IB031 Úvod do strojového učení Tomáš Brázdil

Course Info

Resources:

- Lectures & tutorials (the main source)
- Many books, few perfect for introductory level One relatively good, especially the first part:
 A. Géron. Hands-On Machine Learning with Scikit-Learn, Keras, and TensorFlow: Concepts, Tools, and Techniques to Build Intelligent Systems. O'Reilly Media; 3rd edition, 2022
- (Almost) infinitely many online courses, tutorials, materials, etc.

Evaluation

The evaluation is composed of three parts:

- Mid-term exam: Written exam from the material of the first half of the semester.
- End-term exam: The "big" one containing everything from the semester (with possibly more stress in the second half).
- Projects: During tutorials, you will work on larger projects (in pairs or triples).
- Each part contributes the following number of points:
 - Mid-term exam: 25
 - End-term exam: 50
 - Project: 25

To pass, you need to obtain at least 60 points.

Distinguishing Properties of the Course

- Introductory, prerequisites are held to a minimum
- Formal and precise: Be prepared for a complete and "mathematical" description of presented methods.

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- I assume that you have basic knowledge of
 - Elementary mathematical notation (operations on sets, logic, etc.)
 - ► Linear algebra: Vectors in Rⁿ, operations on vectors (including the dot product). Geometric interpretation!
 - Calculus: Functions of multiple real variables, partial derivatives, basic differential calculus.
 - Probability: Notion of probability distribution, random variables/vectors, expectation.

What Is Machine Learning?

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Machine learning is the field of study that allows computers to learn without being explicitly programmed.

And a more engineering-oriented one:

Tom Mitchell, 1997

A computer program is said to learn from experience E concerning some task T and some performance measure P if its performance on T, as measured by P, improves with experience E.

Example

In the context of spam filtering:

- The task T is to flag spam in new emails.
- The experience E is represented by a set of emails labeled either spam or ham by hand (the training data).
- The performance measure P could be the accuracy, which is the ratio of the number of correctly classified emails and all emails.

There are many more performance measures; we will study the basic ones later.

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In the context of housing price prediction:

- The task T is to predict prices of new houses based on their basic parameters (size, number of bathrooms, etc.)
- The experience E is represented by information about existing houses.
- The performance measure P could be, e.g., an absolute difference between the predicted and the real price.

Examples (cont.)

In the context of game playing:

- ▶ The task *T* is to play chess.
- The experience E is represented by a series of self-plays where the computer plays against itself.
- The performance measure P is winning/losing the game. Here, the trick is to spread the delayed and limited feedback about the result of the game throughout the individual decisions in the game.

Examples (cont.)

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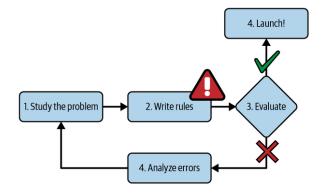
In the context of customer behavior:

- The task T is to group customers with similar shopping habits in an e-shop.
- The experience E consists of lists of items individual customers bought in the shop.
- The performance measure P? Measure how "nicely" the customers are grouped. (whether people with similar habits, as seen by humans, fall into the same group).

Comparison of Programming and Learning

How to code the spam filter?

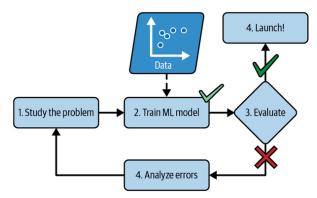
- Examine what spam mails typically contain: Specific words ("Viagra"), sender's address, etc.
- ▶ Write down a rule-based system that detects specific features.
- Test the program on new emails and (most probably) go back to look for more spam features.



Comparison of Programming and Learning

The machine learning way:

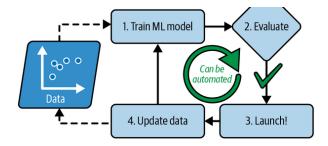
- Study the problem and collect lots of emails, labeling them spam or ham.
- Train a machine learning model that reads an email and decides whether it's spam or ham.
- Test the model and (most probably) go back to collect more data and adjust the model.



ML Solutions are Adaptive

Spam filter: Authors of spam might and will adapt to your spam filter (possibly change the wording to pass through).

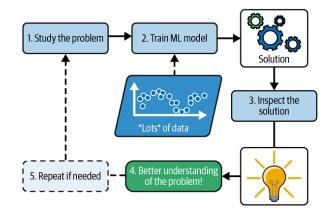
ML systems can be adjusted to new situations by retraining on new data (unless the data becomes ugly).



ML for Human Understanding

Spam filter: A trained system can be inspected for notorious spam features.

Some models allow direct inspection, such as decision trees or linear/logistic regression models.



Usage of Machine Learning

Machine learning suits various applications, especially where traditional methods fall short. Here are some areas where it excels:

- Solving complex problems where fine-tuning and rule-based solutions are inadequate.
- Tackling complex issues that resist traditional problem-solving approaches.
- Adapting to fluctuating environments through retraining on new data.
- Gaining insights from large and complex datasets.

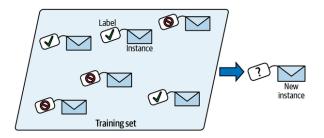
In summary, machine learning offers innovative solutions and adaptability for today's complex and ever-changing problems, (sometimes) providing insights beyond the reach of traditional approaches.

Types of Learning

There are main categories based on information available during the training:

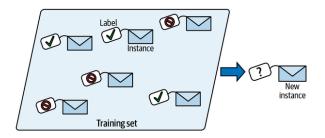
- Supervised learning
- Unsupervised learning
- Semi-supervised learning
- Self-supervised learning
- Reinforcement learning

Supervised Learning



Labels are available for all input data.

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Typical supervised learning tasks are

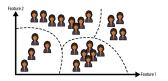
 Classification where the aim is to classify inputs into (typically few) classes

(e.g., the spam filter where the classes are spam/ham)

 Regression where a numerical value is output for a given input (e.g., housing prices)

Unsupervised Learning

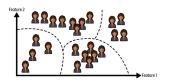




No labels are available for input data.

Unsupervised Learning





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Typical unsupervised learning tasks are

Clustering where inputs are grouped according to their features

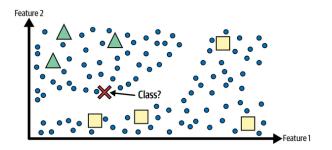
(e.g., clients of a bank grouped according to their age, wealth, etc.)

 Association where interesting relations and rules are discovered among the features of inputs

(e.g., market basket mining where associations between various types of goods are being learned from the behavior of customers)

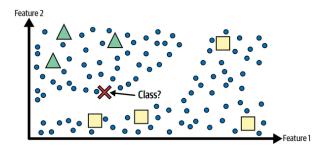
 Dimensionality reduction reduce high-dimensional data to few dimensions (e.g., images to few image features)

Semi-Supervised Learning



Labels for some data.

Semi-Supervised Learning

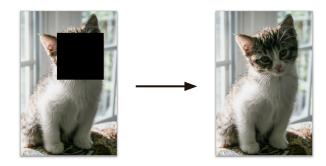


Labels for some data.

For example, Medical data, where elaborate diagnosis is available only for some patients.

Combines supervised and unsupervised learning: e.g., clusters all data and labels the unlabeled inputs with the most common labels in their clusters.

Self-Supervised Learning

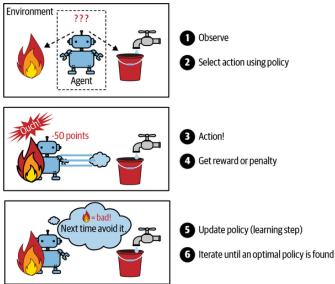


Generate labels from (unlabeled) inputs.

The goal is to learn typical features of the data.

It can be later modified to generate images, classify, etc.

Reinforcement Learning



Learn from performing actions and getting feedback from environment.

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 - The basis forms a generative language model, i.e., a text-generating model trained on texts in a self-supervised way
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Various image recognition and processing tasks

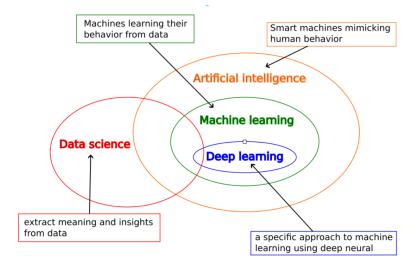
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- Game playing: More fancy than useful, learning models beating humans in several difficult games.

ML in Context



Supervised Learning

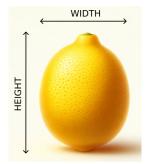
Example - Fruit Recognition

The goal: Create an automatic system for fruit recognition, concretely apple, lemon, and mandarin.

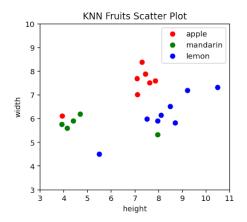
Inputs: Measures of *height* and *width* of each fruit.

Suppose we have a dataset of dimensions of several fruits labeled with the correct class.





Data



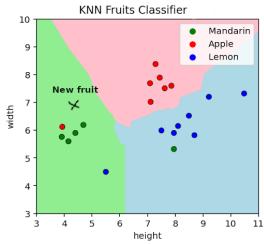
Use similarity to solve the problem.

	height	width	fruit
0	3.91	5.76	Mandarin
1	7.09	7.69	Apple
2	10.48	7.32	Lemon
3	9.21	7.20	Lemon
4	7.95	5.90	Lemon
5	7.62	7.51	Apple
6	7.95	5.32	Mandarin
7	4.69	6.19	Mandarin
8	7.50	5.99	Lemon
9	7.11	7.02	Apple
10	4.15	5.60	Mandarin
11	7.29	8.38	Apple
12	8.49	6.52	Lemon
13	7.44	7.89	Apple
14	7.86	7.60	Apple
15	3.93	6.12	Apple
16	4.40	5.90	Mandarin
17	5.50	4.50	Lemon
18	8.10	6.15	Lemon
19	8.69	5.82	Lemon

KNN Classification

Given a new fruit. What is it?

Find five closest examples



Where is the machine learning?

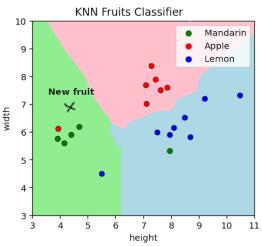
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Among the five closest:

- M = 4 mandarins
- A = 1 apples
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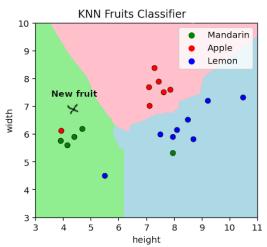
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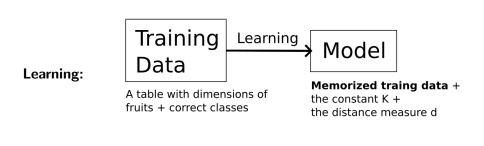
- M = 4 mandarins
- A = 1 apples
- L = 0 lemons

It is a mandarin!



Where is the machine learning?

Learning in Fruit Classification with KNN





Fruit Classification Algorithm

Input: A fruit *F* with dimensions *height*, *width* **Output:** *mandarin*, *lemon*, *apple*

- 1: Find K examples $\{E_1, \ldots, E_K\}$ in the dataset whose dimensions are closest to the dimensions of the fruit F
- 2: Count the number of examples of each class in $\{E_1, \ldots, E_K\}$

$$M$$
 mandarins in $\{E_1, \ldots, E_K\}$

L lemons in
$$\{E_1,\ldots,E_K\}$$

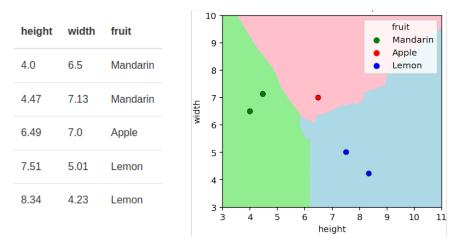
A apples in $\{E_1, \ldots, E_K\}$

- 3: if $M \ge L$ and $M \ge A$ then return mandarin
- 4: else if $L \ge A$ then return lemon
- 5: else return apple
- 6: end if

Does it work?

Testing the Model for Fruit Classification

Consider a test set of new instances (K = 5, d is Euclidean):



Perfect classification of new data! Just deploy and sell!!

K Nearest Neighbors

Learning and Inference

Two crucial components of machine learning are the following:



Training Data

x ₁₁ x ₂₁	x ₁₂ x ₂₂	 	x _{1n} x _{2n}	с ₁ с ₂
÷	:	۰.	: X _{pn}	:
x_{p1}	x_{p2}	•••	x _{pn}	Ср

Formally, we define training dataset

$$\mathcal{T} = \{ (\vec{x}_k, c_k) \mid k = 1, \dots, p \}$$

Here each $\vec{x}_k \in \mathbb{R}^n$ is an input vector and $c_k \in C$ is the correct class.

height	width	fruit
4.0	6.5	Mandarin
4.47	7.13	Mandarin
6.49	7.0	Apple
7.51	5.01	Lemon
8.34	4.23	Lemon

$$\mathcal{T} = \{(4.0, 6.5), M), \\ (4.47, 7.13), M), \\ (6.49, 7.0), A), \\ \dots \}$$

KNN: Learning

Consider the training set:

$$\mathcal{T} = \{(\vec{x}_k, c_k) \mid k = 1, \dots, p\}$$

and memorize it exactly as it is.

Store in a table.

Possibly use a clever representation allowing fast computation of nearest neighbors such as KDTrees (out of the scope of this lecture).

Also,

- determine the number of neighbors $K \in \mathbb{N}$,
- ▶ and the distance measure *d*.

Inference in KNN

Assume a KNN "trained" by memorizing $\mathcal{T} = \{(\vec{x}_k, c_k) \in \mathbb{R}^n \times C \mid k = 1, ..., p\}$, a constant $K \in \mathbb{N}$ and a distance measure d.

For d, consider Euclidean distance, but different norms may also be used to define different distance measures.

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Input: A vector $\vec{z} = (z_1, ..., z_n) \in \mathbb{R}^n$ **Output:** A class from *C*

1: Find K indices of examples $X = \{i_1, \ldots, i_K\} \subseteq \{1, \ldots, p\}$ with minimum distance to \vec{z} , i.e., satisfying

 $\max \big\{ d(\vec{z}, \vec{x_\ell}) \mid \ell \in X \big\} \leq \min \big\{ d(\vec{z}, \vec{x_\ell}) \mid \ell \in \{1, \dots, p\} \smallsetminus X \big\}$

- 2: For every $c \in C$ count the number #c of elements ℓ in X such that $c_\ell = c$
- 3: Return some

```
c_{max} \in \underset{c \in C}{\operatorname{arg\,max}} \# c
```

A class $c_{max} \in C$ which maximizes #c.

The resulting model

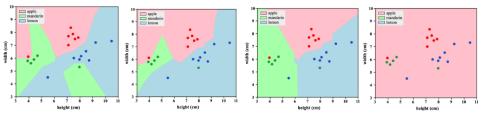
What exactly constitutes the model? The model consists of

- The trained parameters: In this case the memorized training data.
- ► The *hyperparameters* set "from the outside": In this case, the number of neighbors *K* and the distance measure *d*.

The resulting model

What exactly constitutes the model? The model consists of

- The trained parameters: In this case the memorized training data.
- The hyperparameters set "from the outside": In this case, the number of neighbors K and the distance measure d.
 Note that different settings of K lead to different classifiers (for the same d):



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- Deal with issues in the data
 - Data almost always comes in weird formats, with inconsistencies, missing values, wrong values, etc.
 - Data rarely have the ideal form for a given learning model.

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- Deal with the wrong model by testing and validation in as realistic conditions as possible.
- Deal with deployment real-world application issues involving, e.g., implementation in embedded devices with limited resources.

Models Considered in This Course

Throughout this course, we will meet the following models:

- KNN (already did)
- Decision trees
- (Naive) Bayes classifier
- Clustering: K-means and hierarchical
- Linear and logistic regression
- Support Vector Machines (SVM)
- Kernel linear models
- Neural networks (light intro to feed-forward networks)
- Ensemble methods + random forests
- (maybe some reinforcement learning)

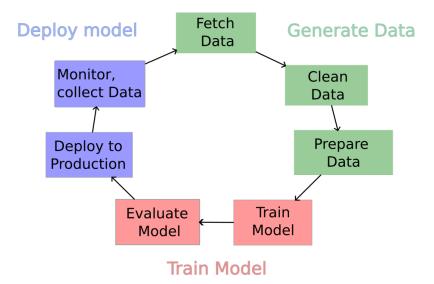
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... but first, let us see the whole machine-learning pipeline.

