# **CSI5180.** Machine Learning for Bioinformatics Applications

Fundamentals of Machine Learning — Training

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# Preamble

#### Fundamentals of Machine Learning — Training

In this lecture, we introduce we focus on training learning algorithms. This will include the need for 2, 3 or k sets, tuning the hyperparameters values, as well as concepts such as under- and over-fitting the data.

General objective :

**Describe** the fundamental concepts of machine learning

### Learning objectives

- **Describe** the role of the **training**, **validation**, and **test** sets
- Clarify the concepts of under- and over- fitting the data
- **Explain** the process of tuning hyperparameters values

#### Reading:

- Chicco, D. Ten quick tips for machine learning in computational biology. *BioData Mining* 10:35 (2017).
- Boulesteix, A.-L. Ten simple rules for reducing overoptimistic reporting in methodological computational research. *PLoS Comput Biol* **11**:e1004191 (2015).
- Domingos, P. A few useful things to know about machine learning. Commun Acm 55:7887 (2012).



#### 1. Preamble

#### 2. Problem

3. Testing

- 4. Under- and over- fitting
- 5. 7-Steps workflow
- 6. Prologue

# The 7 Steps of Machine Learning

#### 7 Steps of Machine Learning

- Gathering Data
- Preparing that Data
- Choosing a Model
- Training
- Evaluation
- Hyperparameter Tuning
- Prediction



https://youtu.be/nKW8Ndu7Mjw

# Problem

### **Supervised learning - regression**

The **data set** is a collection of **labelled** examples.

- $\{(x_i, y_i)\}_{i=1}^N$ 
  - Each  $x_i$  is a **feature vector** with D dimensions.
  - ▶  $x_i^{(j)}$  is the value of the **feature** *j* of the example *i*, for  $j \in 1...D$  and  $i \in 1...N$ .
- The label  $y_i$  is a real number.
- Problem: given the data set as input, create a "model" that can be used to predict the value of y for an unseen x.

# QSAR

#### QSAR stands for Quantitative Structure-Activity Relationship

- As a machine learning problem,
  - Each x<sub>i</sub> is a **chemical compound**
  - $y_i$  is the **biological activity** of the compound  $x_i$ 
    - Examples of biological activity include toxicology and biodegradability



Viira, B., García-Sosa, A. T. & Maran, U. Chemical structure and correlation analysis of HIV-1 NNRT and NRT inhibitors and database-curated, published inhibition constants with chemical structure in diverse datasets. J Mol Graph Model **76**:205223 (2017).

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- "Due to mutations and other influencing factors, the search for new inhibitor molecules for HIV-1 is ongoing."
- "Our recent design, modelling, and synthesis effort in the search for new compounds has resulted in two new, small, low toxicity (...) inhibitors."

# HIV Life Cycle



HIV medicines in seven drug classes stop (2) HIV at different stages in the HIV life cycle.



#### https://aidsinfo.nih.gov/understanding-hiv-aids

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- A possible solution, a model, would look something like this:

$$\hat{y} = 44.418 - 35.133 \times x^{(1)} - 13.518 \times x^{(2)} + 0.766 \times x^{(3)}$$



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- If the training error is high, we say that the model is underfitting the training data.

# **Under- and over- fitting**

- Underfitting and overfitting are two important concepts for machine learning projects
- We will use a **regression** task to illustrate those two concepts

A linear model assumes that the value of the label,  $\hat{y}_i$ , can be expressed as a linear combination of the feature values,  $x_i^{(j)}$ :

$$\hat{y}_i = h(x_i) = \theta_0 + \theta_1 x_i^{(1)} + \theta_2 x_i^{(2)} + \ldots + \theta_D x_i^{(D)}$$

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- Problem: find values for all the model parameters so that the model "best fit" the training data.
  - The Root Mean Square Error is a common performance measure for regression problems.

$$\sqrt{\frac{1}{N}\sum_{1}^{N}[h(x_i)-y_i]^2}$$

### sklearn.linear\_model.LinearRegression



from sklearn.linear\_model import LinearRegression
lin\_reg = LinearRegression()
lin\_reg.fit(X, y)

```
import numpy as np
```

from sklearn.linear\_model import LinearRegression

```
lin_reg = LinearRegression()
lin_reg.fit(X, y)
X new = np.array([[-4], [2]])
```

y\_pred = lin\_reg.predict (X\_new)

```
plt.plot(X, y, "b.")
plt.plot(X_new, y_pred, "r-")
plt.xlabel("$x$", fontsize=18)
plt.ylabel("$y$", rotation=0, fontsize=18)
plt.axis([-4, 2, -1, 35])
save_fig("regression_linear-01")
plt.show()
```

```
import os
import matplotlib as mpl
import matplotlib.pyplot as plt
def save_fig(fig_id, tight_layout=True, fig_extension="pdf", resolution=300):
    path = os.path.join(fig_id + "." + fig_extension)
    print("Saving figure", fig_id)
    if tight_layout:
        plt.tight_layout()
    plt.savefig(path, format=fig_extension, dpi=resolution)
```
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- Solution: we might want to "test" alternative hypotheses.

