

CSI5180. Machine Learning for Bioinformatics Applications

Support Vector Machines

by
Marcel Turcotte

Preamble

Support Vector Machines

In this lecture, we consider one of the most popular **kernel methods**, the **support vector machines**. We informally discuss their main concepts: **separating hyperplane**, **maximum-margin hyperplane**, the **soft margin**, and **kernel functions**. As a running example, we consider the case of classifying acute leukemias patients using DNA microarray data.

General objective :

- ✚ **Explain** in your own words support vector machines

Learning objectives

- ❖ **Discuss** the concept of separating hyperplane
- ❖ **Explain** why soft margin is needed
- ❖ **Describe** in your own words the maximum-margin hyperplane
- ❖ **Justify** the need for a kernel function

Reading:

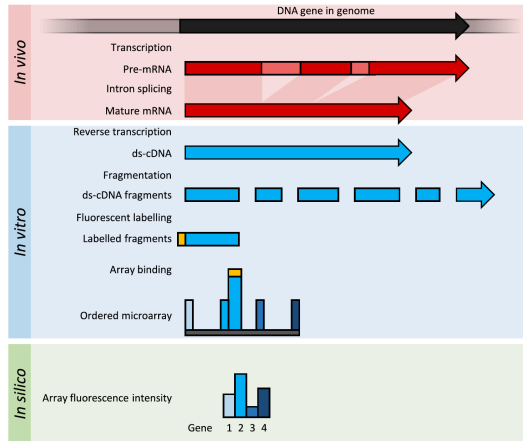
- ❖ Noble, W. S. What is a support vector machine? *Nat Biotechnol* **24**:1565-1567 (2006).

Plan

1. Preamble
2. Problem
3. Introduction
4. Implementation
5. Prologue

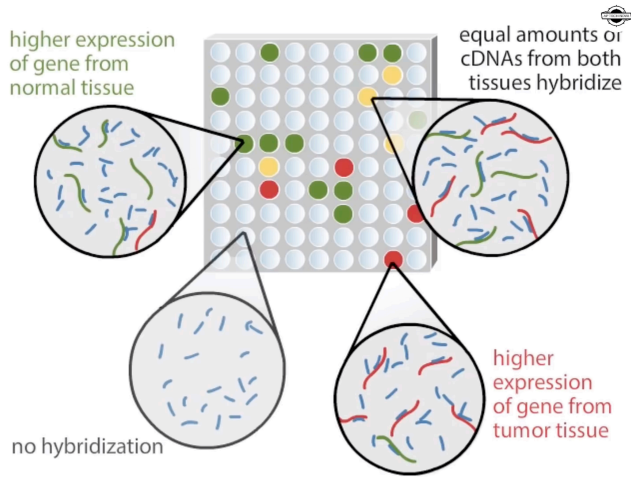
Problem

DNA Microarrays



- Lowe, R., Shirley, N., Bleackley, M., Dolan, S. & Shafee, T. Transcriptomics technologies. *PLoS Comput Biol* **13**, (2017).

DNA microarrays



<https://youtu.be/yzBVOCwRanI>

Classification of cancer

- ✚ Affymetrix microarrays with **6,817 genes**

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Sources:

- ❖ T R Golub, D K Slonim, P Tamayo, C Huard, M Gaasenbeek, J P Mesirov, H Coller, M L Loh, J R Downing, M A Caligiuri, C D Bloomfield, and E S Lander, Molecular classification of cancer: class discovery and class prediction by gene expression monitoring, *Science* **286**:5439, 5317, 1999.
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- ❖ A **binary classification** task.

Introduction

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 - ❖ **Maximum-margin hyperplane**