Machine Learning Pipeline



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In our example, the sources are hospitals. It would be best to persuade them to give you the data and sign a contract.

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Integrate data from various sources.

A serious diagnostic system must be trained/tested on data from many hospitals. You must blend the data from various sources (different formats, etc.).

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The test data are supposed to simulate the actual conditions, i.e., they should be "unseen".

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Data Exploration

Compute basic statistics to identify missing values, outliers, etc.

Clean Data

The cleaning usually comprises the following steps:

- Fix or remove incorrect or corrupted values.
- Identify outliers and decide what to do with them.
 Outliers may harm some training methods and are not "representative".
 However, sometimes, they naturally belong to the dataset, and expert insight is needed.
- Fix formatting.

For example, the Date may be expressed in many ways, and a simple $\ensuremath{\mathsf{Yes}}\xspace/No$ answer.

 Resolve missing values (by either removing the whole examples or imputing)

Many methods have been developed for missing values imputation. It is a susceptible issue because new values may strongly bias the model.

Remove duplicates.

The above steps often affect the training and need expertise in the application domain.

Later in this course, we will discuss techniques for data cleaning.

ID	Age	Income	Gender	Customer_Satisfaction
1	38	46641.356413713	nan	Unsatisfied
2	42	49129.0615585107	female	Neutral
3	18	119965.049731014	Male	nan
4	18	66828.0762224329	nan	very unsatisfied
5	58	57422.2721106762	female	very unsatisfied
6	28	59502.8174855665	Other	Satisfied
7	18	42659.6675768587	Other	Neutral
8	18	54019.1173206374	Other	Satisfied
9	40	25429.1604541137	female	Unsatisfied
10	21	15595.5862129548	Other	Satisfied
11	18	58094.2328460069	Other	very unsatisfied
12	18	39097.3278583155	female	Very Satisfied
13	30		Other	Satisfied
14	50	30617.3914472273	Female	Very Satisfied
15	18		nan	Neutral
16	34	39902.4430953214	male	nan
17	49	68381.6997683133	Female	Very Satisfied
18	33	44796.0962271524	Other	Very Satisfied
19	47	39218.9560738814	Female	very unsatisfied
20		14544.9226784447	Other	Satisfied

Prepare Data

Unlike cleaning, which is application-dependent, data preparation/transformation is model-dependent. This usually subsumes:

Scaling: Settings values of inputs to a similar range.

Some models, especially those utilizing distance, are sensitive to large differences between input sizes.

Encoding: Encode non-numeric data using real-valued vectors. Many models, especially those based on geometry, work only with numeric data. Non-numeric data such as Yes/No, Short/Medium/Long must be encoded appropriately.

 Binning or Discretization Convert continuous features into discrete bins to capture patterns in ranges.

Comment: Sometimes **Normalization**, that is changing the distribution of inputs to resemble the normal distribution, is mentioned. However, this step is typically not essential for machine learning itself. However, it is important to use statistical inference to test the significance of learned parameters.

Prepare Data

 Feature selection Throw out input features that are too "similar" to other features.

For example, if the temperature is measured both in Celsius and in Kelvin, keep one of them. The relationship can, of course, be a more complex (non-linear) correlation.

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▶ Dimensionality reduction Transforming data from \mathbb{R}^n to \mathbb{R}^m where $m \ll n$.

Growing dimension means growing difficulty of training for all models. Some models cease to work for high-dimensional data. The reduction typically searches for a few important characteristic features of inputs.

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▶ Dimensionality reduction Transforming data from ℝⁿ to ℝ^m where m << n.</p>

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 Feature aggregation Introducing new features using operations on the original ones.

We will see kernel transformations later in this course, allowing simple models to solve complex problems.

Train Model

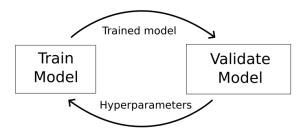
Now the dataset has been cleaned; we may train a model.

Train Model

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Before training, we should split the dataset into

- training dataset on which the model will learn
- validation dataset on which we fine-tune hyperparameters



The resulting model is obtained after several iterations of the above process.

Evaluate Model

Here, we use the test set that we separated during data fetching. In some cases, a brand new test set can be generated. patients are examined regularly, creating new records continuously. In some cases, it is tough to obtain new data. For example, new expensive and difficult measurements are needed to obtain new data.

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Critical issue: Make sure that you are truly testing

exactly the whole inference process.

Often, just a model is tested, and the testing and production inference engines are separated. This leads to truly nasty errors in the production!

We will discuss various generic metrics helpful in measuring the quality of the resulting model.

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From the technical point of view, the typical issues solved by ML Ops teams are

- how to extract/process data in real-time
- how much storage is required
- how to store/collect model (and data) artifacts/predictions
- how to set up APIs, tools, and software environments
- What the period of predictions (instantaneous or batch predictions) should be
- how to set up hardware requirements (or cloud requirements for on-cloud environments) by the computational resources required
- how to set up a pipeline for continuous training and parameter tuning

From the user's point of view:

- How to get a sensible and valuable user output?
 - Al researchers will be satisfied with tons of running text in terminals.
 - "Normal" people need a graphical interface with understandable output.
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 - Experts working in other domains typically demand speed and clarity at the extreme.
- How do you persuade users that the AI is working for them?
 - Especially if safety is at stake, you need to have outstanding arguments and explanations ready for end-users.
 - In many areas, the devices need to be certified (medicine, automotive) for ML-based systems.

This complex subject will be only touched on in this course.

Monitor, collect Data

Deployed machine learning models must be constantly monitored. Because of the influx of new data, ML models work in highly dynamic environments.

For example, an image-processing medical diagnostic model suddenly misdiagnosed a patient because a nurse marked the sample with a marker pen.

Every customer has a different infrastructure and may produce data slightly differently.

Data for retraining and improvement should be stored.

Also, many areas allow the *active learning* where users provide feedback for (continuous) retraining of the models.

Data

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The data consists of a 1000 lines table with five columns:

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After a few days, you have trained a model that predicts numbers resembling the ones in the table.

You contact the medical researcher and discuss the results.

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Data Miner: No.

Researcher: But surely you heard about what happened to field 4? It's supposed to be measured on a scale from 1 to 10, with 0 indicating a missing value, but because of a data entry error, all 10's were changed into 0's. Unfortunately, since some of the patients have missing values for this field, it's impossible to say whether a 0 in this field is a real 0 or a 10. Quite a few of the records have that problem.

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Data Miner: Interesting. Were there any other problems? **Researcher:** Yes, fields 2 and 3 are basically the same, but I assume that you probably noticed that.

Data Miner: Yes, but these fields were only weak predictors of field 5.

Researcher: Anyway, given all those problems, I'm surprised you were able to accomplish anything.

Data Miner: True, but my results are really quite good. Field 1 is a very strong predictor of field 5. I'm surprised that this wasn't noticed before.

Researcher: What? Field 1 is just an identification number.

Data Miner: Nonetheless, my results speak for themselves.

Researcher: Oh, no! I just remembered. We assigned ID numbers after we sorted the records based on field 5. There is a strong connection, but it isn't very sensible. Sorry.

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OK, what's the point?

You have to

Understand the task you want to solve and the data!

Data Objects

Data objects represent entities we work with (e.g., classify them). For example, in cancer prediction, the data objects are patients. In fruit classification, the data objects are individual fruits. Data objects represent entities we work with (e.g., classify them).

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Data objects are described by *attributes* (or *features* or *variables*). For example, the age, weight, genetic profile, and other patient

characteristics. Or the width and height of a fruit.

Attributes vs Features vs Variables

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So, the following names are usually used as synonyms:

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- Features used mostly by machine learning experts.
- Variables used mostly by statisticians.

One may make some distinctions

- Attributes represent information about the object without any additional assumptions.
- Features assume that their values are somewhat characteristic of the object.
- Variables assume that there is some process behind them (typically a random process in the case of statistics).

Data Types - Categorical Attributes

Categorical attributes (nominal attributes) are symbols or names of things.

- Each value represents some kind of category, code, or state.
- Values are not ordered and should not be used quantitatively (in computer science, the values are known as enumerations).

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- Examples:

 $\mathsf{hair_color} \in \{\mathsf{black}, \mathsf{brown}, \mathsf{blond}, \mathsf{red}, \mathsf{auburn}, \mathsf{gray}, \mathsf{white}\}$

```
marital\_status \in {single, married, divorced, widowed}
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 $\mathsf{customer_ID} \in \{0, 1, 2, \ldots\}$

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Binary attributes are categorical attributes with only two values.

DataTypes - Ordinal Attributes

Ordinal attribute is an attribute with values that have a meaningful order or ranking among them.

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Examples:

```
\mathsf{drink\_size} \in \{\mathsf{small}, \mathsf{medium}, \mathsf{large}\}
```

```
\mathsf{grades} \in \{\mathsf{A},\mathsf{B},\mathsf{C},\mathsf{D},\mathsf{E},\mathsf{F}\}
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It can also be obtained by discretizing numeric quantities into series of intervals.

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Categorical and ordinal attributes are called *qualitative* attributes. Next, we look at numeric, i.e., *quantitative* attributes.

Data Types - Numeric Attributes

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Distinguish two types: Interval-scale and ratio-scale.

	INTERVAL SCALE	RATIO SCALE	
Measurement	Equal intervals between	Equal intervals with	
interval	consecutive points.	the presence of a true zero.	
Absolute	Lacks a true zero point.	Possesses a true	
zero		zero point.	
Statistical	Limited to addition	Allows for meaningful	
analysis	and subtraction	multiplication and division.	
Meaningful	Ratios are not meaningful	Ratios are meaningful	
ratios	due to the lack of zero.	due to the presence of zero.	
Examples	Celsius temperature	Height, duration, etc.	
	(20 degrees not twice as hot	(20 meters is twice as large	
	as 10 degrees)	as 10 meters)	

Discrete vs Continuous Attributes

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► Discrete

A finite or countably infinite range of values, i.e., integers may represent the values.

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► Discrete

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Continuous

A continuous range of values, an interval.

There are several more or less formal definitions of continuous attributes in the literature. For example:

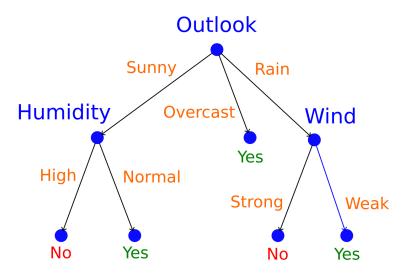
- All non-discrete variables.
- Have an infinite number of values between any two values.
- Their values are measured (??).

Deeper characteristics of data (statistical properties, etc.) will be examined at tutorials.

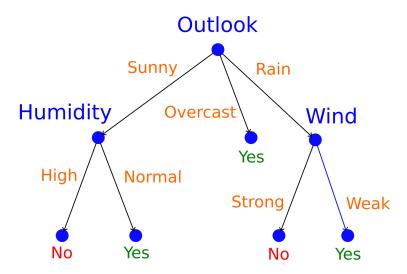
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- Basis for random forests (a powerful model).
- We will consider the ID3 algorithm. Quinlan, 1979
- Various adjustments that appear in C4.5, CART, etc.

Consider the weather forecast for tennis playing. How would you decide whether to play today?



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How do we obtain such a tree based on experience/data?

Consider data represented as follows:

• A finite set of *attributes* $\mathcal{A} = \{A_1, \ldots, A_n\}$.

• Each attribute $A \in A$ has its set of values V(A).

We start with trees on discrete datasets, that is, assume V(A) finite for all $A \in A$.

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Objects to be classified are described by vectors of values of all attributes:

$$\vec{x} = (x_1, \ldots, x_n) \in V(A_1) \times \cdots \times V(A_n)$$

Given \vec{x} and an attribute A_k we denote by $A_k(\vec{x})$ the value x_k of the attribute A_k in \vec{x} .

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Consider a set *C* of *classes*.

We consider a multiclass classification in general, i.e., C is an arbitrary finite set.

The tennis problem:

The attributes are:

 $A_1 = Outlook, A_2 = Temperature, A_3 = Humidity, A_4 = Wind$

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- \blacktriangleright V(A₁) = {Sunny, Overcast, Rain}
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$$\bullet C = \{Yes, No\}$$

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A decision tree is

• a tree $\mathcal{T} = (T, E)$ where

• each leaf $au \in T_{leaf}$ is assigned a class $C(au) \in C$,

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Inference: Given an input \vec{x} , we traverse the tree from the root to a leaf, always choosing edges labeled with values of attributes from \vec{x} . The output is the class labeling the leaf.

$$T = \{O, H, W, z_1, z_2, z_3, z_4, z_5\}$$

$$T_{leaf} = \{z_1, z_2, z_3, z_4, z_5\}, T_{int} = \{O, H, W\}$$

$$E = \{(O, H), (O, W), (H, z_1), (H, z_2), (O, z_3), (W, z_4), (W, z_5)\}$$

$$C(z_1) = C(z_4) = No, C(z_2) = C(z_3) = C(z_5) = Yes$$

$$A(O) = Outlook, A(H) = Humidity, A(W) = Wind$$

$$V(O, H) = Sunny, V(O, z_3) = Overcast, V(O, W) = Rain$$

$$V(H, z_1) = High, V(H, z_2) = Normal$$

$$V(W, z_4) = Strong, V(W, z_5) = Weak$$

Inference: For (*Rain*, *Hot*, *High*, *Strong*) we reach z_4 , yielding *No*.

Consider a training dataset

$$\mathcal{D} = \{ (\vec{x}_k, c_k) \mid k = 1, \dots, p \}$$

Here $\vec{x}_k \in V(A_1) \times \cdots \times V(A_k)$ and $c_k \in C$ for every k.

Technically $\ensuremath{\mathcal{D}}$ can be a multiset containing several occurrences of the same vector.

Index	Outlook	Temperature	Humidity	Wind	PlayTennis
1	Sunny	Hot	High	Weak	No
2	Sunny	Hot	High	Strong	No
3	Overcast	Hot	High	Weak	Yes
4	Rain	Mild	High	Weak	Yes
5	Rain	Cool	Normal	Weak	Yes
6	Rain	Cool	Normal	Strong	No
7	Overcast	Cool	Normal	Strong	Yes
8	Sunny	Mild	High	Weak	No
9	Sunny	Cool	Normal	Weak	Yes
10	Rain	Mild	Normal	Weak	Yes
11	Sunny	Mild	Normal	Strong	Yes
12	Overcast	Mild	High	Strong	Yes
13	Overcast	Hot	Normal	Weak	Yes
14	Rain	Mild	High	Strong	No

 $\mathcal{D} = \{((Sunny, Hot, High, Weak), No), \\ ((Sunny, Hot, High, Strong), No)$

. . .

((Rain, Mild, High, Strong), No)

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- Otherwise, identify an attribute A ∈ A which best classifies the examples in D. For every v ∈ V(A) we obtain

$$\mathcal{D}_{\mathbf{v}} = \{ \vec{x} \mid \vec{x} \in \mathcal{D}, A(\vec{x}) = \mathbf{v} \}$$

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- for every $v \in V(A)$ introduce an edge (τ, τ_v) assigned v.

- 1: function ID3(dataset \mathcal{D} , attribute set \mathcal{A})
- 2: Create a root node τ for the tree
- 3: if $\mathcal{D} = \emptyset$ then
- 4: Return the single node τ assigned with a default class.
- 5: else if all examples in \mathcal{D} are of the same class c then
- 6: Return the single-node tree, where au is assigned c
- 7: else if set of attributes \mathcal{A} is empty then
- 8: Return the single-node tree where τ is assigned the most common class in \mathcal{D}
- 9: else
- 10: Choose attribute $A \in A$ best classifying examples in \mathcal{D} .
- 11: Set the decision attribute for τ to A
- 12: for each value $v \in D(A)$ do
- 13: Compute a decision tree ID3($\mathcal{D}_{v}, \mathcal{A} \setminus \{A\}$) with root τ_{v} ,
- 14: add a new edge (τ, τ_v) assigned v.
- 15: end for
- 16: end if
- 17: return au
- 18: end function

Best Classifying Attribute

We aim to choose an attribute that best informs us about the class. As a result, we would possibly use as few attributes as possible and obtain a small tree containing only class-relevant decisions.

How to choose an attribute that best classifies examples in \mathcal{D} ?

There are several measures used in practice.

The most common are

- information gain
- Gini impurity decrease

The information gain is based on the notion of entropy.

