

MACHINE LEARNING IN SYSTEMS BIOLOGY I

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INTRODUCTION

WHAT IS MACHINE LEARNING?

'A computer program is said to learn from experience E with respect to some class of tasks T and performance measure P if its performance at tasks in T , as measured by P , improves with experience E '

- Tom M. Mitchell [Mit97]

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- >2006 Companies such as Netflix, Facebook, Microsoft, Google fund projects/prizes in and use machine learning/artificial intelligence

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8. Apply model to problems, learn more

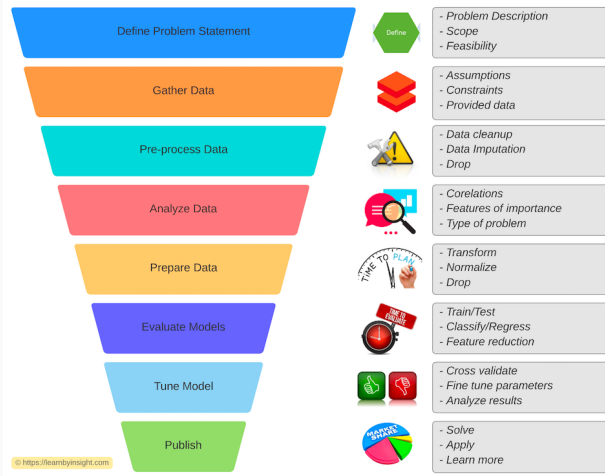


Figure 1: Machine Learning workflow [Mew20]

CONCEPTS

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This section follows [GKMJ21].

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- ▶ Can have huge performance benefits compared to unsupervised learning

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- ▶ Validation: Use separate dataset to test model.

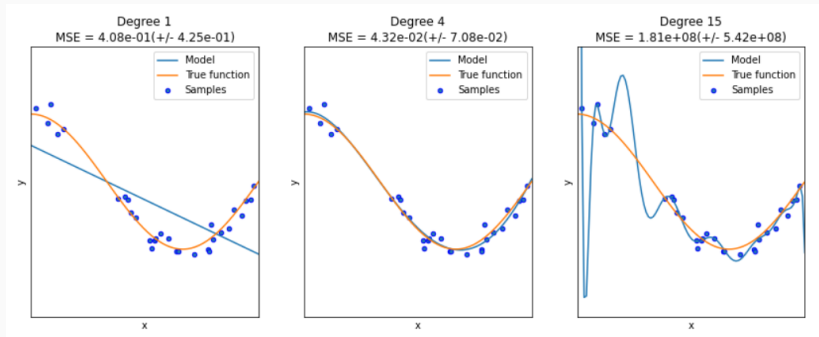


Figure 2: Underfitting, Optimal Fitting and Overfitting [Tri20]

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MACHINE LEARNING TECHNIQUES

TRADITIONAL MACHINE LEARNING TECHNIQUES

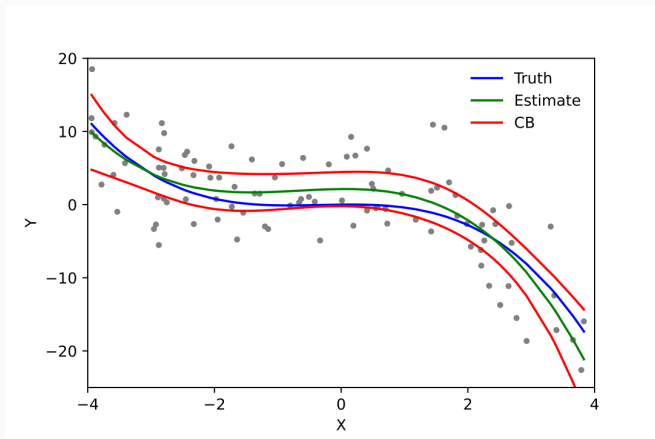


Figure 3: Polynomial Regression [Skb09]

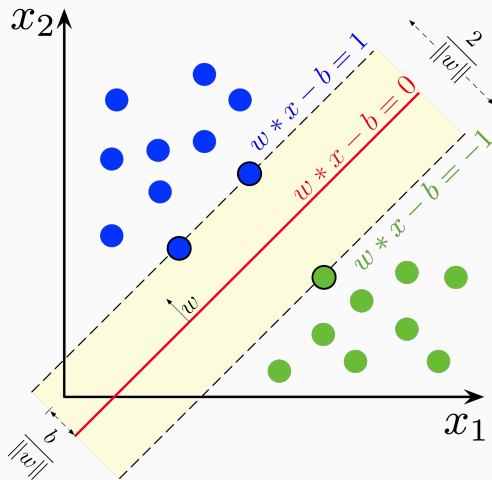


Figure 4: Support Vector Machine [Lar18]