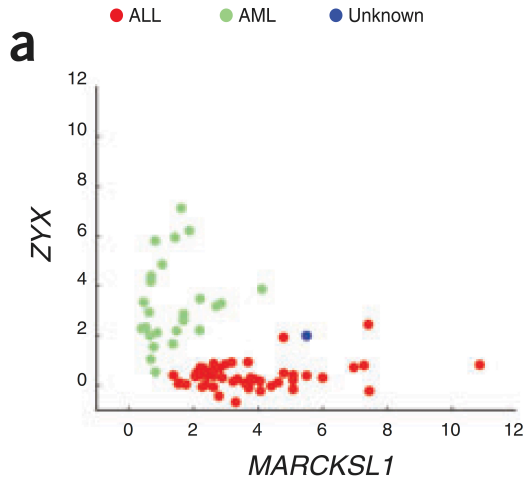
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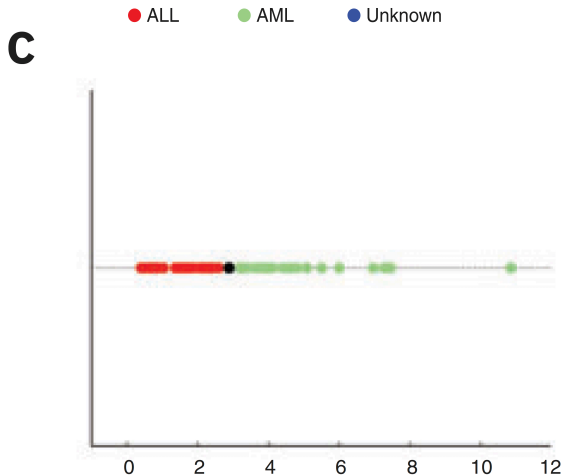
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 - ❖ **Soft-margin**
 - ❖ **Kernel function**

Separating hyperplane - 2 genes (features)



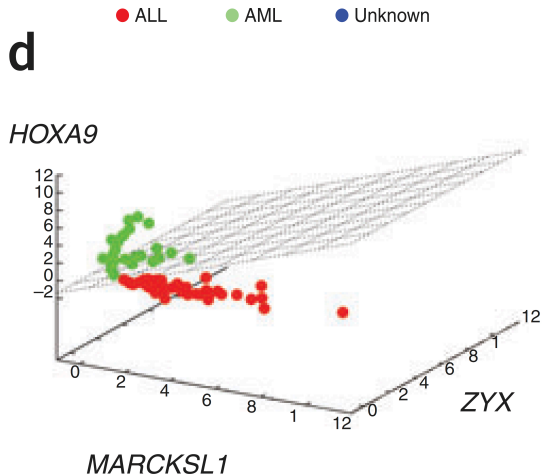
Source: [1] Figure 1a

Separating hyperplane - 1 genes (feature)



Source: [1] Figure 1c

Separating hyperplane - 3 genes (features)

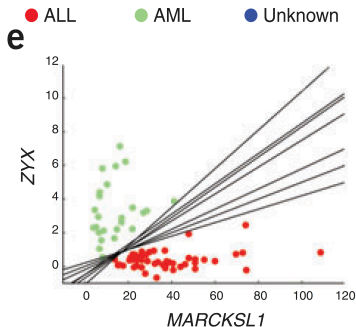


Source: [1] Figure 1d

Separating hyperplane - D genes (features)

- ❖ Given D features (genes), $D \gg 3$, the **decision boundary** is a **hyperplane**.
- ❖ “The general term for a **straight** line in a **high-dimensional space** is a **hyperplane**, and so the **separating hyperplane** is, essentially, the **line that separates the ALL and AML samples.**” [1]

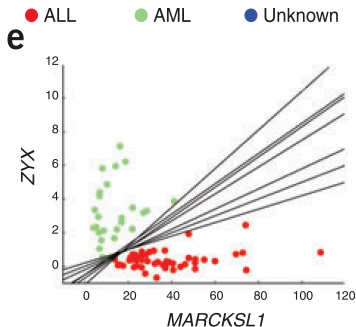
Many separating hyperplanes



Source: [1] Figure 1e

- ❖ There are generally infinitely **many separating hyperplanes**, which one to **choose**?

Many separating hyperplanes

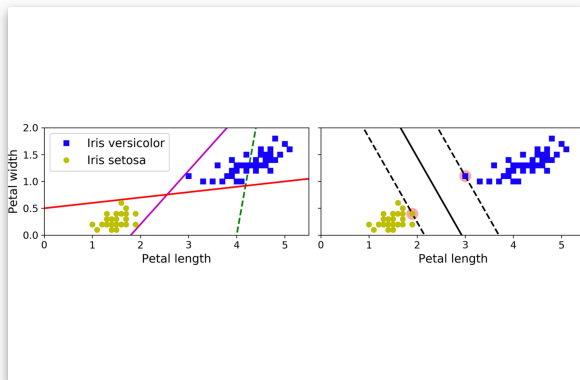


Source: [1] Figure 1e

- ❖ There are generally infinitely **many separating hyperplanes**, which one to **choose**?
- ❖ What would be a good **guiding principle**?