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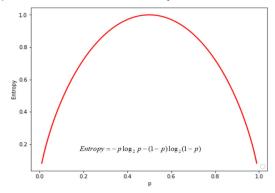
▶ The *information gain* of an attribute A is then defined by

$$extsf{Gain}(\mathcal{D}, \mathcal{A}) = extsf{Entropy}(\mathcal{D}) - \sum_{v \in V(\mathcal{A})} rac{|\mathcal{D}_v|}{|\mathcal{D}|} extsf{Entropy}(\mathcal{D}_v)$$

In every step of the ID3 algorithm, we choose an attribute maximizing the information gain for the current dataset \mathcal{D} .

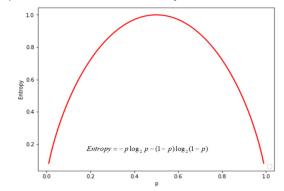
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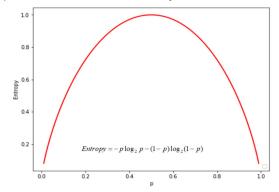
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∑_{v∈V(A)} |D|/|D| Entropy(D_v) is weighted uncertainty of classes in each D_v (weighted by the relative size of D_v).
 Gain(D, A) measures reduction in uncertainty of classes by splitting D according to A.

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The *impurity decrease* of an attribute A is then defined similarly to the gain in the entropy case

$$\mathit{ImpDec}(\mathcal{D}, A) = \mathit{Gini}(\mathcal{D}) - \sum_{v \in V(A)} \frac{|\mathcal{D}_v|}{|\mathcal{D}|} \mathit{Gini}(\mathcal{D}_v)$$

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What is the intuition behind $Gini(\mathcal{D})$?

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Assume we randomly independently choose objects from \mathcal{D} .

 $1 - \sum_{c \in C} p_c^2$ is the probability of choosing two objects of different classes in two consecutive independent trials. Indeed, p_c is the probability of choosing an object of class c, p_c^2 the probability of choosing objects of the class c twice, and $\sum_{c \in C} p_c^2$ the probability of choosing two objects of the same class.

In what follows (and at the exam), we will work only with the Gini impurity as it is easier to compute by hand.

Consider our tennis example (see the table).

Consider the whole dataset
$$D$$
.
 $p_{Yes} = 9/14$
 $p_{No} = 5/14$
 $Gini(D) = 1 - (9/14)^2 - (5/14)^2 = 0.459$

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 $Gini(\mathcal{D}) = 1 - (9/14)^2 - (5/14)^2 = 0.459$
For $A = Outlook$ we get
 $Gini(\mathcal{D}_{Sunny}) = 1 - (2/5)^2 - (3/5)^2 = 0.48$
 $Gini(\mathcal{D}_{Overcast}) = 1 - 1^2 - 0^2 = 0$
 $Gini(\mathcal{D}_{Rain}) = 1 - (3/5)^2 - (2/5)^2 = 0.48$
Thus

 $ImpDec(\mathcal{D}, Outlook) =$ $0.459 - (5/14) \cdot 0.48 - (4/14) \cdot 0 - (5/14) \cdot 0.48$ = 0.117

•
$$ImpDec(\mathcal{D}, Temperature) = 0.018$$

• $ImpDec(\mathcal{D}, Humidity) = 0.091$

So the largest information gain is given by the Outlook.

Going further on, consider $\mathcal{D} = \mathcal{D}_{Sunny}$. We get

- $ImpDec(\mathcal{D}, Temperature) = 0.279$
- $ImpDec(\mathcal{D}, Humidity) = 0.48$
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Now consider $\mathcal{D} = \mathcal{D}_{Rain}$.

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- how close they are to the root of \mathcal{T} ,
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Then define the importance as the average decrease in Gini impurity (i.e., average ImpDec) in the nodes of T[A]:

$$\textit{GiniImportance}(\textit{A}) = \sum_{ au \in \mathcal{T}[\textit{A}]} rac{|\mathcal{D}[au]|}{|\mathcal{D}|}\textit{ImpDec}(\mathcal{D}[au],\textit{A})$$

Continuous-Valued Attributes

What if values of an attribute A come from a continuous variable? A is a numerical attribute that can take any value in an interval, such as temperature, size, time, etc.

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Consider an internal node $\tau \in T_{int}$ assigned such a continuous attribute *A*. Then

- τ is assigned a threshold value called a *cut point* $H \in \mathbb{R}$,
- there are two edges e_{true} , e_{false} from τ ,
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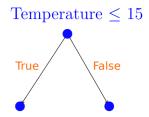
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During inference, when considering an example \vec{x} in the node τ ,

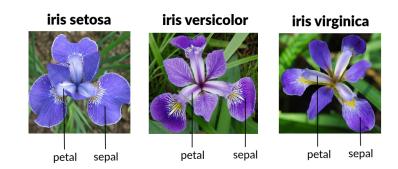
- evaluate $A(\vec{x}) \leq H$,
- ▶ if $A(\vec{x}) \leq H$, then follow e_{true} ,

else follow e_{false}.



In training, the cut point is chosen from the attribute values in the training set using information gain/impurity decrease similar to discrete attributes.

Iris Example



Attributes

Sepal.Length, Sepal.Width, Petal.Length, Petal.Width

Classes (Variety) Setosa, Versicolor, Virginica

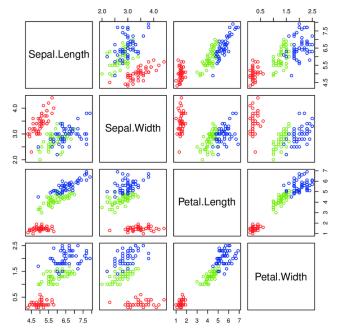
Iris Example

_

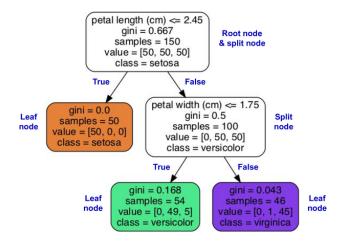
The dataset (150 examples):

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Variety
5.5	3.5	1.3	0.2	Setosa
6.8	2.8	4.8	1.4	Versicolor
6.7	3.1	4.7	1.5	Versicolor
6.9	3.1	5.1	2.3	Virginica
7.3	2.9	6.3	1.8	Virginica
5.4	3.7	1.5	0.2	Setosa
4.6	3.4	1.4	0.3	Setosa
6.2	2.8	4.8	1.8	Virginica
5.4	3.0	4.5	1.5	Versicolor
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5.9	3.2	4.8	1.8	Versicolor
5.6	2.8	4.9	2.0	Virginica

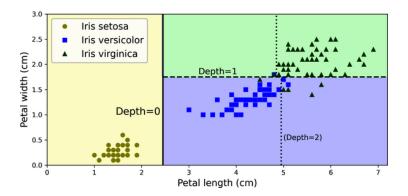
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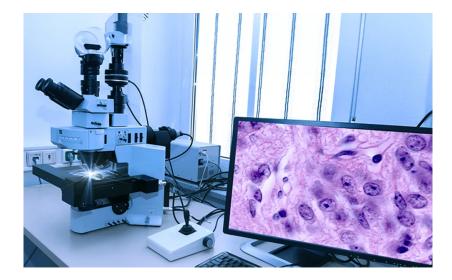
Iris Example - Decision Tree



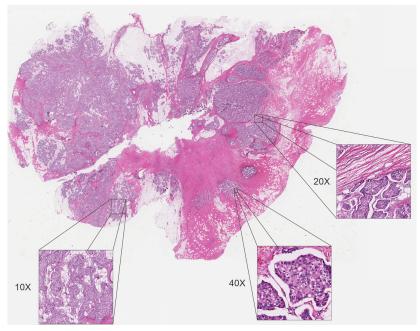
Iris Example - Decision Tree Boudaries



If the leaves are split further, the Depth = 2 boundary would be added.



Wisconsin Breast Cancer Dataset



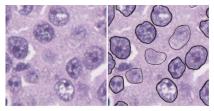
The Wisconsin Breast Cancer Dataset (WBCD) is used for binary classification of tumors.

- Origin: Created by Dr. William H. Wolberg at the University of Wisconsin-Madison.
- **Samples**: 569 breast cancer cases.

Target Variable:

- 0 = Benign (non-cancerous)
- 1 = Malignant (cancerous)

Features: 30 numerical attributes describing cell nuclei.



Each sample is characterized by 10 different measurements:

- Radius, Texture, Perimeter, Area
- Smoothness, Compactness, Concavity
- Concave Points, Symmetry, Fractal Dimension
- Each feature has three statistical measures:
 - Mean (Average over cells in the sample)
 - Standard Error (SE) (Variation within the sample)
 - Worst (Largest value in the sample)

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	
0	842302	м	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	
1	842517	M	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	
2	84300903	M	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	
3	84348301	M	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	
4	84358402	м	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	

Just asked ChatGPT: Train a decision tree predicting the diagnosis and show me graphically the result.

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I'll train a decision tree classifier to predict the **diagnosis** from your **cleaned_breast_cancer_dataset.csv** and visualize the tree. Let me first inspect the dataset to confirm its structure.

The dataset has 569 samples and 32 columns, including an ID column and a diagnosis column (target variable). The diagnosis is encoded as 1 (Malignant) and 0 (Benign).

I will:

- 1. Remove the **ID** column.
- 2. Train a Decision Tree Classifier on the remaining features.
- 3. Visualize the trained tree.

(see the result shown separately; too large for a slide) Training Accuracy: 0.9956 Test Accuracy: 0.9474

```
import pandas as pd
import matplotlib.pvplot as plt
from sklearn.model selection import train test split
from sklearn.tree import DecisionTreeClassifier, plot tree
from sklearn.metrics import accuracy score
# Load dataset
file path = "cleaned breast cancer dataset.csv"
df = pd.read csv(file path)
# Remove ID column
df = df.drop(columns=["id"])
# Split data into features and target
X = df.drop(columns=["diagnosis"])
v = df["diagnosis"]
# Split into training and test sets
X train, X test, y train, y test = train test split(
   X, y, test size=0.2, random state=42)
# Train decision tree classifier
clf = DecisionTreeClassifier(max depth=4, random state=42)
clf.fit(X_train, y_train)
# Evaluate model
train accuracy = accuracy score(v train, clf.predict(X train))
test accuracy = accuracy score(y test, clf.predict(X test))
# Print accuracy
print(f"Training Accuracy: {train accuracy:.4f}")
print(f"Test Accuracy: {test accuracy:.4f}")
# Plot decision tree
plt.figure(figsize=(20,10))
plot tree(clf, feature names=X.columns, class names=["Benign", "Malignant"],
          filled=True. rounded=True)
plt.show()
```

Decision Trees

Practical Issues

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- Data preprocessing
- Model tunning (overfitting and underfitting)
- Sensitivity to changes in data/hyperparameters
- Learning representation problems (the XOR)

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Imbalanced classes might cause problems because of small information gain/impurity decrease in splitting.

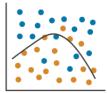
The behavior of the model on the training set:

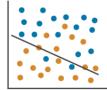


Right Fit

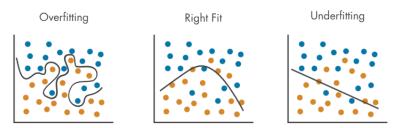
Underfitting





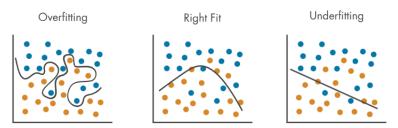


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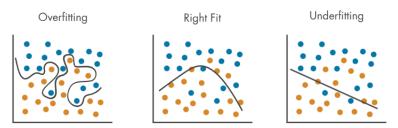
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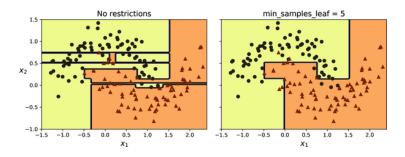
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- The left one is strongly overfitting. It would possibly not work well on new data.
- The right one is strongly underfitting. It would probably give poor classification results.
- The middle one seems good (but still needs to be tested on fresh data).

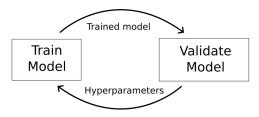
Model Tuning - Overfitting in Decision Trees



See the overfitting on the left and the "nice" model on the right. Both overfitting and underfitting are best avoided. But how do we find out?

Model Tuning (In General)

Recall from the first lecture:

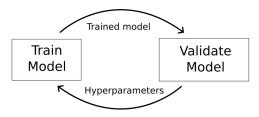


The validation should be done on a **validation set** separated from the training set.

We will discuss more sophisticated techniques later.

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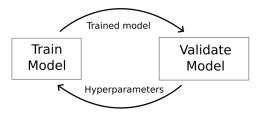
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What to observe? In the case of decision trees, one should observe the difference between performance measures (e.g., classification accuracy) on the training and validation sets.

The too-large difference implies an improperly fitting model.

There are several approaches available for decision trees.

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The post-pruning approach has been more successful in practice than the pre-pruning because it is usually hard to say when to stop growing the tree.

We shall meet this controversy also in deep learning, where recent history shows a similar phenomenon.

The ensemble methods will be covered later when we discuss random forests.

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- Minimum information gain/impurity decrease A small impurity decrease means that the split does not contribute too much to the classification (their proportions after a split are similar to proportions before a split). However, keep in mind that it is *weighted average impurity* after the split.

Post-Pruning - Reduced Error Pruning

Train a large tree and then remove nodes that make classification worse on the validation set.

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Given a decision tree \mathcal{T} and its internal node $\tau \in T_{int}$, we denote by $\mathcal{T}_{-\tau}$ the tree obtained from \mathcal{T} by removing the subtree rooted in τ , i.e., τ is a leaf of $\mathcal{T}_{-\tau}$.

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- 1: Train $\mathcal T$ to maximum fit on the *training dataset*.
- 2: while true do
- 3: $Err[\mathcal{T}] \leftarrow$ the error of \mathcal{T} on the validation set.

4: for
$$\tau \in T_{int}$$
 do

- 5: $Err[\mathcal{T}_{-\tau}] \leftarrow$ the error of $\mathcal{T}_{-\tau}$ on the validation set.
- 6: end for

7: **if**
$$Err[\mathcal{T}] \leq \min\{Err[\mathcal{T}_{-\tau}] \mid \tau \in T_{int}\}\}$$
 then return \mathcal{T}

8: **else**

9:
$$\mathcal{T} \leftarrow \operatorname{argmin}\{\operatorname{Err}[\mathcal{T}_{-\tau}] \mid \tau \in T_{\operatorname{int}}\}$$

10: end if

11: end while

The error $Err[\mathcal{T}]$ can be any measure of the "badness" of the decision tree \mathcal{T} . For example, 1 - Accuracy.

Other Pruning Methods

There are more pruning methods.

- Rule Post-Pruning:
 - Transform the tree into a set of rules. Rules correspond to paths in the tree; they have a form of implication: Specific values of attributes imply a class.
 - Remove the attribute conditions from the premises of the implications.

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Using cost complexity measure: Evaluate trees not only based on the classification error but also based on their size.

Typically introduce regularization into the error functions: Given a decision tree $\ensuremath{\mathcal{T}}$

 $Err_{\alpha}(\mathcal{T}) = Err(\mathcal{T}) + \alpha |\mathcal{T}|$

The original paper by Breiman et al. (1984) defined $Err(\mathcal{T})$ to be the misclassification rate on the training dataset, and $|\mathcal{T}|$ is the number of nodes of the tree \mathcal{T} .

Sensitivity to Small Changes and Randomness

 Decision trees are sensitive to small changes in data and hyperparameters.
 Several attributes may provide (almost) identical information gain but

divide the training dataset very differently.

Some implementations choose attributes partially in random (sci-kit-learn). You may get completely different trees. Sensitivity to Small Changes and Randomness

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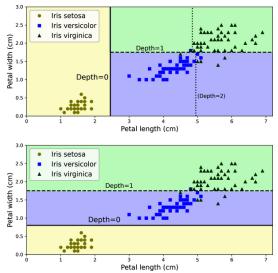
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A solution is to train an ensemble of many decision trees and then use majority voting for classification.

This is the fundamental idea behind random forests (see later lectures).

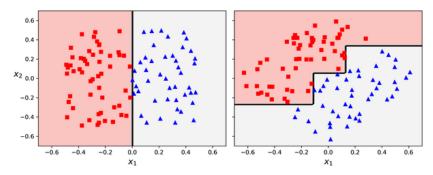
Iris - Illustration



Decision trees trained on the Iris dataset.

