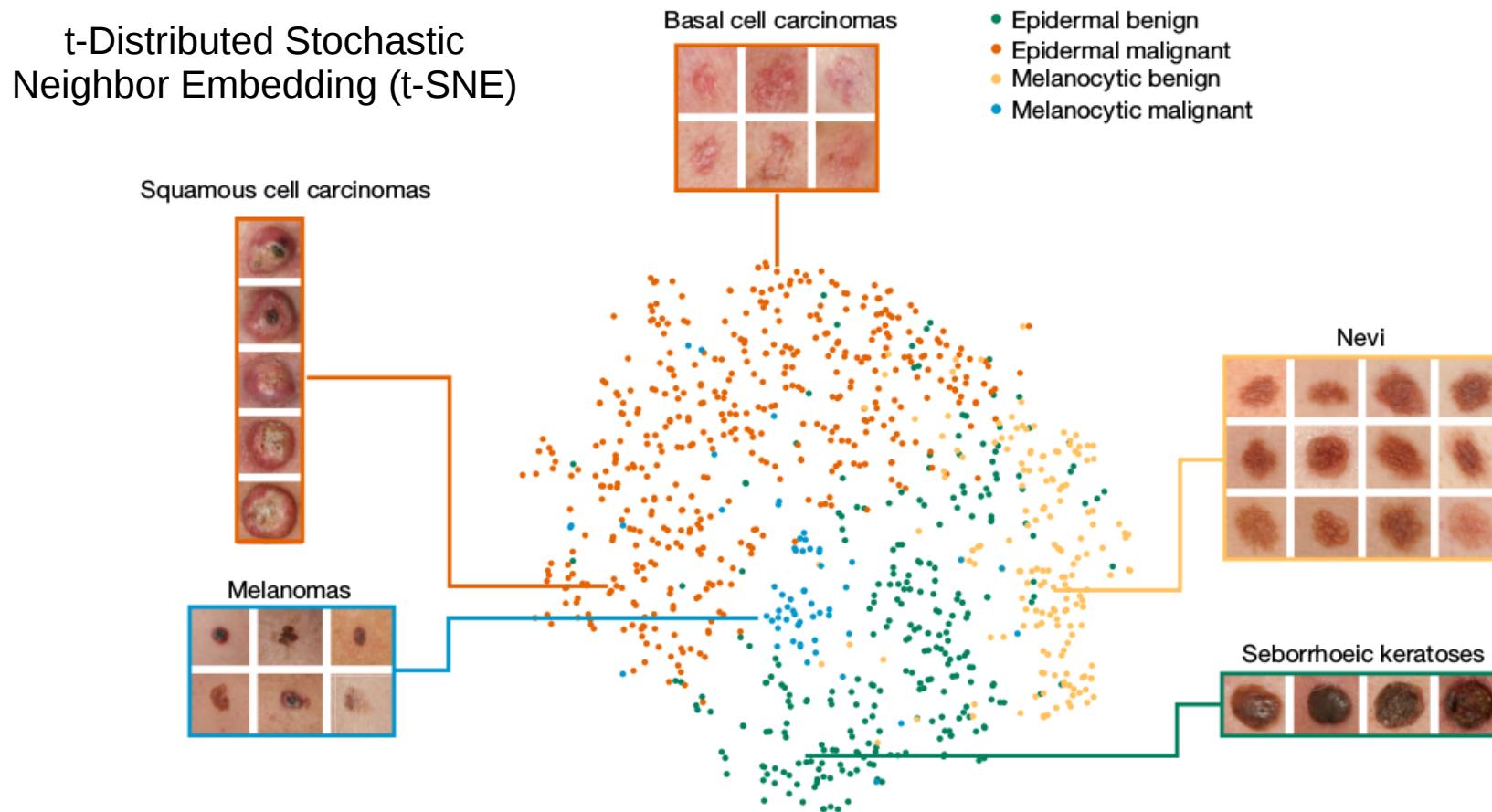


# Standard Unsupervised ML: dimensionality reduction

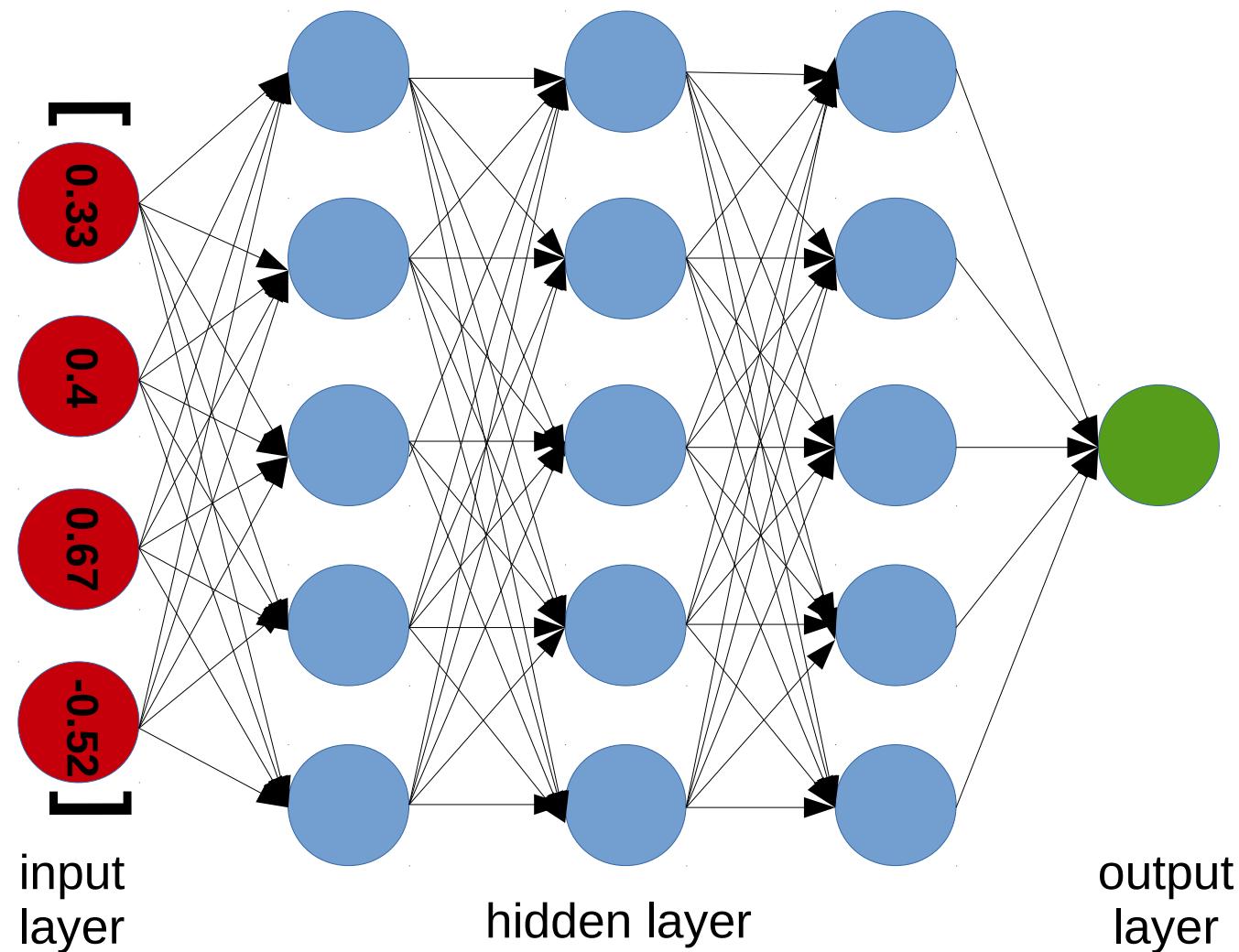


- preparation of data for further classification, regression, etc.
- visualization and analysis
- generative models