Maximum-margin hyperplane

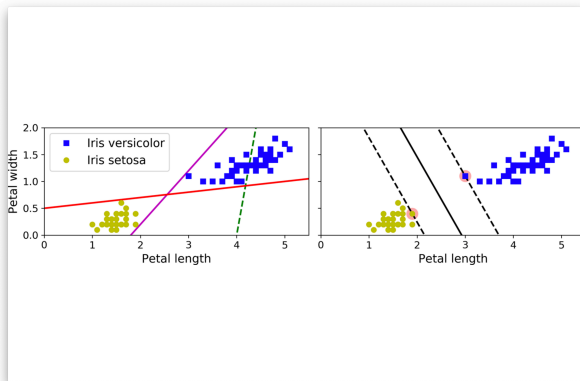
- ❖ The **support vectors** are the examples **closest** to the **separating hyperplane**.



Source: [4] Figure 5.1

Maximum-margin hyperplane

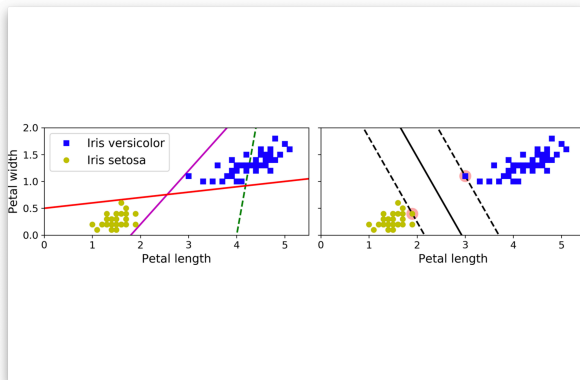
- ❖ The **support vectors** are the examples **closest** to the **separating hyperplane**.
- ❖ The **margin** is the distance between the **separating hyperplane** (decision boundary) and the **support vectors**.



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Maximum-margin hyperplane

- ❖ The **support vectors** are the examples **closest** to the **separating hyperplane**.
- ❖ The **margin** is the distance between the **separating hyperplane** (decision boundary) and the **support vectors**.
- ❖ **Problem:** of all possible **separating hyperplanes** find the one with the **largest margin**.



Source: [4] Figure 5.1

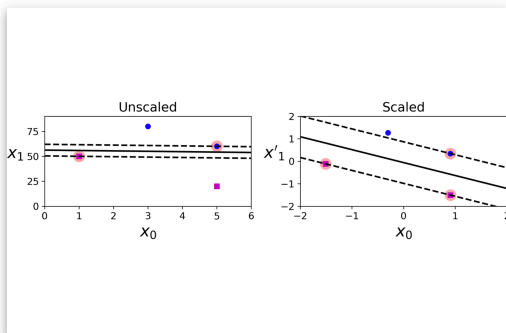
Maximum-margin hyperplane (continued)

- ✦ Selecting a **decision boundary** with maximum distance to any example is supported by **statistical learning theory**.

Maximum-margin hyperplane (continued)

- ❖ Selecting a **decision boundary** with maximum distance to any example is supported by **statistical learning theory**.
- ❖ A **large margin** should decrease the **generalization error** (errors on new cases).

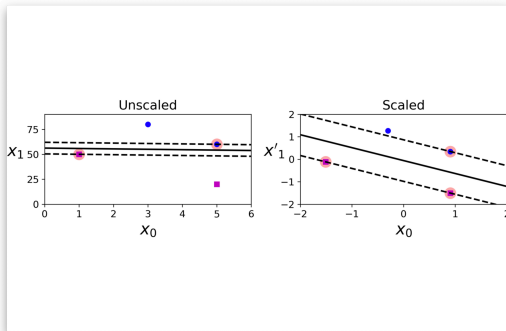
Warning



Source: [4] Figure 5.2

- ❖ **Support vector machines** can be negatively affected by **features having different scales**. On the left, x_1 ranges from 0 to 75, whereas x_2 ranges from 0 to 6.