Iris Setosa is perfectly separated by many choices for the first split.

Axis Sensitivity



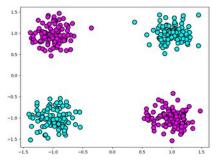
The decision makes divisions along particular axes:

That is, rotated data may result in a completely different model.

That is why decision trees are often preceded by the *principal component analysis (PCA)* transformation, which aligns data along the axes of maximum data variance.

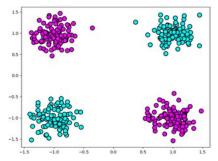
XOR Training Problem

Consider the following training dataset:

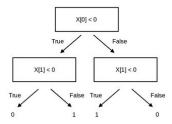


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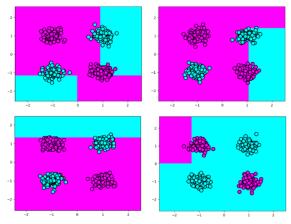


An ideal decision tree would look like this:



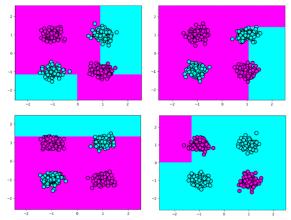
Attempts at Training on XOR

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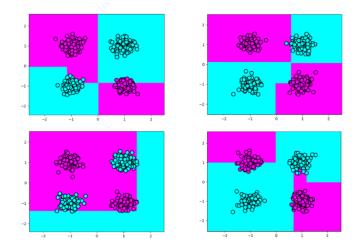


The problem: Both information gain and decrease in impurity consider only the relationship of a *single* attribute and the class.

However, there is no relationship between a single attribute and the class; both attributes need to be considered together!

More Attempts at Training on XOR

Max depth = 3:



It's better but still fails occasionally.

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- Little data preparation, unlike other techniques requiring normalization, dummy variables, or missing value removal.
- Handles numerical and categorical data.
- Not sensitive to outliers since the splitting is based on the proportion of examples within the split ranges and not on absolute values.
- The cost of using a well-balanced tree is logarithmic in the number of data points used to train it.

- Overfitting: Trees can be over-complex and not generalize well, needing pruning or limits on tree depth.
- Instability: Small data variations can result in very different trees. This is mitigated in ensemble methods.
- Non-smooth predictions: Decision trees make piecewise constant approximations, which are not suitable for extrapolation.

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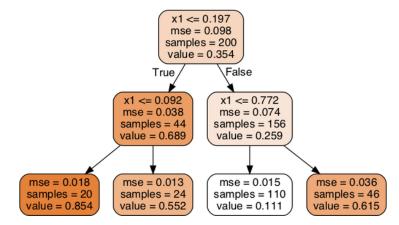
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- Difficulty learning certain concepts, such as XOR.
- Bias in trees: Decision trees can create biased trees if some classes dominate. Balancing the dataset is recommended.
- Learning optimal trees is NP-complete: Heuristic algorithms like greedy algorithms are used, which do not guarantee globally optimal trees. Ensemble methods can help.

History of Decision Trees

- Hunt and colleagues use exhaustive search decision-tree methods (CLS) to model human concept learning in the 1960's.
- In the late 70's, Quinlan developed ID3 with the information gain heuristic to learn expert systems from examples.
- Simultaneously, Breiman, Friedman, and colleagues develop CART (Classification and Regression Trees), similar to ID3.
- In the 1980s, various improvements were introduced to handle noise, continuous features, missing features, and improved splitting criteria. Various expert-system development tools results.
- Quinlan's updated decision-tree package (C4.5) released in 1993.

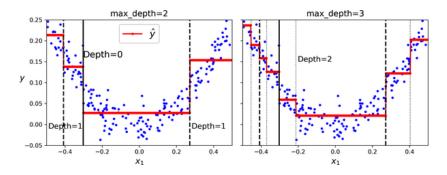
Comment on Regression Trees

Decision trees can also be used to approximate functions. Assign a function value to the leaves instead of classes.



Here, "mse" is the mean-squared-error.

Comment on Regression Trees



Intuitively, for every subinterval of x_1 , the value (the red line) is at the average y over the subinterval.

How are the subintervals being set?

A regression tree is a decision tree whose leaves are labeled by values from $\mathbb R.$

We follow the same procedure as in decision trees during inference on an input \vec{x} .

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The training procedure is the same as for the decision trees, except that the splits and cut points are selected differently.

Given a dataset $\mathcal{D} = \{(\vec{x_1}, d_1), \dots, (\vec{x_p}, d_p)\}$, we denote by $\overline{\mathcal{D}}$ the average *desired* value in \mathcal{D} , that is $\overline{\mathcal{D}} = \frac{1}{p} \sum_{k=1}^{p} d_k$.

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We are looking for a value H of the attribute A such that the split:

 $\mathcal{D}_{\leq H} = \{ (\vec{x}, d) \in \mathcal{D} \mid A(\vec{x}) \leq H \} \quad \mathcal{D}_{>H} = \{ (\vec{x}, d) \in \mathcal{D} \mid A(\vec{x}) > H \}$ Minimizes the following *split error*:

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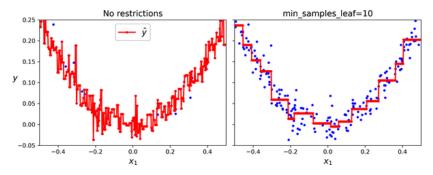
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If Δ is large enough, split on A and H that minimize the split error. Otherwise, step splitting and label the leaf with \overline{D}

Without any lower bound on the number of examples in the leaves, the algorithm will eventually overfit by splitting into (possibly) singleton leaves.



Probabilistic Classification

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The degree of belief (Bayesian), or the relative frequency (frequentists), is the *probability*.

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Experiment: Roll one dice once. Sample space: $\Omega = \{1, \dots, 6\}$

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 for all $\omega \in \Omega$,

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► Basic laws: $P(\Omega) = 1$, $P(\emptyset) = 0$, given disjoint sets A, B we have $P(A \cup B) = P(A) + P(B)$, $P(\Omega \setminus A) = 1 - P(A)$.

Conditional Probability and Independence

► P(A | B) is the probability of A given B (assume P(B) > 0) defined by

 $P(A \mid B) = P(A \cap B)/P(B)$

(We assume that B is all and only information known.)

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• A and B are independent if $P(A \cap B) = P(A) \cdot P(B)$.

It is easy to show that if P(B) > 0, then A, B are independent iff P(A | B) = P(A). Random Variables and Random Vectors

- ► A random variable X is a function $X : \Omega \to \mathbb{R}$. A dice: $X : \{1, ..., 6\} \to \{0, 1\}$ such that $X(n) = n \mod 2$.
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We use $X = (X_1, ..., X_d)$ where X_i is a random variable returning the *i*-th component of X.

Consider random variables X₁, X₂ and Y. The variables X₁, X₂ are *conditionally independent given* Y if for all x₁, x₂ and y we have that

$$P(X_1 = x_1, X_2 = x_2 | Y = y) = P(X_1 = x_1 | Y = y) \cdot P(X_2 = x_2 | Y = y)$$

Let Ω be a space of colored geometric shapes that are divided into two categories (1 and 0).

Assume a random vector $X = (X_{color}, X_{shape}, X_{cat})$ where

•
$$X_{color} : \Omega \to \{red, blue\},\$$

•
$$X_{shape} : \Omega \rightarrow \{circle, square\},\$$

$$\blacktriangleright X_{cat}: \Omega \to \{\mathbf{1}, \mathbf{0}\}.$$

The following tables give probability distribution of values:

category 1:

category	0 :
----------	------------

	circle	square
red	0.2	0.02
blue	0.02	0.01

	circle	square
red	0.05	0.3
blue	0.2	0.2

Example: $P(red, circle, \mathbf{1}) = P(X_{color} = red, X_{shape} = circle, X_{cat} = \mathbf{1}) = 0.2$

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$$P(red, circle) = P(X_{color} = red, X_{shape} = circle)$$

= P(red, circle, 1) + P(red, circle, 0)
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Thus also, all conditional probabilities can be computed:

$$P(\mathbf{1} \mid red, circle) = \frac{P(red, circle, \mathbf{1})}{P(red, circle)} = \frac{0.2}{0.25} = 0.8$$

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- Let Y be the random variable for the category which takes values in {0,1}.
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 - Denote by $\vec{x} \in \mathbb{R}^n$ values of X,
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Bayes classifier: Given a vector of feature values \vec{x} ,

$$C^{Bayes}(\vec{x}) := \begin{cases} \mathbf{1} & \text{if } P(Y = \mathbf{1} \mid X = \vec{x}) \ge P(Y = \mathbf{0} \mid X = \vec{x}) \\ \mathbf{0} & \text{otherwise.} \end{cases}$$

Intuitively, C^{Bayes} assigns to \vec{x} the most probable category it might be in.

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The Bayes classifier compares $P(Y = \mathbf{1} | X = (40g, 5cm))$ with $P(Y = \mathbf{0} | X = (40g, 5cm))$ and selects the more probable category given the features.

Crucial question: Is such a classifier good?

There are other classifiers, e.g., one which compares the weight divided by 10 with the diameter and decides based on the answer, or maybe a classifier that sums the weight and the diameter and compares the result with a constant, etc.

Bayes Classifier

Let C be an arbitrary *classifier*, that is a function that to every feature vector $\vec{x} \in \mathbb{R}^n$ assigns a class from $\{0, 1\}$.

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Define the error of the classifier C by

$$E_C = P(Y \neq C)$$

(Here we slightly abuse notation and apply *C* to samples, technically we apply the composition $C \circ X$ of *C* and *X* which first determines the features using *X* and then classifies according to *C*).

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Theorem

The Bayes classifier C^{Bayes} minimizes E_C , that is

 $E_{C^{Bayes}} = \min_{C \text{ is a classifier}} E_C$

Practical Use of Bayes Classifier

The crucial problem: The probability *P* is not known! In particular, where to get $P(Y = \mathbf{1} | X = \vec{x})$? Note that $P(Y = \mathbf{0} | X = \vec{x}) = 1 - P(Y = \mathbf{1} | X = \vec{x})$

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Given no other assumptions, this requires a table showing the probability of the category **1** for each possible feature vector \vec{x} . Where do you get these probabilities?

In some cases, the probabilities might come from the knowledge of the solved problem (e.g., applications in physics might be supported by a theory giving the probabilities).

In most cases, however, P is estimated from sampled data by

$$\bar{P}(Y = \mathbf{1} \mid X = \vec{x}) = \frac{\text{number of samples with } Y = \mathbf{1} \text{ and } X = \vec{x}}{\text{number of samples with } X = \vec{x}}$$

(We use \overline{P} to denote an estimate of P from data.)

Estimating P

Consider a problem with $X = (X_1, X_2, X_3)$ where each X_i returns either 0 or 1. What might the data look like?

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Part of the data table:

All data with $X_1 = 1$, $X_2 = 0$, $X_3 = 1$:

Y	X_1	<i>X</i> ₂	<i>X</i> ₃
1	1	0	1
1	0	1	1
0	1	0	1
0	0	0	1
1	0	0	0
0	1	1	1

Y	X_1	X_2	<i>X</i> ₃
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Estimate: $\bar{P}(\mathbf{1} \mid 1, 0, 1) = 2/3$

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The probability table and the necessary data are typically too large!

Concretely, if all X_1, \ldots, X_n are binary, there are 2^n probabilities $P(Y = \mathbf{1} \mid X = \vec{x})$, one for each possible $\vec{x} \in \{0, 1\}^n$.

Let's Look at It the Other Way Round

Theorem (Bayes, 1764)

$$P(A \mid B) = \frac{P(B \mid A) \cdot P(A)}{P(B)}$$

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Proof.

$$P(A \mid B) = \frac{P(A \cap B)}{P(B)} = \frac{\frac{P(A \cap B)}{P(A)} \cdot P(A)}{P(B)} = \frac{P(B \mid A) \cdot P(A)}{P(B)}$$

Determine the category for \vec{x} by computing

$$P(Y = y \mid X = \vec{x}) = \frac{P(Y = y) \cdot P(X = \vec{x} \mid Y = y)}{P(X = \vec{x})}$$

for both $y \in \{0, 1\}$ and deciding whether or not the following holds:

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for both $y \in \{0, 1\}$ and deciding whether or not the following holds:

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So, to make the classifier, we need to compute the following:

- The prior P(Y = 1) (then P(Y = 0) = 1 P(Y = 1))
- ► The conditionals $P(X = \vec{x} | Y = y)$ for $y \in \{0, 1\}$ and for every \vec{x}

Estimating the Prior and Conditionals

• P(Y = 1) can be easily estimated from data by

$$\bar{P}(Y = \mathbf{1}) = \frac{\text{number of samples with } Y = \mathbf{1}}{\text{number of all samples}}$$

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If the dimension of features is small, P(X = x | Y = y) can be estimated from data similarly as P(Y = 1 | X = x) by

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Unfortunately, for higher dimensional data too many samples are needed to estimate all $P(X = \vec{x} | Y = y)$ (there are too many \vec{x} 's).

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So where is the advantage of using the Bayes thm.??

We introduce *independence assumptions* about the features!

Naive Bayes

We assume that features are (conditionally) independent given the category. That is for all x = (x₁,...,x_n) and y ∈ {0,1} we assume:

$$P(X = x | Y = y) = P(X_1 = x_1, \cdots, X_n = x_n | Y)$$
$$= \prod_{i=1}^n P(X_i = x_i | Y = y)$$

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► Therefore, we only need to specify P(X_i = x_i | Y = y) for each possible pair of a feature-value x_i and y ∈ {0,1}.

Note that if all X_i are binary (values in $\{0, 1\}$), this requires specifying only 2n parameters:

$$P(X_i = 1 \mid Y = \mathbf{1})$$
 and $P(X_i = 1 \mid Y = \mathbf{0})$ for each X_i

as
$$P(X_i = 0 | Y = y) = 1 - P(X_i = 1 | Y = y)$$
 for $y \in \{0, 1\}$.

Compared to specifying 2^n parameters without any independence assumption.

Estimating the marginal probabilities

Estimate the probabilities $P(X_i = x_i | Y = y)$ by

$$\bar{P}(X_i = x_i \mid Y = y) = \frac{\text{number of samples with } X_i = x_i \text{ and } Y = y}{\text{number of samples with } Y = y}$$

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Example: Consider a problem with $X = (X_1, X_2, X_3)$ where each X_i returns either 0 or 1. The data is

Y	X_1	X_2	<i>X</i> ₃
1	1	0	1
1	0	1 1	
0	1	0	1
0	0	0	1
1	0	0	0
0	1	1	1

$$\bar{P}(X_1 = 1 | Y = \mathbf{1}) = 1/3 \qquad \bar{P}(X_1 = 1 | Y = \mathbf{0}) = 2/3
\bar{P}(X_2 = 1 | Y = \mathbf{1}) = 1/3 \qquad \bar{P}(X_2 = 1 | Y = \mathbf{0}) = 1/3
\bar{P}(X_3 = 1 | Y = \mathbf{1}) = 2/3 \qquad \bar{P}(X_3 = 1 | Y = \mathbf{0}) = 1$$

Naive Bayes - Example

Consider classification of geometric shapes:

- $X_1 \in \{\textit{small}, \textit{medium}, \textit{large}\}$
- $X_2 \in \{red, blue, green\}$
- $X_3 \in \{ square, triangle, circle \}$

Naive Bayes – Example

Consider classification of geometric shapes:

- $X_1 \in \{ small, medium, large \}$
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Assume that we have already estimated the following probabilities:

	Y = 1	Y = 0
$\bar{P}(Y)$	0.5	0.5
$\bar{P}(small \mid Y)$	0.4	0.4
$\bar{P}(medium \mid Y)$	0.1	0.2
$\bar{P}(large \mid Y)$	0.5	0.4
$\bar{P}(red \mid Y)$	0.9	0.3
$\overline{P}(blue \mid Y)$	0.05	0.3
$\bar{P}(green \mid Y)$	0.05	0.4
$\bar{P}(square \mid Y)$	0.05	0.4
$\bar{P}(triangle \mid Y)$	0.05	0.3
$\bar{P}(circle \mid Y)$	0.9	0.3

Does (*medium*, *red*, *circle*) belong to the category **1** ?