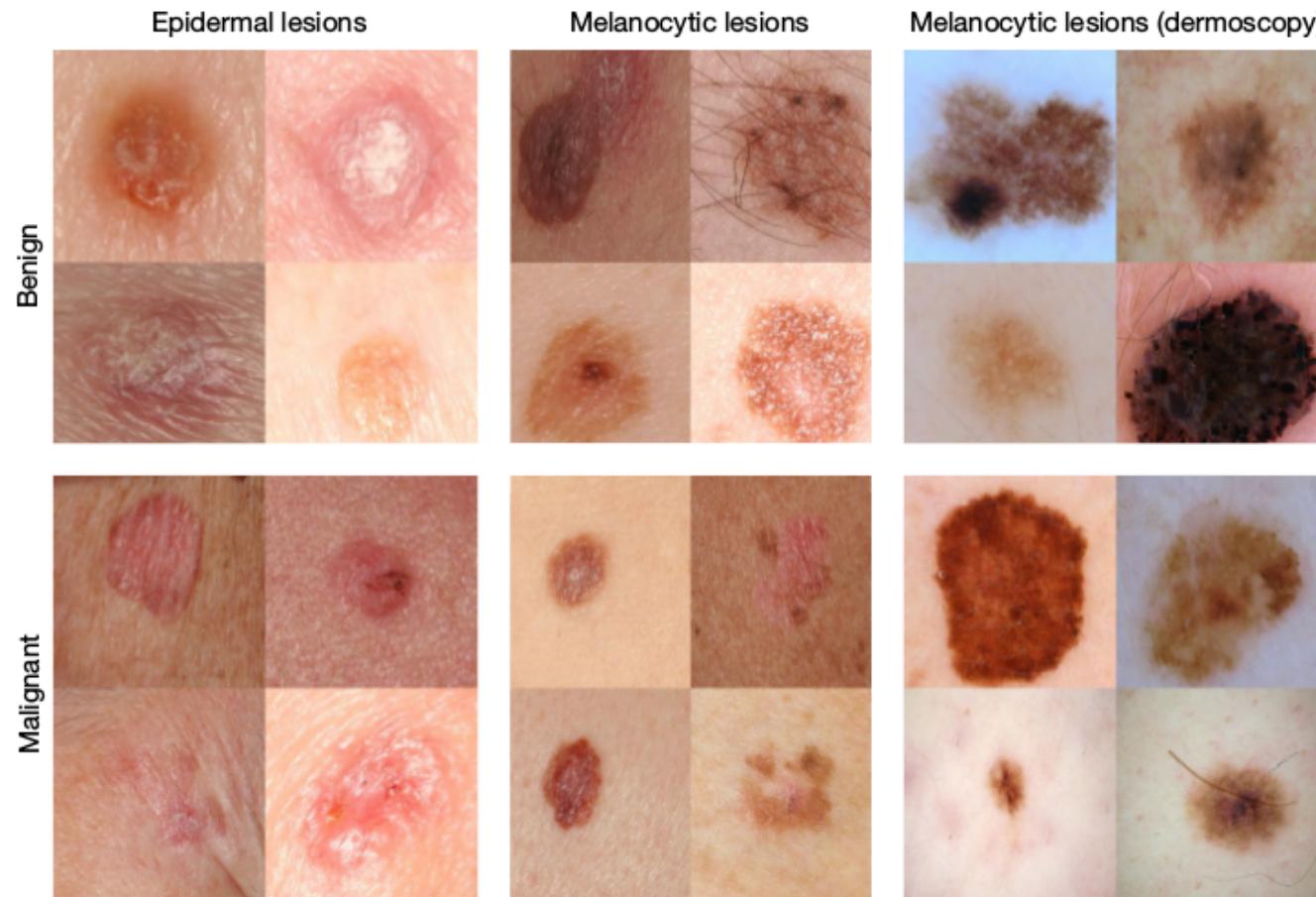
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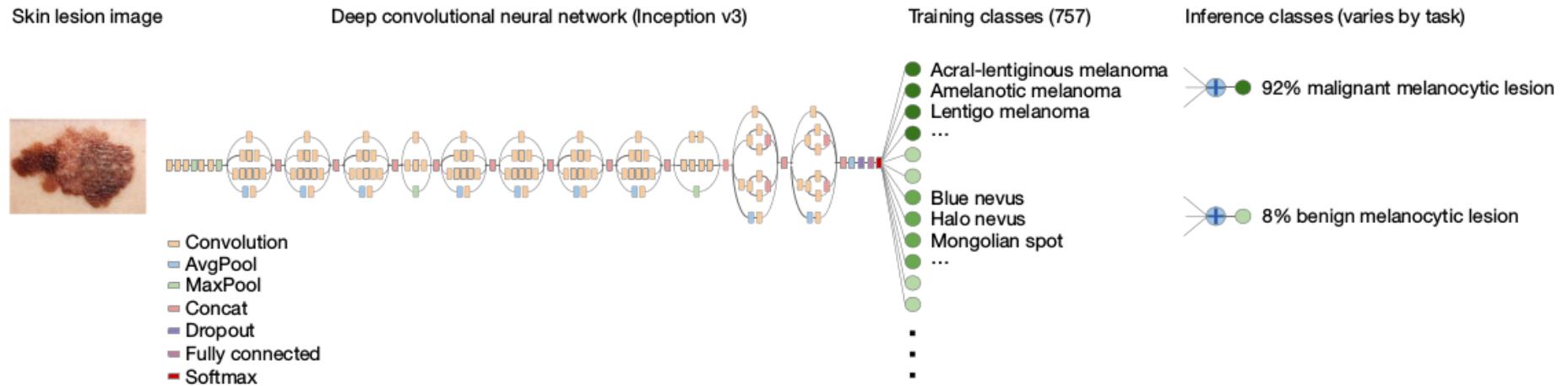
# Deep Learning (Neural Networks)