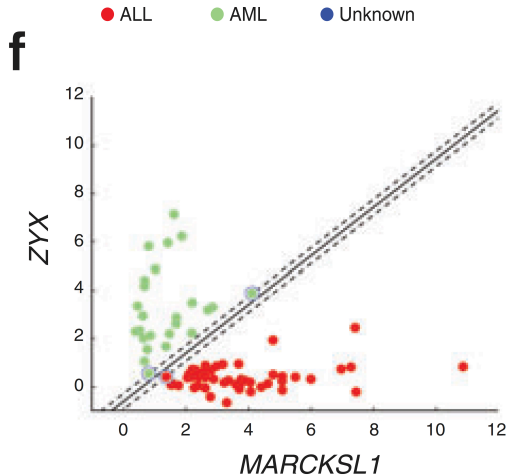
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- ❖ **Suggestion:** use `sklearn.preprocessing.StandardScaler`.

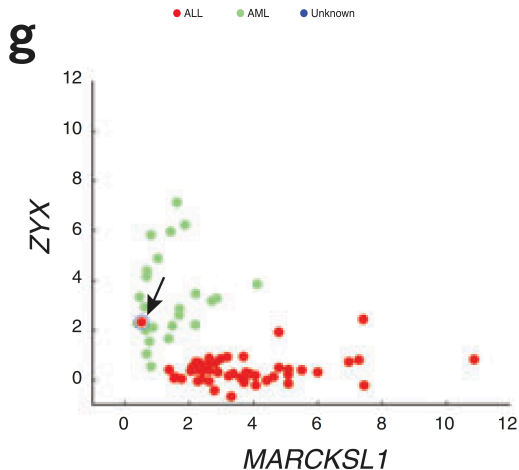
Maximum-margin hyperplane



Source: [1] Figure 1f

Linearly separable?

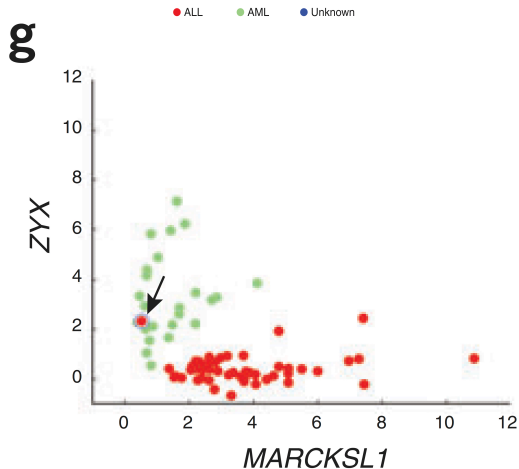
- ❖ So far, we have assumed that our data set is **linearly separable**.



Source: [1] Figure 1g

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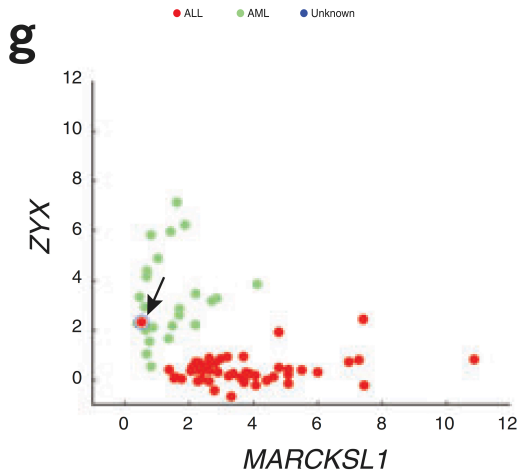
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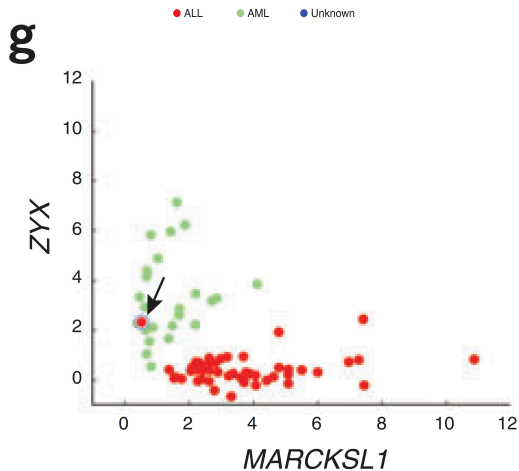
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- ❖ First, we might want to be able to allow for a **small number of classification errors**.