	Y = 1	Y = 0
$\bar{P}(Y)$	0.5	0.5
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$\bar{P}(medium \mid Y)$	0.1	0.2
$\bar{P}(red \mid Y)$	0.9	0.3
$\overline{P}(circle \mid Y)$	0.9	0.3

$$P(Y = \mathbf{1} | X = \vec{x}) =$$

= P(1) · P(medium | 1) · P(red | 1) · P(circle | 1) / P(X = \vec{x})
= 0.5 · 0.1 · 0.9 · 0.9 / P(X = \vec{x}) = 0.0405/P(X = \vec{x})

	Y = 1	Y = 0
$\bar{P}(Y)$	0.5	0.5
$\bar{P}(medium \mid Y)$	0.1	0.2
$\bar{P}(red \mid Y)$	0.9	0.3
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$$P(Y = \mathbf{1} | X = \vec{x}) =$$

= P(\mathbf{1}) \cdot P(medium | \mathbf{1}) \cdot P(red | \mathbf{1}) \cdot P(circle | \mathbf{1}) / P(X = \vec{x})
\delta 0.5 \cdot 0.1 \cdot 0.9 \cdot 0.9 / P(X = \vec{x}) = 0.0405 / P(X = \vec{x})

$$P(Y = \mathbf{0} | X = \vec{x}) =$$

= P(\mathbf{0}) \cdot P(medium | \mathbf{0}) \cdot P(red | \mathbf{0}) \cdot P(circle | \mathbf{0}) / P(X = \vec{x})
\delta 0.5 \cdot 0.2 \cdot 0.3 \cdot 0.3 / P(X = \vec{x}) = 0.009 / P(X = \vec{x})

(Note that we used the estimates \overline{P} of P to finish the computation above.)

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\delta 0.5 \cdot 0.1 \cdot 0.9 \cdot 0.9 / P(X = \vec{x}) = 0.0405 / P(X = \vec{x})

$$P(Y = \mathbf{0} | X = \vec{x}) =$$

= P(\mathbf{0}) \cdot P(medium | \mathbf{0}) \cdot P(red | \mathbf{0}) \cdot P(circle | \mathbf{0}) / P(X = \vec{x})
\delta 0.5 \cdot 0.2 \cdot 0.3 \cdot 0.3 / P(X = \vec{x}) = 0.009 / P(X = \vec{x})

(Note that we used the estimates \bar{P} of P to finish the computation above.) Apparently,

$$P(Y = \mathbf{1} \mid X = \vec{x}) \doteq 0.0405 / P(X = \vec{x}) > 0.009 / P(X = \vec{x}) \doteq P(\mathbf{0} \mid X = \vec{x})$$

So we classify \vec{x} to the category **1**.

Estimating Probabilities in Practice

We already know that $P(X_i = x_i | Y = y)$ can be estimated by

$$\bar{P}(X_i = x_i \mid Y = y) = \ell_{y, x_i} / \ell_y$$

where

Estimating Probabilities in Practice

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$$\bar{P}(X_i = x_i \mid Y = y) = \ell_{y,x_i} / \ell_y$$

where

Problem: If, by chance, a rare value x_i of a feature X_i never occurs in the training data, we get

$$\bar{P}(X_i = x_i \mid Y = y) = 0$$
 for both $y \in \{\mathbf{0}, \mathbf{1}\}$

But then $\overline{P}(X = x) = 0$ for x containing the value x_i for X_i , and thus $\overline{P}(Y = y \mid X = x)$ is not well defined. Moreover, $\overline{P}(Y = y) \cdot \overline{P}(X = x \mid Y = y) = 0$ (for $y \in \{0, 1\}$) so even this cannot be used for classification.

Probability Estimation Example

Estimated probabilities:

					Y = 1	Y = 0
				$\overline{P}(Y)$	0.5	0.5
Training data:		$\bar{P}(small \mid Y)$	0.5	0.5		
Size	Color	Shape	Class	$\bar{P}(medium \mid Y)$	0	0
small	red	circle	1	$\bar{P}(large \mid Y)$	0.5	0.5
large	red	circle	1	$\bar{P}(red \mid Y)$	1	0.5
small	red	triangle	0	$\overline{P}(blue \mid Y)$	0	0.5
large	blue	circle	0	$\overline{P}(green \mid Y)$	0	0
				$\overline{P}(square \mid Y)$	0	0
				$\overline{P}(triangle \mid Y)$	0	0.5
				$\overline{P}(circle \mid Y)$	1	0.5

Note that $\overline{P}(medium \mid \mathbf{1}) = P(medium \mid \mathbf{0}) = 0$ and thus also $\overline{P}(medium, red, circle) = 0$.

So what is $\overline{P}(1 \mid medium, red, circle)$?

Smoothing

To account for estimation from small samples, probability estimates are adjusted or *smoothed*.

Smoothing

- To account for estimation from small samples, probability estimates are adjusted or *smoothed*.
- Laplace smoothing adds one to every count of feature values

$$\tilde{P}(X_i = x_i \mid Y = y) = \frac{\ell_{y,x_i} + 1}{\ell_y + v_i}$$

where

To understand note that

$$\ell_y = \sum_{x_i \text{ is a value of } X_i} \ell_{y,x_i}$$

and thus

$$\begin{split} \bar{P}(X_i = x_i \mid Y = y) &= \ell_{y, x_i} / \sum_{x_i \text{ is a value of } X_i} \ell_{y, x_i} \\ \tilde{P}(X_i = x_i \mid Y = y) &= (\ell_{y, x_i} + 1) / \sum_{x_i \text{ is a value of } X_i} (\ell_{y, x_i} + 1) \end{split}$$

Laplace Smoothing Example

Assume training set contains 10 samples of category 1:

- 4 small
- 0 medium
- ▶ 6 large

Laplace Smoothing Example

Assume training set contains 10 samples of category 1:

- 4 small
- 0 medium
- 6 large

Estimate parameters as follows

- $\tilde{P}(small \mid \mathbf{1}) = (4+1)/(10+3) = 0.384$
- $\tilde{P}(medium \mid \mathbf{1}) = (0+1)/(10+3) = 0.0769$
- $\tilde{P}(large \mid \mathbf{1}) = (6+1)/(10+3) = 0.538$

Continuous Features

 Ω may be (potentially) continuous, X_i may assign a continuum of values in \mathbb{R} .

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The probabilities are computed using *probability density p*: ℝ → ℝ⁺.
 A random variable X : Ω → ℝ⁺ has a density *p* : ℝ → ℝ⁺ if for every interval [*a*, *b*] we have

$$P(a \le X \le b) = \int_a^b p(x) dx$$

Usually, $P(X_i | Y = y)$ is used to denote the *density* of X_i conditioned on Y = y.

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Usually, $P(X_i | Y = y)$ is used to denote the *density* of X_i conditioned on Y = y.

- The densities $P(X_i | Y = y)$ are usually estimated using Gaussian densities as follows:
 - Estimate the mean μ_{iy} and the standard deviation σ_{iy} based on training data.

Then put

$$ar{P}(X_i \mid Y = y) = rac{1}{\sigma_{iy}\sqrt{2\pi}} \exp\left(rac{-(X_i - \mu_{iy})^2}{2\sigma_{iy}^2}
ight)$$

Tends to work well despite rather a strong assumption of conditional independence of features.

- Tends to work well despite rather a strong assumption of conditional independence of features.
- Experiments show that it is quite competitive with other classification methods.

Even if the probabilities are not accurately estimated, it often picks the correct maximum probability category.

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- Typically handles outliers and noise well in the discrete version. In the continuous case depends on the way the parameters are estimated (e.g., the mean is very sensitive to outliers).
- Missing values are easy to deal with; use only non-missing values in the computation of P
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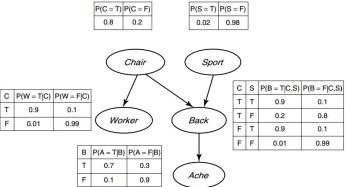
Bayesian networks are a graphical model that uses a directed acyclic graph to specify dependencies among variables.

Bayesian Networks - Frample P(S = T) | P(S = F)P(C = T) P(C = F)0.8 0.2 0.02 0.98 Chair Sport P(B = T|C,S) P(B = F|C,S)S С С P(W = T|C) P(W = F|C)т т 0.9 0.1 т 0.9 0.1 т F 0.2 0.8 Worker Back F 0.01 0.99 F Т 0.9 0.1 F F 0.01 0.99 P(A = T|B) P(A = F|B)в т 0.7 0.3 Ache F 0.1 0.9

Now, e.g.,

 $P(C, S, W, B, A) = P(C) \cdot P(S) \cdot P(W \mid C) \cdot P(B \mid C, S) \cdot P(A \mid B)$

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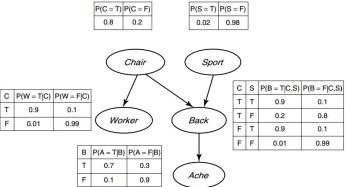


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Now, we may, e.g., infer the probability P(C = T | A = T) that we sit in the wrong chair, assuming that our back aches. We have to store only 10 numbers as opposed to $2^5 - 1$ possible probabilities for all vectors of values of C, S, W, B, A.

Bayesian Networks – Learning & Naive Bayes

Many algorithms have been developed for learning:

- the structure of the graph of the network,
- the conditional probability tables.

The methods are based on maximum-likelihood estimation, gradient descent, etc.

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Can you express the naive Bayes for Y, X_1, \ldots, X_n using a Bayesian network?

Classifier Evaluation

Assume binary classification into two classes $\{0, 1\}$.

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There are many possible metrics ...

I will call the class 1 *positive* and the class 0 *negative*. Note that the class 0 is not negative in the numerical sense but in the absence of something (e.g., predicted illness).

		Pred	icted
		1	0
Actual	1	ΤP	FN
Actual	0	FP	ΤN

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Index	1	2	3	4	5	6	7	8	9	10	11	12
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Predicted	0	0	1	1	1	1	1	1	1	0	0	0
Result	FN	FN	ΤP	ΤP	ΤP	ΤP	ΤP	ΤP	FP	ΤN	ΤN	ΤN

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Terminology

- TP aka hit
- TN aka correct rejection
- ▶ FP aka type I error, false alarm, overestimation
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In what follows, we also use

- P = TP + FN of all cases with the *actual* class 1
- ▶ N = TN + FP of all cases with the *actual* class 0
- ▶ PP = TP + FP of all cases with the *predicted* class 1

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There is a large number of derived metrics. We consider some of the most used in practice.

Accuracy

$$\mathsf{Accuracy} = \frac{\mathsf{TP} + \mathsf{TN}}{\mathsf{P} + \mathsf{N}}$$

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The Accuracy is

$$\mathsf{ACC} = \frac{\mathsf{TP} + \mathsf{TN}}{\mathsf{P} + \mathsf{N}} = \frac{6+3}{12} = \frac{3}{4}$$

Accuracy can be misleading when the classes are imbalanced:

- Consider 100 cases, 90 in the class 0 and 10 in the class 1,
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However, the classifier is pretty bad in the positive cases. In the case of cancer prediction, such a classifier would be a disaster.

Precision & Recall

To mitigate the defect of the Accuracy, we may compute the following metrics:

$$Precision = \frac{TP}{PP} \quad (= how often is predicted positive actually positive)$$

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$$Recall = \frac{TP}{P} \quad (= how often is actually positive predicted positive)$$

Recall is also known as true positive rate, sensitivity, hit rate, and power.

Precision & Recall - Example

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- Precision measures how often is the patient predicted to be ill truly ill (in our case, 6/7)
- Recall measures how often is an ill patient found to be ill (in our case, 6/8)

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$$\begin{aligned} &\mathsf{Precision} = 1\\ &\mathsf{Recall} = \frac{1}{10} \end{aligned}$$

You can see that the predictor is very precise (on the class 1) but useless due to the weak Recall.

Let us get back to our cancer example:

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Consider Precision and Recall.

By now, you should remember what they measure.

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Which of the two is more important in medicine?

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Can we get a single number summarizing both Precision and Recall?

For example, to compare two classifiers.

F₁ Score

 F_1 score is the harmonic mean of Recall and Precision:

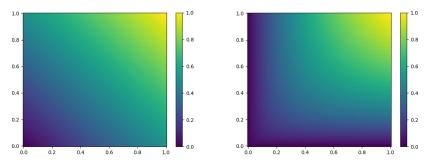
$$\mathsf{F}_{1} = \frac{2}{\mathsf{Recall}^{-1} + \mathsf{Precision}^{-1}} = \frac{2\mathsf{TP}}{2\mathsf{TP} + \mathsf{FP} + \mathsf{FN}}$$

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Compare the arithmetic (left) and harmonic (right) mean:



The harmonic mean prefers the two values closer to each other. For example, the harmonic mean of 2/3 and 1/3 is (approx) 0.44444.

F₁ Score - Examples

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Our imbalanced example:

Actual	Predicted	
	Pos	Neg
Pos	1	9
Neg	0	90
Total	90 + 10 = 100	

Here $F_1 = \frac{2\text{TP}}{2\text{TP}+\text{FP}+\text{FN}} = (2 \cdot 1)/((2 \cdot 1) + 0 + 9) = 0.18$. Note that the average of Precision and Recall is 0.55, which would give us a much less severe warning that the classifier is bad.

Imbalanced Classes Once More

Note that the standard definitions of Precision and Recall for binary classifiers reveal only part of the truth.

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Precision = 90/99 Recall = 90/90 $F_1 = \frac{2\text{TP}}{2\text{TP} + \text{FP} + \text{FN}} = (2 \cdot 90)/(2 \cdot 90 + 9 + 0) = 0.95$

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All great, except that the classifier sucks on the negative cases. If you are concerned with the negative cases, swap the classes and compute another set of metrics.

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Works better with imbalanced classes.

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 Fowlkes-Mallows index is a geometric mean of Precision and Recall (used in clustering).

The geometric mean is between the arithmetic and harmonic mean. For example, the geometric mean of 2/3 and 1/3 is (approx) 0.4714.

More Derived Metrics

Positive predictive value (PPV),	False omission
precision = $\frac{TP}{PP}$ = 1 - FDR	rate (FOR) = $\frac{FN}{PN}$ = 1 - NPV
False discovery rate (FDR) = $\frac{FP}{PP}$ = 1 - PPV	Negative predictive value (NPV) $= \frac{TN}{PN} = 1 - FOR$

You can see that the negative predictive value becomes the Precision when we swap the classes (and vice versa).

More Derived Metrics

True positive rate (TPR), recall, sensitivity (SEN), probability of detection, hit rate, power $=\frac{TP}{P} = 1 - FNR$	False negative rate (FNR), miss rate = $\frac{FN}{P} = 1 - TPR$
False positive rate (FPR),	True negative rate (TNR),
probability of false alarm, fall-out	specificity (SPC), selectivity
$= \frac{FP}{N} = 1 - TNR$	$= \frac{TN}{N} = 1 - FPR$

Note that *specificity* becomes Recall when we swap the classes (and vice versa).

For example, medical doctors communicate in terms of *sensitivity* and *specificity*.

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 $\mathsf{TPR} = \mathsf{Sensitivity} = \mathsf{Recall} = \mathsf{TP}/\mathsf{P} = 6/8$

How often is positive predicted positive?

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TPR = Sensitivity = Recall = TP/P = 6/8

How often is positive predicted positive?

$$TNR = Specificity = TN/N = 3/4$$

How often is negative predicted negative?

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$$FNR = Miss rate = FN/P = 2/8$$

How often is positive predicted negative?

Evaluating Multi-class Classifiers

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Here each h_k has been predicted for the k-the example (\vec{x}_k, c_k) .

How good are the predictions h_1, \ldots, h_p w.r.t. c_1, \ldots, c_p ? There are many possible metrics ...

Consider an arbitrary (finite) number of classes in C.

Confusion Matrix

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Now, given two classes $i, j \in C$ we denote by M_{ij} the number of samples of class *i* classified into the class *j*.

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Formally,

$$M_{ij} = |\{k \mid c_k = i \land h_k = j\}|$$

Actual	Predicted				
	1	•••	j	•••	т
1	<i>M</i> ₁₁	•••	M_{1j}	•••	M_{1m}
÷	÷		÷		÷
i	M_{i1}	• • •	M _{ij}	• • •	M _{im}
:	÷		÷		÷
т	M_{m1}	•••	M _{mj}	•••	M_{mm}

Example

Actual	Predicted
big	big
big	big
small	big
medium	medium
big	small
big	big
small	small
small	small
medium	medium
medium	small
small	small
big	big
medium	small
small	medium
big	big

Example

Actual	Predicted
big	big
big	big
small	big
medium	medium
big	small
big	big
small	small
small	small
medium	medium
medium	small
small	small
big	big
medium	small
small	medium
big	big

Actual	Predicted		
	big	medium	small
big	5	0	1
medium	0	2	2
small	1	1	3

Note that the diagonal counts the correctly classified samples.