# Deep Learning (Neural Networks): example

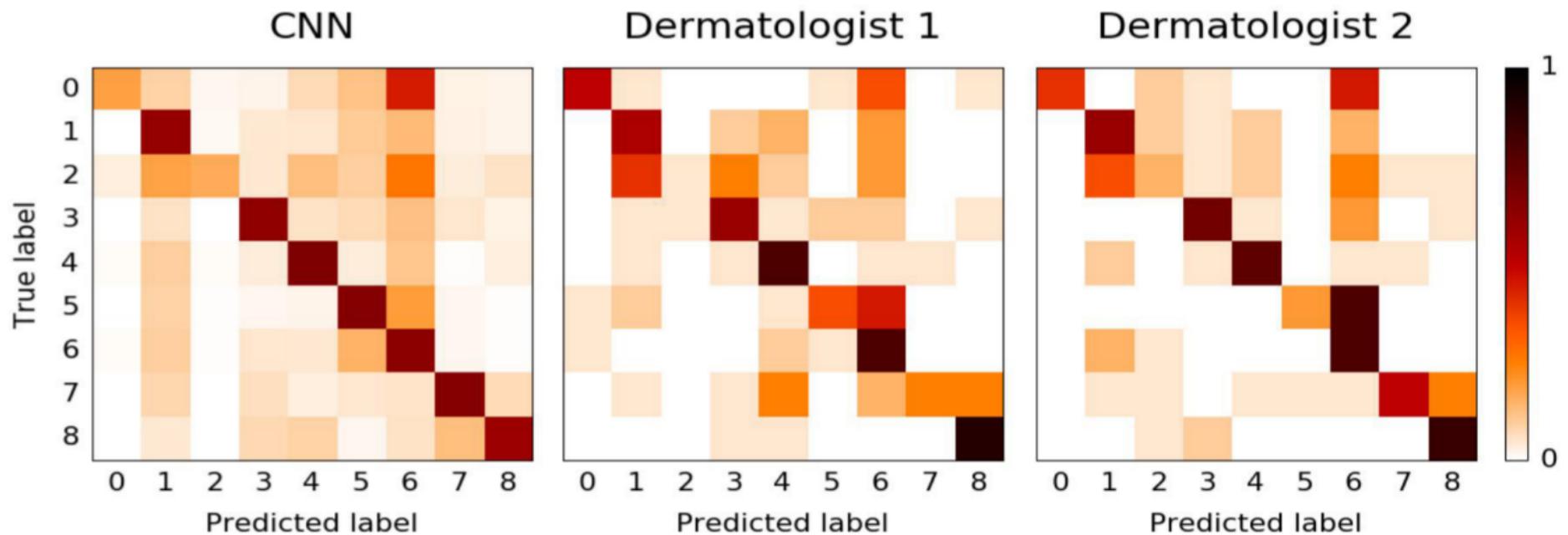


# Deep Learning (Neural Networks): example



- base model: Google Inception v3 CNN (pretrained 1.28 million images / 1,000 classes)
- transfer learning: 129,450 skin lesions / 757 classes (2,032 different diseases)