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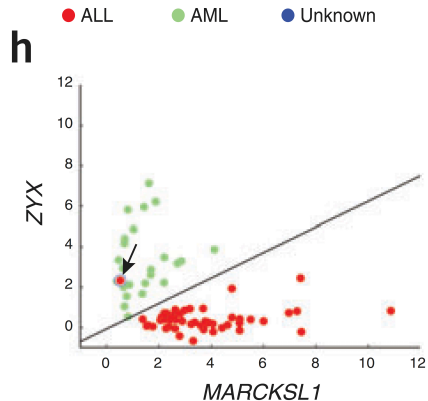
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 - ❖ These might actually represent **errors in our training set**.



Source: [1] Figure 1g

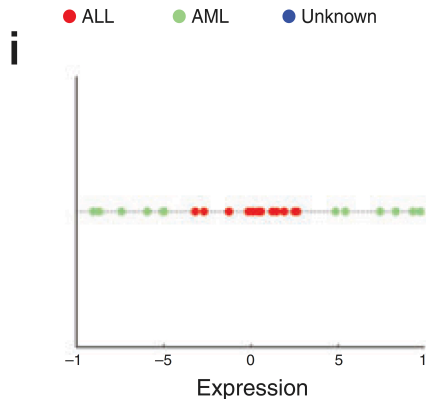
Soft margin



Source: [1] Figure 1h

- A user defined parameter, the **soft margin** (C), controls how many misclassification errors are allowed.

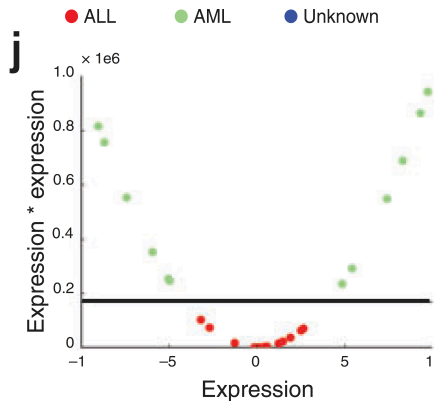
Linearly separable? (Take 2) — one feature



Source: [1] Figure 1i

❖ **No** single point can separate the two classes!

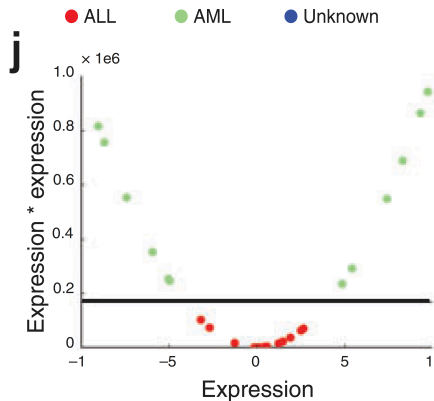
Kernel function



Source: [1] Figure 1j

- Adding a **new dimension** to our data.

Kernel function



Source: [1] Figure 1j

- ✦ Adding a **new dimension** to our data.
- ✦ Here, simply taking the square values of our feature.

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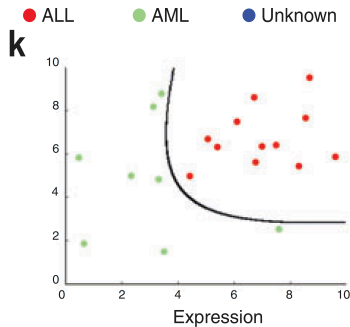
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- ❖ “It is possible to prove that, **for any given data set** with consistent labels (where consistent simply means that the data set does not contain two identical objects with opposite labels) **there exists a kernel function** that will **allow the data to be linearly separated**.” [1]

Kernels

- ❖ Linear
- ❖ Polynomial
- ❖ Gaussian RBF (radial basis function)
- ❖ Sigmoid

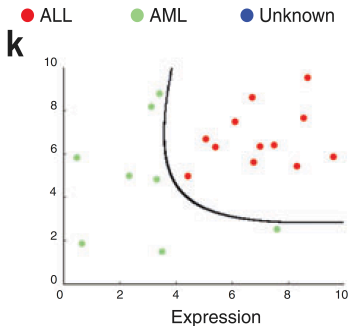
Kernel function



Source: [1] Figure 1k

- ✦ The result of projecting up the two-dimensional data into a four-dimensional space.