The off-diagonal elements correspond to misclassified samples.

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Accuracy =
$$\frac{\sum_{k=1}^{m} M_{kk}}{M_{\bullet \bullet}}$$

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For a given class $i \in C$:

$$Precision[i] = \frac{M_{ii}}{M_{\bullet i}} \qquad \text{Recall}[i] = \frac{M_{ii}}{M_{i\bullet}}$$

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Now, the metrics:

Accuracy =
$$\frac{\sum_{k=1}^{m} M_{kk}}{M_{\bullet \bullet}}$$

For a given class $i \in C$:

$$\begin{aligned} &\mathsf{Precision}[i] = \frac{M_{ii}}{M_{\bullet i}} \quad \mathsf{Recall}[i] = \frac{M_{ii}}{M_{i\bullet}} \\ &\mathsf{F}_1[i] = \frac{2 * \mathsf{Precision}[i] * \mathsf{Recall}[i]}{\mathsf{Precision}[i] + \mathsf{Recall}[i]} \end{aligned}$$

Note that Precision, Recall, and F_1 can be defined only for a given class!

Example

Actual	Predicted		
	big	medium	small
big	5	0	1
medium	0	2	2
small	1	1	3

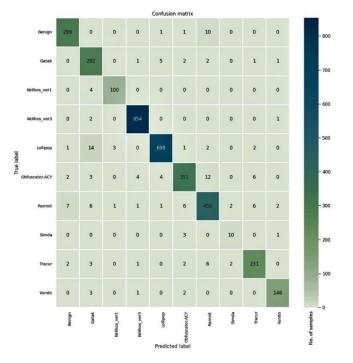
Compute the metrics.

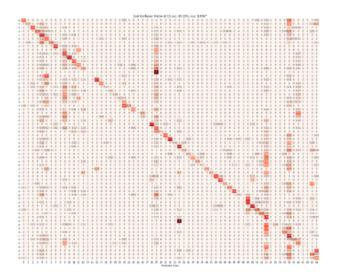
Example

Accuracy = $(5+2+3)/15 = 0.66$	5
Precision[big] = 5/6	Actual
Precision[medium] = 2/3	big
Precision[small] = 3/6	medium
Recall[big] = 5/6	small
Recall[medium] = 2/4	
Recall[small] = 3/5	
$F_1[\text{big}] = \frac{2 * (5/6) * (5/6)}{(5/6) + (5/6)} = 5$	/6 = 0.83
F_1 [medium] = 0.57	
F_1 [medium] = 0.54	

How do you get a single number out of these? Average Precision, Recall, and F_1 are usually computed, but one needs to be careful about the variance.

Actual	Predicted		
	big	medium	small
big	5	0	1
medium	0	2	2
small	1	1	3





Machine learning/data mining is needed to understand the matrix.

Probabilistic Classifier Evaluation

Assume binary classification into two classes $\{0, 1\}$.

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Consider a classification dataset:

 $\{(\vec{x}_k, c_k) \mid k = 1, \ldots, p\}$

Here \vec{x}_k is a vector of attributes/features and $c_k \in C$ for all k.

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Consider a sequence of predictions generated by a classifier. Now the classifier returns *probability of class* 1 for a given input:

$$h_1,\ldots,h_p\in[0,1]$$

Here each h_k has been predicted for the k-the example (\vec{x}_k, c_k) .

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Here each h_k has been predicted for the k-the example (\vec{x}_k, c_k) .

How to interpret the predictions h_1, \ldots, h_p ? How good are the predictions h_1, \ldots, h_p w.r.t. c_1, \ldots, c_p ?

Let us fix predictions h_1, \ldots, h_p .

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$$h_k^T = \begin{cases} 1 & \text{if } h_k \ge T \\ 0 & \text{if } h_k < T \end{cases}$$

For every T we can compute all the metrics (Precision, Recall, etc.)

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We obtain

$$\mathsf{TP}[T] = |\{k \mid h_k^T = 1 \land c_k = 1\}|$$

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and

 $TN[T], FP[T], FN[T], Accuracy[T], Precision[T], Recall[T], F_1[T], \dots$

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and

 $TN[T], FP[T], FN[T], Accuracy[T], Precision[T], Recall[T], F_1[T], \dots$

However, all metrics are now functions of the threshold T.

Index	1	2	3	4	5	6	7	8	9	10	11	12
Actual	1	1	1	1	1	0	0	1	1	0	0	0
Predicted	.98	.95	.9	.86	.66	.48	.43	.42	.36	.15	.1	.05
T=0.5	ΤP	ΤP	ΤP	TP	ΤP	ΤN	ΤN	FN	FN	ΤN	ΤN	ΤN
T=0.42	ΤP	TP	ΤP	TP	TP	FP	FP	TP	FN	ΤN	ΤN	ΤN
T=0.1	ΤP	TP	ΤP	TP	TP	FP	FP	TP	ΤP	FP	FP	ΤN

Index	1	2	3	4	5	6	7	8	9	10	11	12
Actual	1	1	1	1	1	0	0	1	1	0	0	0
Predicted	.98	.95	.9	.86	.66	.48	.43	.42	.36	.15	.1	.05
T=0.5	ΤP	ΤP	ΤP	TP	ΤP	ΤN	ΤN	FN	FN	ΤN	ΤN	ΤN
T=0.42	ΤP	ΤP	ΤP	TP	ΤP	FP	FP	ΤP	FN	ΤN	ΤN	ΤN
T=0.1	ΤP	ΤP	ΤP	TP	ΤP	FP	FP	TP	ΤP	FP	FP	ΤN

For example, consider T = 0.42, then

Index	1	2	3	4	5	6	7	8	9	10	11	12
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Predicted	.98	.95	.9	.86	.66	.48	.43	.42	.36	.15	.1	.05
T=0.5	TP	TP	ΤP	TP	ΤP	ΤN	TN	FN	FN	ΤN	ΤN	ΤN
T=0.42	TP	TP	ΤP	TP	ΤP	FP	FP	ΤP	FN	ΤN	ΤN	ΤN
T=0.1	TP	TP	ΤP	TP	ΤP	FP	FP	TP	ΤP	FP	FP	ΤN

For example, consider T = 0.42, then

 $\mathsf{TP}[T] = 6$ $\mathsf{FP}[T] = 2$ $\mathsf{FN}[T] = 1$ $\mathsf{TN}[T] = 3$

Index	1	2	3	4	5	6	7	8	9	10	11	12
Actual	1	1	1	1	1	0	0	1	1	0	0	0
Predicted	.98	.95	.9	.86	.66	.48	.43	.42	.36	.15	.1	.05
T=0.5	ΤP	ΤP	ΤP	TP	TP	ΤN	TN	FN	FN	ΤN	ΤN	ΤN
T=0.42	ΤP	ΤP	ΤP	TP	TP	FP	FP	TP	FN	ΤN	ΤN	ΤN
T=0.1	ΤP	ΤP	ΤP	TP	ΤP	FP	FP	TP	ΤP	FP	FP	ΤN

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 $\mathsf{TP}[T] = 6$ $\mathsf{FP}[T] = 2$ $\mathsf{FN}[T] = 1$ $\mathsf{TN}[T] = 3$

Accuracy
$$[T] = rac{3+6}{12}$$
 Precision $[T] = rac{6}{6+2}$ Recall $[T] = rac{6}{6+1}$

Index	1	2	3	4	5	6	7	8	9	10	11	12
Actual	1	1	1	1	1	0	0	1	1	0	0	0
Predicted	.98	.95	.9	.86	.66	.48	.43	.42	.36	.15	.1	.05
T=0.5	TP	TP	ΤP	TP	ΤP	ΤN	ΤN	FN	FN	ΤN	ΤN	ΤN
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For example, consider T = 0.42, then

 $\mathsf{TP}[T] = 6$ $\mathsf{FP}[T] = 2$ $\mathsf{FN}[T] = 1$ $\mathsf{TN}[T] = 3$

Accuracy[T] =
$$\frac{3+6}{12}$$
 Precision[T] = $\frac{6}{6+2}$ Recall[T] = $\frac{6}{6+1}$
 $F_1[T] = \frac{2 \cdot 6/8 \cdot 6/7}{6/8 + 6/7} = 0.8$

Consider two metrics for a given T:

$$\mathsf{TPR}[T] = \frac{\mathsf{TP}[T]}{\mathsf{P}[T]} \qquad (\mathsf{True Positive Rate})$$

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$$\begin{aligned} \mathsf{TPR}[T] &= \frac{\mathsf{TP}[\mathsf{T}]}{\mathsf{P}[T]} & (\mathsf{True Positive Rate}) \\ \mathsf{FPR}[T] &= \frac{\mathsf{FP}[T]}{\mathsf{N}[T]} & (\mathsf{False Positive Rate}) \end{aligned}$$

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(True Positive Rate)
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ROC curve is then a function $\mathsf{ROC}:[0,1] \to [0,1]^2$ defined by

ROC(T) = (TPR[T], FPR[T])

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ROC curve is then a function $\mathsf{ROC}:[0,1] \to [0,1]^2$ defined by

ROC(T) = (TPR[T], FPR[T])

Observe that

ROC(0) = (1, 1)

Because the classifier with T = 0 simply classifies everything as positive, i.e., into the class 1.

Both TPR[T] and FPR[T] are non-increasing in T.

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Predicted	.98	.95	.9	.86	.66	.48	.43	.42	.36	.15	.1	.05

Index	1	2	3	4	5	6	7	8	9	10	11	12
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▶ $0.05 < T \le 0.10$: TPR = 1 and FPR = 4/5

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Index	1	2	3	4	5	6	7	8	9	10	11	12
Actual	1	1	1	1	1	0	0	1	1	0	0	0
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• $0.15 < T \le 0.36$: TPR = 1 and FPR = 2/5

Index	1	2	3	4	5	6	7	8	9	10	11	12
Actual	1	1	1	1	1	0	0	1	1	0	0	0
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- ▶ 0.43 < $T \le 0.48$: TPR = 5/7 and FPR = 1/5
- $0.48 < T \le 0.66$: TPR = 5/7 and FPR = 0

Index	1	2	3	4	5	6	7	8	9	10	11	12
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- $0.36 < T \le 0.42$: TPR = 6/7 and FPR = 2/5
- $0.42 < T \le 0.43$: TPR = 5/7 and FPR = 2/5
- 0.43 < $T \le$ 0.48: TPR = 5/7 and FPR = 1/5
- $0.48 < T \le 0.66$: TPR = 5/7 and FPR = 0
- $0.66 < T \le 0.86$: TPR = 4/7 and FPR = 0

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- 0.43 < $T \le$ 0.48: TPR = 5/7 and FPR = 1/5
- 0.48 < $T \le 0.66$: TPR = 5/7 and FPR = 0
- $0.66 < T \le 0.86$: TPR = 4/7 and FPR = 0
- $0.86 < T \le 0.90$: TPR = 3/7 and FPR = 0

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- $0.42 < T \le 0.43$: TPR = 5/7 and FPR = 2/5
- 0.43 < $T \le$ 0.48: TPR = 5/7 and FPR = 1/5
- 0.48 < $T \le 0.66$: TPR = 5/7 and FPR = 0
- $0.66 < T \le 0.86$: TPR = 4/7 and FPR = 0
- $0.86 < T \le 0.90$: TPR = 3/7 and FPR = 0
- $0.90 < T \le 0.95$: TPR = 2/7 and FPR = 0

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- 0.43 < $T \le$ 0.48: TPR = 5/7 and FPR = 1/5
- $0.48 < T \le 0.66$: TPR = 5/7 and FPR = 0
- $0.66 < T \le 0.86$: TPR = 4/7 and FPR = 0
- $0.86 < T \le 0.90$: TPR = 3/7 and FPR = 0
- $0.90 < T \le 0.95$: TPR = 2/7 and FPR = 0

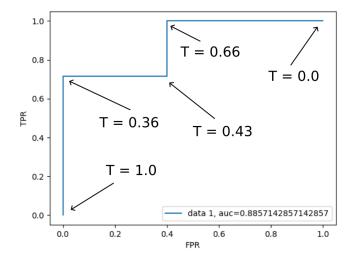
• $0.95 < T \le 0.98$: TPR = 1/7 and FPR = 0

Index	1	2	3	4	5	6	7	8	9	10	11	12
Actual	1	1	1	1	1	0	0	1	1	0	0	0
Predicted	.98	.95	.9	.86	.66	.48	.43	.42	.36	.15	.1	.05

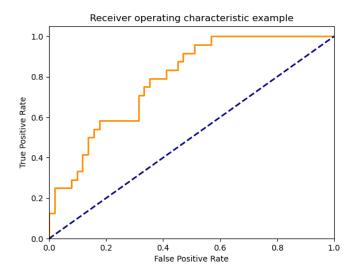
- $0.05 < T \le 0.10$: TPR = 1 and FPR = 4/5
- $0.10 < T \le 0.15$: TPR = 1 and FPR = 3/5
- 0.15 < $T \le$ 0.36: TPR = 1 and FPR = 2/5
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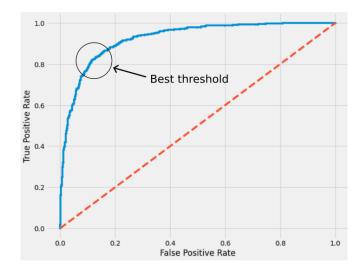


Iris Dataset - A Classifier



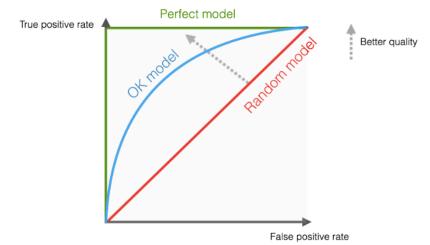
 $\mathsf{Example}$ from the scikit-learn manual - SVM classifier trained in Iris

Using ROC and Threshold



Search for the best threshold at the elbow of the ROC curve.

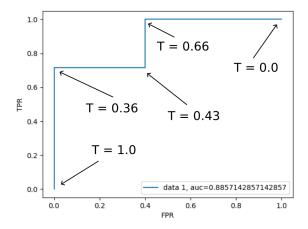
ROC - Explanation



The larger the *area under the ROC curve (ROC-AUC)*, the better. ROC-AUC ranges from 0 to 1. ROC-AUC \approx 0.5 indicates random guessing.

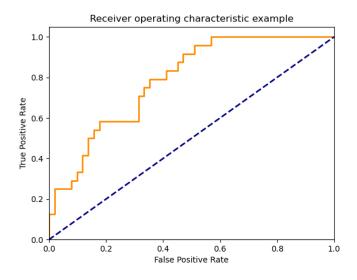
ROC-AUC

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 $\mathsf{ROC}\text{-}\mathsf{AUC} = 0.8857$

Iris - ROC-AUC



ROC-AUC = 0.79

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The ROC-AUC is the probability of succeeding in the $h_i > h_j$ test.

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There are still several questions unanswered:

- When to use the metrics.
- ▶ How to estimate the influence of sampling the dataset.

Use of Evaluation Metrics

In our case, the following scenarios are typical:

Final test: Evaluate the model on the test set (separated at the beginning of training) and then compute the metrics. May inform the user about the quality of the model.

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- Hyperparameter fine-tuning.
- Comparison of different models (e.g., KNN and decision trees).

Keep in mind that the metrics are artificial, and the results of the model are roughly summarized.

It would be best if you always strived to test the proper functionality of your model in as natural conditions as possible.

For example, a model for medical diagnosis should be evaluated by medical doctors who may observe many features of its behavior that are difficult to express quantitatively.

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We will consider these issues in some later lecture. Concretely,

- ► *Bias-variance* tradeoff
- Statistical tests for testing
 - significance of the metrics values,
 - paired t-tests for comparing models.

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Thresholding

- Introduce a threshold $0 \le t \le 1$
- Demand, one of the two metrics (typically the Recall), to be at least t. That is

 $\operatorname{Recall}_1 \geq t \qquad \operatorname{Recall}_2 \geq t$

Compare the values of the other metric numerically. In our case, decide whether

 $Precision_1 \ge Precision_2$

(Still need to be concerned about the statistical significance.)