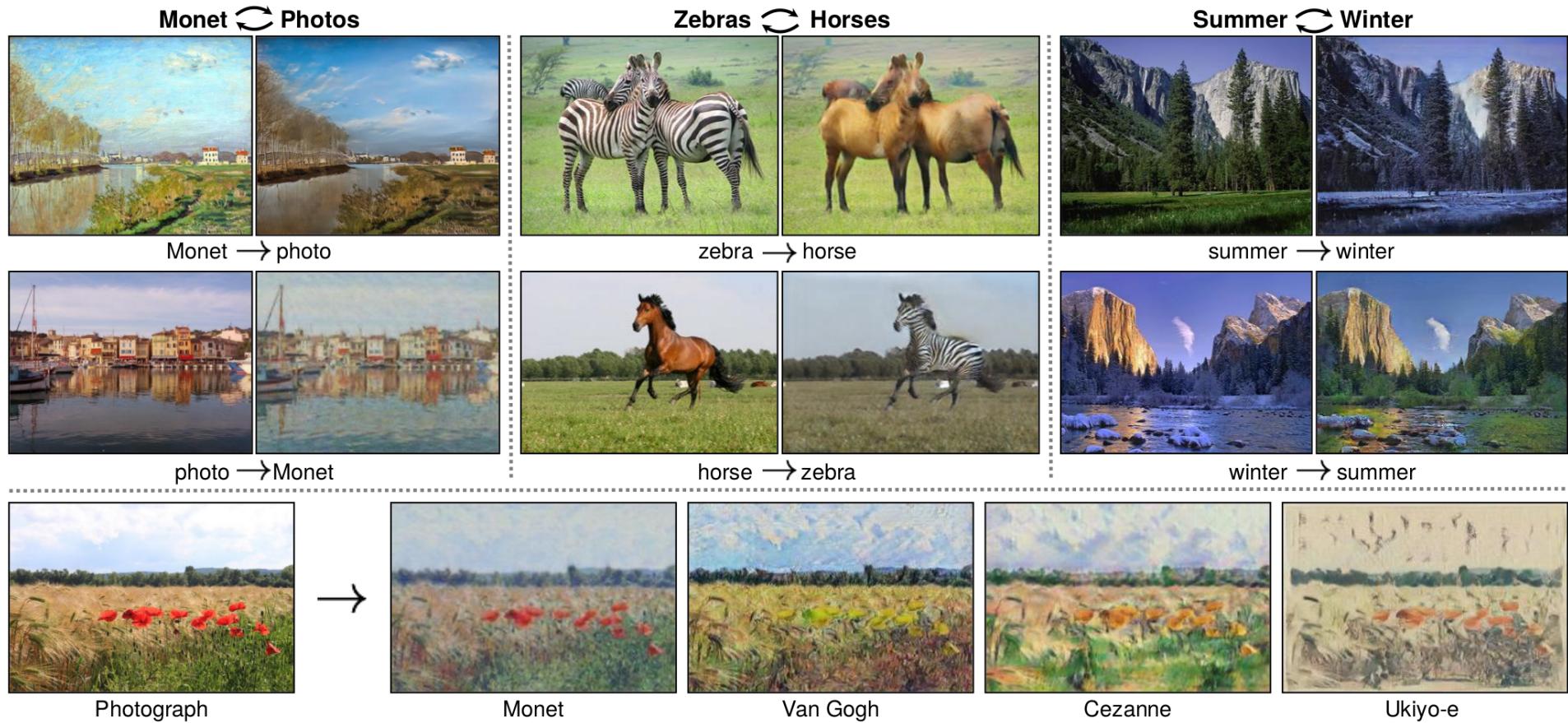
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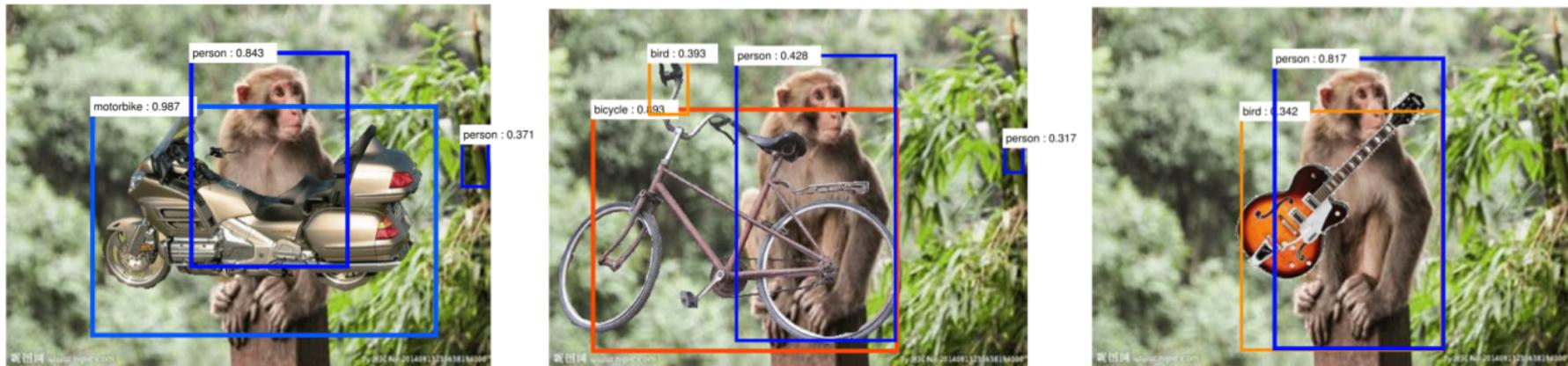
**Extended Data Figure 2 | Confusion matrix comparison between CNN and dermatologists.** Confusion matrices for the CNN and both dermatologists for the nine-way classification task of the second validation strategy reveal similarities in misclassification between human experts and the CNN. Element  $(i, j)$  of each confusion matrix represents the empirical probability of predicting class  $j$  given that the ground truth was class  $i$ , with  $i$  and  $j$  referencing classes from Extended Data Table 2d. Note that both the CNN and the dermatologists noticeably confuse benign and malignant melanocytic lesions—classes 7 and 8—with each other, with