Kernel function



Source: [1] Figure 1k

- ✦ The result of projecting up the two-dimensional data into a four-dimensional space.
- ✦ Then projecting from the four-dimensional space down to a two-dimensional space (the curved line).

Errors/soft margin/kernel function

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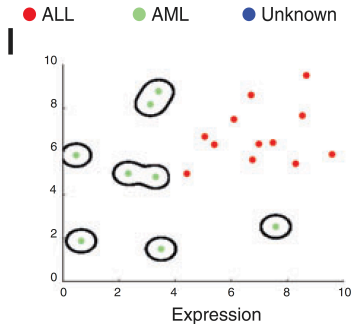
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- ❖ The above suggest that **we do not actually need the concept of soft margin!**
- ❖ Simply project the data into higher a higher dimensionality space where it will be separable!
- ❖ **Sadly**, it is not that simple!

Overfitting



Source: [1] Figure 11

- ❖ The mapping to **higher-dimensional space** can create a **complex decision boundary** and **overfitting**.

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- ❖ Just like **logistic regression**, **support vector machines** are learning the parameters of a **linear decision boundary** separating the data in **two classes**.
- ❖ However, **SVM** algorithms also rely on the concept of **maximum margin hyperplane** as a mechanism to lower generalization errors.
- ❖ In order to handle a **small number of classification errors**, the algorithms introduce the concept of **soft margin**.
- ❖ Finally, because the data is **not always linearly separable**, these algorithms project the data to **higher dimensions** using a **kernel function**.

Multiclass SVM

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 - ❖ Build a classifier to distinguish between Class **K** against the best.

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 - ❖ Build a classifier to distinguish between class **2** against the rest.
 - ❖ ...
 - ❖ Build a classifier to distinguish between Class **K** against the best.
- ❖ In other words, examples of **class k (label = 1)** are the positive examples and all the other examples are the negative examples (**label = -1**), $\forall k \in 1 \dots K$.

Implementation

Worked example on kaggle

- ✦ `https://www.kaggle.com/crawford/gene-expression`
- ✦ `https://www.kaggle.com/varimp/gene-expression-classification`

sklearn.svm.SVC

scikit-learn.org/stable/modules/generated/sklearn.svm.SVC.html

```
svm_param_grid = {'C': [0.1, 1, 10, 100],
                  'kernel': ['linear', 'rbf', 'poly']}

svm_grid = GridSearchCV(SVC(), svm_param_grid, cv=3)

svm_grid.fit(X_train, y_train)

print("Best Parameters:\n", svm_grid.best_params_)

best_svc = svm_grid.best_estimator_

svm_pred = best_svc.predict(X_test)
```

Source: <https://www.kaggle.com/varimp/gene-expression-classification>

Complexity

- ❖ Grows **quadratically** with the **number of examples**.
- ❖ **Linear time** approximations exist.
- ❖ Handles **millions of examples**.

Prologue

Kernel methods

- ❖ As we will see in the next lecture, **kernels** can be defined for inputs that are not vectors.

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- ❖ **Support vector machines** have a **strong foundation**.
- ❖ **Empirical results** show that their performance is excellent.

Next module

▣ Kernel Methods

References

-  William S Noble.
What is a support vector machine?
Nat Biotechnol, 24(12):1565–7, Dec 2006.
-  T R Golub, D K Slonim, P Tamayo, C Huard, M Gaasenbeek, J P Mesirov, H Coller, M L Loh, J R Downing, M A Caligiuri, C D Bloomfield, and E S Lander.
Molecular classification of cancer: class discovery and class prediction by gene expression monitoring.
Science, 286(5439):531–7, Oct 1999.
-  Michael Molla, Michael Waddell, David Page, and Jude W. Shavlik.
Using machine learning to design and interpret gene-expression microarrays.
AI Magazine, 25(1):23–44, 2004.
-  Aurélien Géron.
Hands-on Machine Learning with Scikit-Learn, Keras, and TensorFlow.
O'Reilly Media, 2nd edition, 2019.



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