Example

Actual condition	Predicted condition			Actual condition		edicted ndition
	Canc.	Canc. Non-canc.			Canc.	Non-canc.
Cancer	6	2		Cancer	5	3
Non-canc.	1	3		Non-canc.	0	4
Total	8 + 4 = 12			Total	8 +	- 4 = 12

$$\begin{aligned} & \mathsf{Precision}_1 = \frac{6}{7} \qquad \mathsf{Recall}_1 = \frac{6}{8} \\ & \mathsf{Precision}_2 = \frac{5}{5} = 1 \qquad \mathsf{Recall}_2 = \frac{5}{8} \end{aligned}$$

Consider a threshold t on the Recall.

The second classifier is better if the threshold t is 5/8.

If the threshold t is 6/8, then the second classifier is unacceptable.

Linear Models

Numerical features

► Throughout this lecture we assume that all features are numerical, i.e., feature vectors belong to ℝⁿ.

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- ► Throughout this lecture we assume that all features are numerical, i.e., feature vectors belong to ℝⁿ.
- Most non-numerical features can be conveniently transformed to numerical ones.

For example:

Colors {blue, red, yellow} can be represented by

 $\{(1,0,0),(0,1,0),(0,0,1)\}$

(one-hot encoding)

- Words can be embedded into vector spaces by various means (word2vec etc.)
- A black-and-white picture of x × y pixels can be encoded as a vector of xy numbers that capture the shades of gray of the pixels.

(Even though this is not the best way of representing images.)

Basic Problems

We consider two basic problems:

► (Binary) classification

Our goal: Classify inputs into two categories.

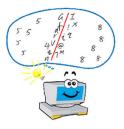


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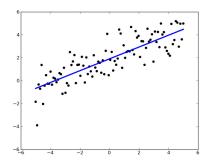
(Binary) classification

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Our goal: Find a (hypothesized) functional dependency in data.



Linear Models Binary Classification

Binary classification in \mathbb{R}^n

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• Given a set D of training examples of the form (\vec{x}, c) where $\vec{x} \in \mathbb{R}^n$ and $c \in \{0, 1\}$,

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Comments:

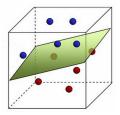
In practice, we often do not strictly demand h(x) = c for all training examples (x, c) ∈ D (often it is impossible)

We are more interested in good generalization, that is how well h classifies new instances that do not belong to D.
 (Recall that we usually evaluate accuracy of the resulting hypothesized function h on a test set.)

Models

We consider two kinds of models:

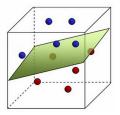
Linear (affine) classifiers (this lecture)



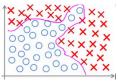
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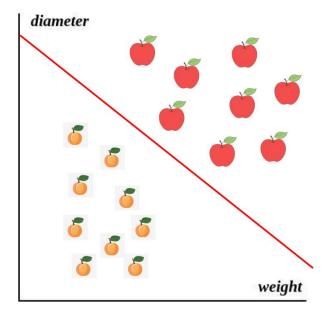
Linear (affine) classifiers (this lecture)



 Non-linear classifiers (kernel SVM, neural networks) (later lectures)



Linear Classifier – Example



Length and Scalar Product of Vectors

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- Scalar product $\vec{x} \cdot \vec{y}$ of vectors $\vec{x} = (x_1, \dots, x_n)$ and $\vec{y} = (y_1, \dots, y_n)$ defined by

$$\vec{x} \cdot \vec{y} = \sum_{i=1}^{n} x_i y_i$$

Recall that x̄ · ȳ = ||x̄|| ||ȳ|| cos θ where θ is the angle between x̄ and ȳ. That is x̄ · ȳ is the length of the projection of ȳ on x̄ multiplied by ||x̄||.

• Note that
$$\vec{x} \cdot \vec{x} = ||\vec{x}||^2$$

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$$h[\vec{w}](\vec{x}) := \begin{cases} 1 & w_0 + \sum_{i=1}^n w_i \cdot x_i \ge 0\\ 0 & w_0 + \sum_{i=1}^n w_i \cdot x_i < 0 \end{cases}$$

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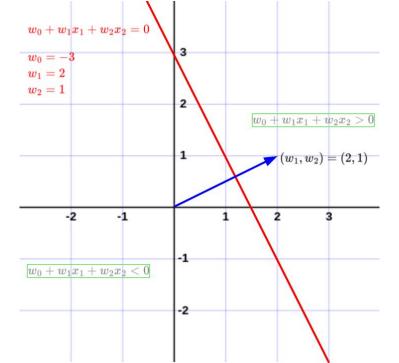
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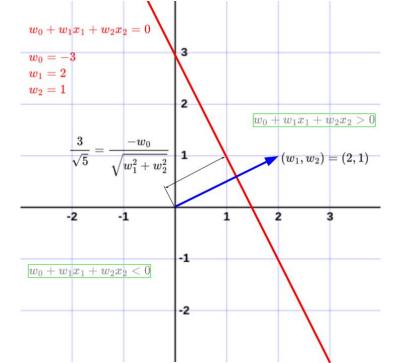
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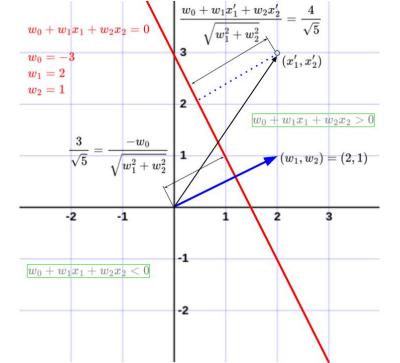
More succinctly:

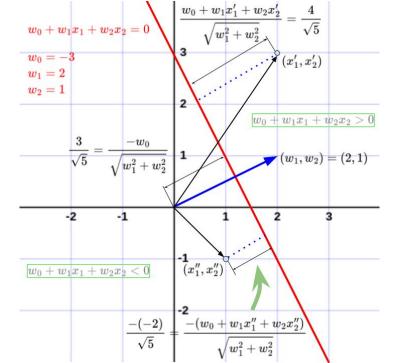
$$h(\vec{x}) = sgn\left(w_0 + \sum_{i=1}^n w_i \cdot x_i\right) \quad \text{where} \quad sgn(y) = \begin{cases} 1 & y \ge 0\\ 0 & y < 0 \end{cases}$$

We define separating hyperplane determined by \vec{w} as the set of all $\vec{x} \in \mathbb{R}^n$ satisfying $w_0 + \sum_{i=1}^n w_i \cdot x_i = 0$.

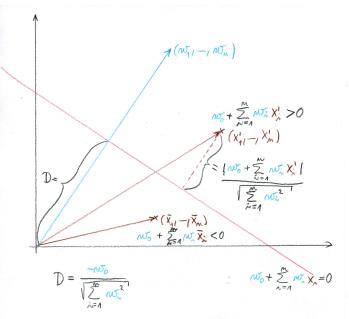








Linear Classifier – Geometry



Linear Classifier – Notation

Given
$$\vec{x} = (x_1, \dots, x_n) \in \mathbb{R}^n$$
 we define an *augmented feature vector*

 $\mathbf{\tilde{x}} = (x_0, x_1, \dots, x_n)$ where $x_0 = 1$

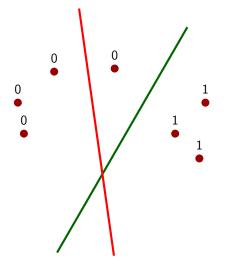
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This makes the notation for the linear classifier more succinct:

$$h[\vec{w}](\vec{x}) = sgn(\vec{w} \cdot \tilde{\mathbf{x}})$$

Linear Classifier – Learning



- classification in the plane using a linear classifier
- if a point is incorrectly classified, the learning algorithm turns the line (hyperplane) to improve the classification

Given a training set

$$D = \{ (\vec{x}_1, c_1), (\vec{x}_2, c_2) \}, \dots, (\vec{x}_p, c_p) \}$$

Here $\vec{x}_k = (x_{k1} \dots, x_{kn}) \in \mathbb{R}^n$ and $c_k \in \{0, 1\}$.

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► A weight vector $\vec{w} \in \mathbb{R}^{n+1}$ is **consistent with** D if $h[\vec{w}](\vec{x}_k) = sgn(\vec{w} \cdot \tilde{\mathbf{x}}_k) = c_k$ for all k = 1, ..., p

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D is **linearly separable** if there is a vector $\vec{w} \in \mathbb{R}^{n+1}$ which is consistent with *D*.

• Our goal is to find a consistent \vec{w} assuming that D is linearly separable.

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Idea: Cyclically go through the training examples in D and adapt weights. Whenever an example is incorrectly classified, turn the hyperplane so that the example becomes closer to its correct half-space.

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- $\vec{w}^{(0)}$ is randomly initialized close to $\vec{0} = (0, ..., 0)$
- ▶ In (t+1)-th step, $\vec{w}^{(t+1)}$ is computed as follows:

$$ec{w}^{(t+1)} = ec{w}^{(t)} - \varepsilon \cdot \left(h[ec{w}^{(t)}](ec{x}_k) - c_k
ight) \cdot \widetilde{\mathbf{x}}_k$$

Online learning algorithm:

Idea: Cyclically go through the training examples in D and adapt weights. Whenever an example is incorrectly classified, turn the hyperplane so that the example becomes closer to its correct half-space.

Compute a sequence of weight vectors $\vec{w}^{(0)}, \vec{w}^{(1)}, \vec{w}^{(2)}, \dots$

- $\vec{w}^{(0)}$ is randomly initialized close to $\vec{0} = (0, \dots, 0)$
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Theorem (Rosenblatt)

If D is linearly separable, then there is t^* such that $\vec{w}^{(t^*)}$ is consistent with D.

Example

Training set:

$$D = \{((2, -1), 1), ((2, 1), 1), ((1, 3), 0)\}$$

That is

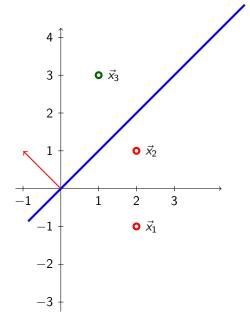
$$\vec{x}_1 = (2, -1) \qquad \qquad \tilde{x}_1 = (1, 2, -1) \\ \vec{x}_2 = (2, 1) \qquad \qquad \tilde{x}_2 = (1, 2, 1) \\ \vec{x}_3 = (1, 3) \qquad \qquad \tilde{x}_3 = (1, 1, 3)$$

$$c_1 = 1$$

 $c_2 = 1$
 $c_3 = 0$

Assume that the initial vector $\vec{w}^{(0)}$ is $\vec{w}^{(0)} = (0, -1, 1)$. Consider $\varepsilon = 1$.

Example: Separating by $\vec{w}^{(0)}$



Denoting $\vec{w}^{(0)} =$ $(w_0, w_1, w_2) = (0, -1, 1)$ the blue separating line is given by $w_0 + w_1x_1 + w_2x_2 = 0$.

The red vector normal to the blue line is (w_1, w_2) .

The points on the side of (w_1, w_2) are assigned 1 by the classifier, the others zero. (In this case $\vec{x_3}$ is assigned one and $\vec{x_1}, \vec{x_2}$ are assigned zero, all of this is inconsistent with $c_1 = 1, c_2 = 1, c_3 = 0.$)

Example: Computing $\vec{w}^{(1)}$

We have

$$\vec{w}^{(0)} \cdot \tilde{\mathbf{x}}_1 = (0, -1, 1) \cdot (1, 2, -1) = 0 - 2 - 1 = -3$$

thus

$$sgn\left(ec{w}^{(0)}\cdot\widetilde{\mathbf{x}}_{1}
ight)=0$$

and thus

$$sgn\left(ec{w}^{(0)}\cdot\widetilde{\mathbf{x}}_{1}
ight)-c_{1}=0-1=-1$$

(I.e., $\vec{x_1}$ is not correctly classified, and $\vec{w}^{(0)}$ is not consistent with D.) Hence,

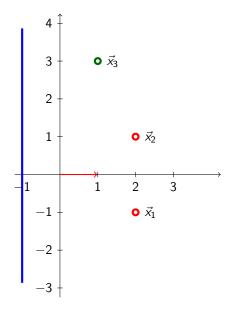
$$\vec{w}^{(1)} = \vec{w}^{(0)} - \left(sgn\left(\vec{w}^{(0)} \cdot \tilde{\mathbf{x}}_1 \right) - c_1 \right) \cdot \tilde{\mathbf{x}}_1$$

$$= \vec{w}^{(0)} + \tilde{\mathbf{x}}_1$$

$$= (0, -1, 1) + (1, 2, -1)$$

$$= (1, 1, 0)$$

Example: Separating by $\vec{w}^{(1)}$



Example: Computing $\vec{w}^{(2)}$

We have

$$\vec{w}^{(1)} \cdot \tilde{\mathbf{x}}_2 = (1, 1, 0) \cdot (1, 2, 1) = 1 + 2 = 3$$

thus

$$sgn\left(ec{w}^{(1)}\cdot\widetilde{\mathbf{x}}_{2}
ight)=1$$

and thus

$$sgn\left(ec{w}^{(1)}\cdot\widetilde{\mathbf{x}}_{2}
ight)-c_{2}=1-1=0$$

(I.e., $\vec{x_2}$ is currently correctly classified by $\vec{w}^{(1)}$. However, as we will see, $\vec{x_3}$ is not well classified.) Hence,

$$\vec{w}^{(2)} = \vec{w}^{(1)} = (1, 1, 0)$$

Example: Computing $\vec{w}^{(3)}$

We have

$$\vec{w}^{(2)} \cdot \tilde{\mathbf{x}}_3 = (1, 1, 0) \cdot (1, 1, 3) = 1 + 1 = 2$$

thus

$$sgn\left(ec{w}^{(2)}\cdot\widetilde{\mathbf{x}}_{3}
ight)=1$$

and thus

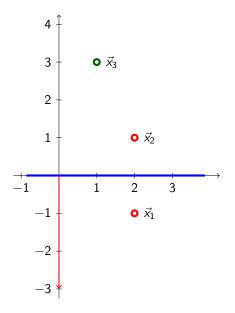
$$sgn\left(ec{w}^{(2)}\cdot\widetilde{\mathbf{x}}_{3}
ight)-c_{3}=1-0=1$$

(This means that \vec{x}_3 is not well classified, and $\vec{w}^{(2)}$ is not consistent with D.) Hence,

$$\vec{w}^{(3)} = \vec{w}^{(2)} - \left(sgn\left(\vec{w}^{(2)} \cdot \tilde{\mathbf{x}}_{3}\right) - c_{3}\right) \cdot \tilde{\mathbf{x}}_{3}$$

= $\vec{w}^{(2)} - \tilde{\mathbf{x}}_{3}$
= $(1, 1, 0) - (1, 1, 3)$
= $(0, 0, -3)$

Example: Separating by $\vec{w}^{(3)}$



Example: Computing $\vec{w}^{(4)}$

We have

$$\vec{w}^{(3)} \cdot \tilde{\mathbf{x}}_1 = (0, 0, -3) \cdot (1, 2, -1) = 3$$

thus

$$sgn\left(ec{w}^{(3)}\cdot\mathbf{\widetilde{x}}_{1}
ight)=1$$

and thus

$$sgn\left(ec{w}^{(3)}\cdot\mathbf{\tilde{x}}_{1}
ight)-c_{1}=1-1=0$$

(I.e., $\vec{x_1}$ is currently correctly classified by $\vec{w}^{(3)}$. However, we shall see that $\vec{x_2}$ is not.) Hence,

$$\vec{w}^{(4)} = \vec{w}^{(3)} = (0, 0, -3)$$

Example: Computing $\vec{w}^{(5)}$

We have

$$\vec{w}^{(4)} \cdot \tilde{\mathbf{x}}_2 = (0, 0, -3) \cdot (1, 2, 1) = -3$$

thus

$$sgn\left(ec{w}^{(4)}\cdot\widetilde{\mathbf{x}}_{2}
ight)=0$$

and thus

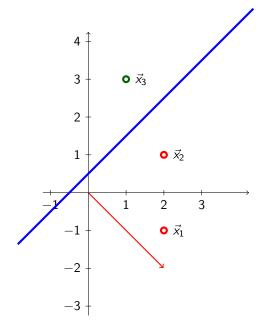
$$sgn\left(ec{w}^{(4)}\cdot\widetilde{\mathbf{x}}_{2}
ight)-c_{2}=0-1=-1$$

(I.e., $\vec{x_2}$ is not correctly classified, and $\vec{w}^{(4)}$ is not consistent with D.) Hence,

$$\vec{w}^{(5)} = \vec{w}^{(4)} - \left(sgn\left(\vec{w}^{(4)} \cdot \tilde{\mathbf{x}}_2\right) - c_2\right) \cdot \tilde{\mathbf{x}}_2$$