dermatologists erring on the side of predicting malignant. The distribution across column 6—inflammatory conditions—is pronounced in all three plots, demonstrating that many lesions are easily confused with this class. The distribution across row 2 in all three plots shows the difficulty of classifying malignant dermal tumours, which appear as little more than cutaneous nodules under the skin. The dermatologist matrices are each computed using the 180 images from the nine-way validation set. The CNN matrix is computed using a random sample of 684 images (equally distributed across the nine classes) from the validation set.

# Deep Learning (Neural Networks)



# Deep Learning (Neural Networks)



# Deep Learning (Neural Networks)



$x$   
“panda”  
57.7% confidence

+ .007 ×



$\text{sign}(\nabla_x J(\theta, x, y))$   
“nematode”  
8.2% confidence

=



$x +$   
 $\epsilon \text{sign}(\nabla_x J(\theta, x, y))$   
“gibbon”  
99.3 % confidence

### Symbolic ML:

- intelligible models
- can use established types of models (if suitable formalisms and algorithms exist)
- can automate various analysis, repair and design tasks
- easy to justify output
- can take advantage of small data
- poor handling of numerical parameters

### Std. Supervised ML:

- models capture numerical patterns from labeled data
- main tasks are classification and regression
- human necessary in model selection and feature engineering
- need (often a lot of) labeled data

### Std. Unsupervised ML:

- no labels needed
- can be used in concert with supervised methods (dimensionality red.)
- or to find patterns in data (semisupervised classification)

### Deep Learning:

- hidden layers allow for feature learning
- state of the art performance on very complex tasks (Moravec's paradox)
- hype (+/-)
- requires huge amount of data
- complex black box (generalisation?)

# How hard is it going to be?

## 1) Are data available?

- quantity/cost: gathering data can be >80% of the work; also slows everything down
- quality: missing data? noise?
- relevance: spurious features? How easy to extract relevant features? (domain knowledge, another 80%)

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## 2) Does the problem match?

- classification/regression: should be straightforward
- deep learning: hard, unless transfer learning used
- symbolic: straightforward, if suitable formalism exists