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- ▶ Genetic Algorithms

- ▶ Traditional machine learning routines should be preferred over neural networks
- ▶ Deep learning can be powerful (and trendy)
However, currently still limited in applicability
Requires lots of data \Rightarrow often not present
- ▶ Traditional Methods are faster to develop and test
They typically expect same number of features with each datapoint
 \Rightarrow Padding and Windowing are methods to circumvent this

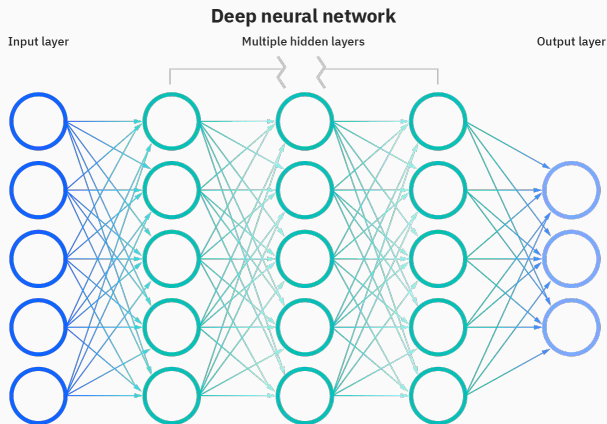


Figure 5: Standard, fully connected neural network [Edu20]

- ▶ Universal function approximators
- ▶ No guarantee that model will yield accurate predictions for new data
- ▶ Question: Is the trained model optimal?
- ▶ Neurons are at the heart of Neural Networks

They apply a function to the input variables x_i to obtain output y by multiplying with learnable weight w_i .

$$y = \sigma \left(\sum_{i=1}^n w_i x_i + b \right) \quad (1)$$

- ▶ Multiple layers \Rightarrow iterate this procedure

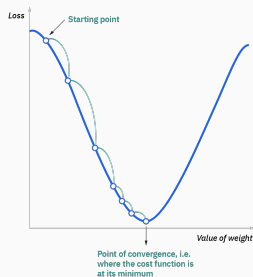


Figure 6: Iterative approach to finding a local optimum of the cost function. It penalizes or rewards good/bad results. An example can be given by the mean squared error [Edu20].

$$\text{MSE} = \frac{1}{2m} \sum_{i=1}^m (\hat{y} - y)^2 \quad (2)$$

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6. To optimize: Go along steepest negative gradient of $\partial C / \partial w$.

BIOLOGICAL APPLICATIONS

Input data	Example prediction tasks	Recommended models	Challenges
Gene sequence	DNA accessibility ¹⁴	1D CNNs	Repetitive regions in genome
	3D genome organization ⁵⁸	RNNs	Sparse regions of interest
	Enhancer–promoter interactions ⁴⁰	Transformers	Very long sequences
Protein sequence	Protein structure ^{23,55}	2D CNNs and residual networks using co-variation data	Metagenome data stored in many places and therefore hard to access
	Protein function ¹³²	Multilayer perceptrons with windowing	Data leakage (from homology) can make validation difficult
	Protein–protein interaction ¹³³	Transformers	
Protein 3D structure	Protein model refinement ¹³⁴	GCNs using molecular graph	Lack of data, particularly on protein complexes
	Protein model quality assessment ¹³⁵	3D CNNs using coordinates	Lack of data on disordered proteins
	Change in stability upon mutation ¹³⁶	Traditional methods using structural features Clustering	
Gene expression	Intergenic interactions or co-expression ¹³⁷	Clustering CNNs	Unclear link between co-expression and function
	Organization of transcription machinery ¹³⁸	Autoencoders	High dimensionality High noise

Figure 7: Different applications in Biological contexts. I [GKMJ21]

Mass spectrometry	Detecting peaks in spectra ¹³⁹ Metabolite annotation ¹⁴⁰	CNNs using spectral data Traditional methods using derived features	Lack of standardized benchmarks ¹⁴¹ Normalization* required between different datasets
Images	Medical image recognition ^{14,62} Cryo-EM image reconstruction ^{60,142} RNA-sequencing profiles ¹⁴³	2D CNNs and residual networks Autoencoders Traditional methods using image features	Systematic differences in data collection affect prediction Hard to obtain large datasets of consistent data
Molecular structure	Antibiotic activity ⁷³ Drug toxicity ⁵⁴ Protein-ligand docking ³⁹ Novel drug generation ¹⁴⁴	GCNs using molecular graph Traditional methods or multilayer perceptrons using molecular properties RNNs using text-based representations of molecular structure such as SMILES Autoencoders	Experimental data available for only a tiny fraction of possible small molecules
Protein-protein interaction network	Polypharmacology side effects ⁷⁷ Protein function ¹⁴⁵	GCNs Graph embedding	Interaction networks can be incomplete Cellular location affects whether proteins interact High number of possible combinations

Figure 8: Different applications in Biological contexts. II [GKMJ21]

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- ▶ How is it going so far?

QUESTIONS?

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