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- Rule of thumb: keep 70 % of your data for training, 15 % of your data is used for validation, and 15 % of your data is used for testing.
- For data sets comprising millions of examples, 1 or 2 % test set might be enough.

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  - A learning curve shows the performance of our model, here using RMSE, on both the training set and the validation set.
  - Multiple measurements are obtained by repeatedly training the model on larger and larger subsets of the data.

# Linear model - underfitting



Source: Géron 2019

#### sklearn.linear\_model.LinearRegression



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- As the size of the data set grows, the performance on the **validation set** improves. Eventually, the performance does not improve.
- "These learning curves are typical of a model thats underfitting. Both curves have reached a plateau; they are close and fairly high." [2]

# Polynomial of degree 10 - overfitting



#### Source: Géron 2019

# **Overfitting and underfitting**



Source: Géron 2019

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- There is a gap between the two curses, the model performs significantly better on the training data compared to the validation data.

### **Overfitting - deep nets - loss**



Training and validation loss



#### **Overfitting - deep nets - accuracy**



Training and validation accuracy



# Summary

#### Underfitting:

- Your model is **too simple** (linear model).
- Uninformative features.
- **Poor** performance on both **training** and **validation** data.

#### • Overfitting:

- Your model is too complex (tall decision tree, deep and wide neural networks...).
- **Too many features** given the number of examples available
- Excellent performance on the training set, but poor performance on the validation set.

What if I have a small number of examples?

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- At the end, one calculates the **mean** and **standard deviation** for the metrics of interest: cost/loss function, precision/recall, etc.
- Open the door to hypothesis testing.

#### Insert a discussion about hypothesis testing

#### sklearn.model\_selection.cross\_val\_score

```
from sklearn.model_selection import cross_val_score
lin_scores = cross_val_score(lin_reg, X, y, cv=10)
print("Scores:", lin_scores)
print("Mean:", lin_scores.mean())
print("Standard deviation:", lin_scores.std())
```

#### sklearn.model\_selection.cross\_val\_score

```
from sklearn.model_selection import cross_val_score
tree_rmse_scores = cross_val_score(tree_reg, X, y, cv=10)
print("Scores:", tree_rmse_scores)
print("Mean:", tree_rmse_scores.mean())
print("Standard deviation:", tree_rmse_scores.std())
```

Scores: [70194.33680785 66855.16363941 72432.58244769 70758.73896782 71115.88230639 75585.14172901 70262.86139133 70273.6325285 75366.87952553 71231.65726027] Mean: 71407.68766037929 Standard deviation: 2439.4345041191004
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  - If time allows, conduct another grid search with values close to the optimal values found in the previous iteration.

#### sklearn.model\_selection.GridSearchCV

See: Géron 2019 §2

```
from sklearn model selection import GridSearchCV
param grid = [
  { 'n_estimators ': [3, 10, 30],
   'max_features': [2, 4, 6, 8]}
1
forest reg = RandomForestRegressor()
grid_search = GridSearchCV(forest_reg, param_grid, cv=5)
grid_search fit (X_train, y_train)
grid search best params
```

{'max\_features': 8, 'n\_estimators': 30}

- What if the number of combinations is large (many hyperparameters, many values for each)
- Scikit-Learn provides RandomizedSearchCV
  - The user can either supply a list of values for each hyperparameters or a probability distribution (a method for sampling values)
  - The user also specifies the number of iterations, that is the number of combinations to try.
  - Makes the execution time more predictable.

# 7-Steps workflow

## Workflow [Deep Learning with Python]

- Defining the problem and assembling the data
- Choosing a measure of success
- Choosing an evaluation protocol
- Preparing the data
- Developing an initial model
- Developing a model that overfits
- Regularization and hyper parameter tuning

Source: [4]





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- We also talked about **cross-validation**: *k*-folds and leave-one-out
- Underfitting and overfitting are important concepts
- We looked at grid search and randomized search

> Training - gradient descent

#### References

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