= $\vec{w}^{(4)} + \tilde{\mathbf{x}}_2$
= $(0, 0, -3) + (1, 2, 1)$
= $(1, 2, -2)$

Example: Separating by $\vec{w}^{(5)}$



Example: The result

The vector $\vec{w}^{(5)}$ is consistent with *D*:

$$sgn\left(\vec{w}^{(5)} \cdot \tilde{\mathbf{x}}_{1}\right) = sgn\left((1, 2, -2) \cdot (1, 2, -1)\right) = sgn(7) = 1 = c_{1}$$
$$sgn\left(\vec{w}^{(5)} \cdot \tilde{\mathbf{x}}_{2}\right) = sgn\left((1, 2, -2) \cdot (1, 2, 1)\right) = sgn(3) = 1 = c_{2}$$
$$sgn\left(\vec{w}^{(5)} \cdot \tilde{\mathbf{x}}_{3}\right) = sgn\left((1, 2, -2) \cdot (1, 1, 3)\right) = sgn(-3) = 0 = c_{3}$$

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Compute a sequence of weight vectors $\vec{w}^{(0)}, \vec{w}^{(1)}, \vec{w}^{(2)}, \dots$

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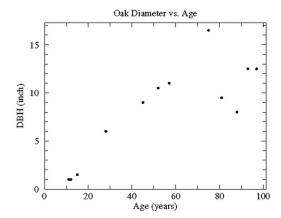
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Linear Regression – Oaks in Wisconsin

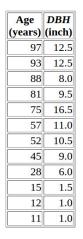
This example is from How to Lie with Statistics by Darrell Huff (1954)

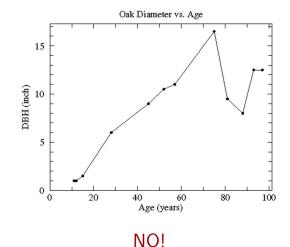
Age	DBH
(years)	(inch)
97	12.5
93	12.5
88	8.0
81	9.5
75	16.5
57	11.0
52	10.5
45	9.0
28	6.0
15	1.5
12	1.0
11	1.0



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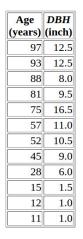
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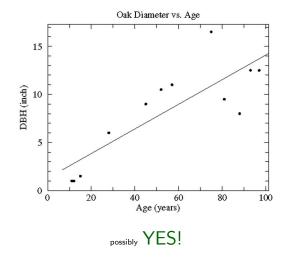




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 $h(\vec{x}) \approx f$ for all training examples $(\vec{x}, f) \in D$

Here \approx means that the values are somewhat close to each other w.r.t. an appropriate *error function E*. Also called *loss function*.

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In what follows we use the squared error defined by

$$E = \frac{1}{2} \sum_{(\vec{x},f)\in D} (h(\vec{x}) - f)^2$$

Our goal is to minimize E.

The main reason is that this function has nice mathematical properties (as opposed, e.g., to $\sum_{(\vec{x},f)\in D} |h(\vec{x}) - f|$).

Linear Function Approximation

▶ Given a set *D* of training examples:

$$D = \{ (\vec{x}_1, f_1), (\vec{x}_2, f_2), \dots, (\vec{x}_p, f_p) \}$$

Here $\vec{x}_k = (x_{k1} \dots, x_{kn}) \in \mathbb{R}^n$ and $f_k \in \mathbb{R}$.

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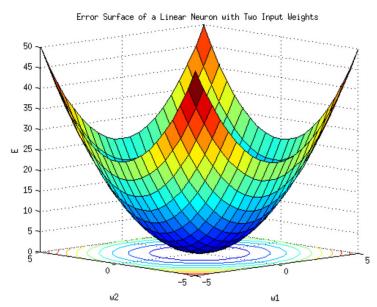
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Squared Error Function:

$$E(\vec{w}) = \frac{1}{2} \sum_{k=1}^{p} (\vec{w} \cdot \tilde{\mathbf{x}}_{k} - f_{k})^{2} = \frac{1}{2} \sum_{k=1}^{p} \left(\sum_{i=0}^{n} w_{i} x_{ki} - f_{k} \right)^{2}$$

Error function



Consider the gradient of the error function:

$$\nabla E(\vec{w}) = \left(\frac{\partial E}{\partial w_0}(\vec{w}), \dots, \frac{\partial E}{\partial w_n}(\vec{w})\right) = \sum_{k=1}^p \left(\vec{w} \cdot \tilde{\mathbf{x}}_k - f_k\right) \cdot \tilde{\mathbf{x}}_k$$

What is the gradient $\nabla E(\vec{w})$? It is a vector in \mathbb{R}^{n+1} which points in the direction of the steepest *ascent* of *E* (its length corresponds to the steepness). Note that here the vectors $\tilde{\mathbf{x}}_k$ are *fixed* parameters of *E*!

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Fact: If $\nabla E(\vec{w}) = \vec{0} = (0, ..., 0)$, then \vec{w} is a global minimum of E.

This follows from the fact that E is a convex paraboloid that has a unique extreme, which is a minimum.



Consider n = 1, which means that $\vec{w} = (w_0, w_1)$ and we write x instead of \vec{x} since $\vec{x} \in \mathbb{R}^n = \mathbb{R}^1 = \mathbb{R}$.

Then the model is $h[\vec{w}](x) = w_0 + w_1 \cdot x$.

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The augmented feature vectors are: (1, 2), (1, 3), (1, 4).

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 $\frac{\partial E}{\partial w_0}$

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$$\nabla E(\vec{w}) = \left(\frac{\partial E}{\partial w_0}, \frac{\partial E}{\partial w_1}\right) = (w_0 + w_1 \cdot 2 - 1) \cdot (1, 2) + (w_0 + w_1 \cdot 3 - 2) \cdot (1, 3) + (w_0 + w_1 \cdot 4 - 5) \cdot (1, 4)$$

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Gradient Descent:

 Weights w⁽⁰⁾ are initialized randomly close to 0.
 In (t + 1)-th step, w^(t+1) is computed as follows: w^(t+1) = w^(t) - ε · ∇E(w^(t)) = w^(t) - ε · ∑^p_{k=1} (w^(t) · x̃_k - f_k) · x̃_k = w^(t) - ε · ∑^p_{k=1} (h[w^(t)](x̃_k) - f_k) · x̃_k

Here $0 < \varepsilon \leq 1$ is a learning rate.

Note that the algorithm is almost similar to the batch perceptron algorithm!

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Note that the algorithm is almost similar to the batch perceptron algorithm!

Proposition

For sufficiently small $\varepsilon > 0$ the sequence $\vec{w}^{(0)}, \vec{w}^{(1)}, \vec{w}^{(2)}, \ldots$ converges (component-wisely) to the global minimum of E.

Training set:

$$D = \{(x_1, f_1), (x_2, f_2), (x_3, f_3)\} = \{(0, 0), (2, 1), (2, 2)\}$$

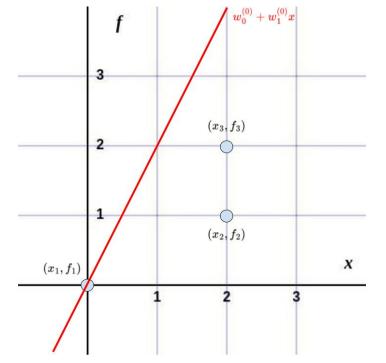
Note that input vectors are one dimensional, so we write them as numbers. That is

$$x_3 = 2$$
 $\tilde{\mathbf{x}}_3 = (1,2)$

$$f_1 = 0$$

 $f_2 = 1$
 $f_3 = 2$

Assume that the initial vector $\vec{w}^{(0)}$ is $\vec{w}^{(0)} = (w_0^{(0)}, w_1^{(0)}) = (0, 2)$. Consider $\varepsilon = \frac{1}{10}$.



Training set: $D = \{(x_1, f_1), (x_2, f_2), (x_3, f_3)\} = \{(0, 0), (2, 1), (2, 2)\}$ Augmented input vectors: $\mathbf{\tilde{x}}_1 = (1, 0), \ \mathbf{\tilde{x}}_2 = (1, 2), \ \mathbf{\tilde{x}}_1 = (1, 2)$

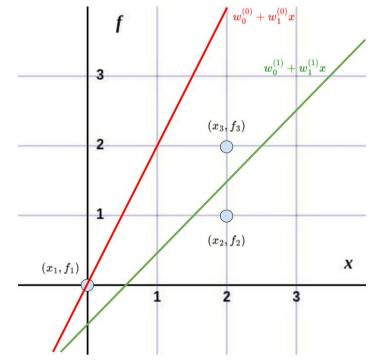
$$\nabla E(\vec{w}) = \left(\frac{\partial E}{\partial w_0}(\vec{w}), \frac{\partial E}{\partial w_1}(\vec{w})\right) = (w_0 + w_1 \cdot x_1 - f_1) \cdot \tilde{\mathbf{x}}_1 + (w_0 + w_1 \cdot x_2 - f_2) \cdot \tilde{\mathbf{x}}_2 + (w_0 + w_1 \cdot x_3 - f_3) \cdot \tilde{\mathbf{x}}_3$$

For $\vec{w}^{(0)} = (0, 2)$ we have

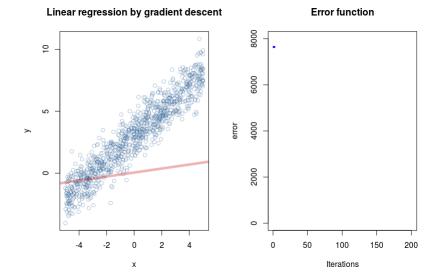
$$\nabla E(\vec{w}^{(0)}) = (0 + 2 \cdot 0 - 0) \cdot (1, 0) \\ + (0 + 2 \cdot 2 - 1) \cdot (1, 2) \\ + (0 + 2 \cdot 2 - 2) \cdot (1, 2) = (3, 6) + (2, 4) = (5, 10)$$

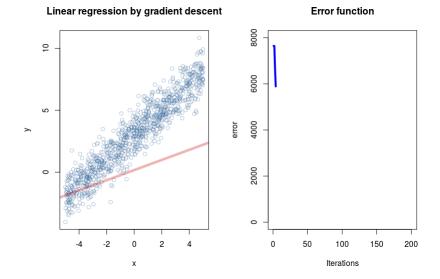
Finally, $\vec{w}^{(1)}$ is computed by

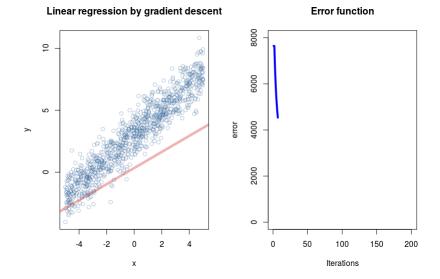
$$ec{w}^{(1)} = ec{w}^{(0)} - arepsilon \cdot
abla E(ec{w}^{(0)}) = (0,2) - rac{1}{10} \cdot (5,10) = (-1/2,1)$$

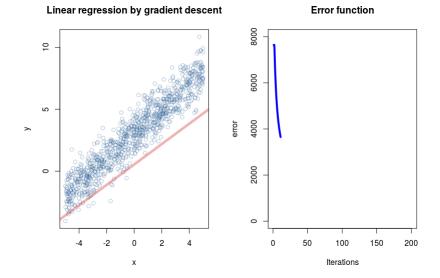


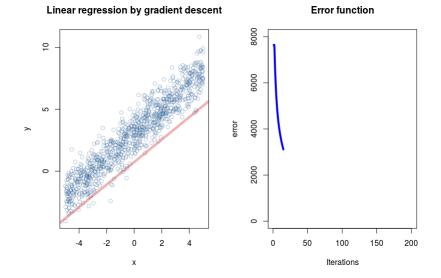
Linear Regression - Animation

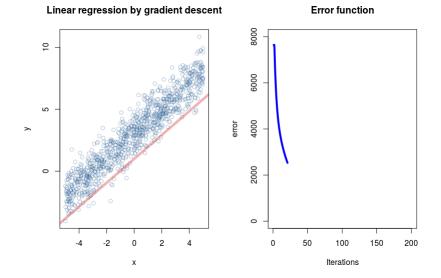


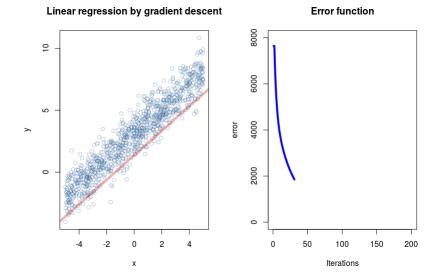


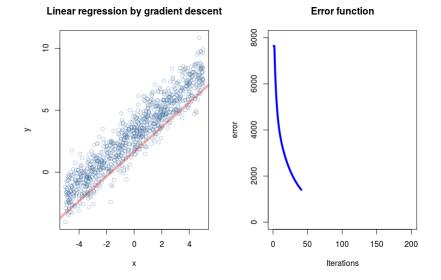


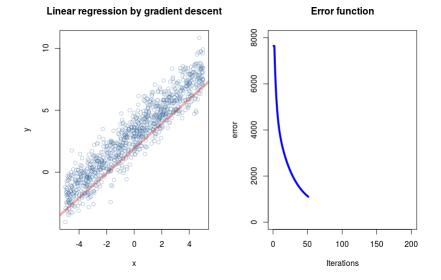


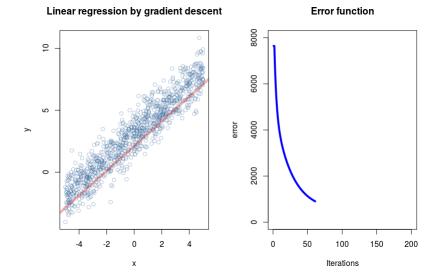


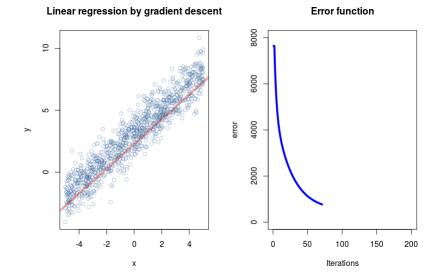


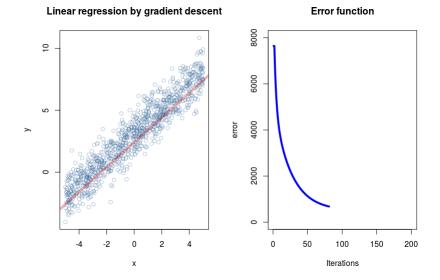


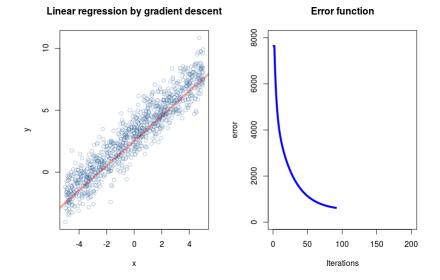


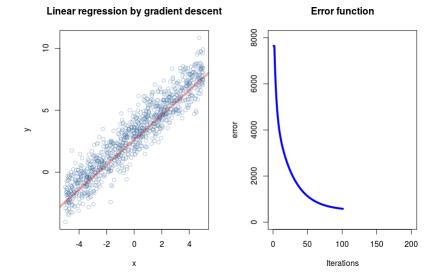


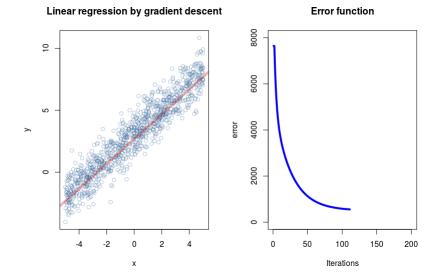


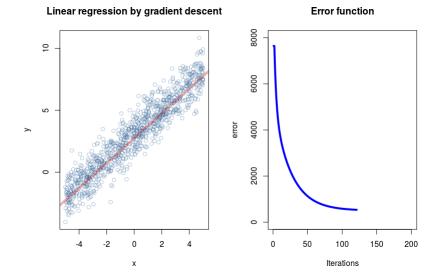


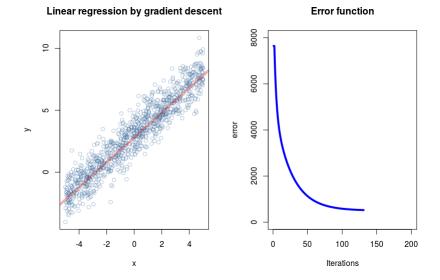


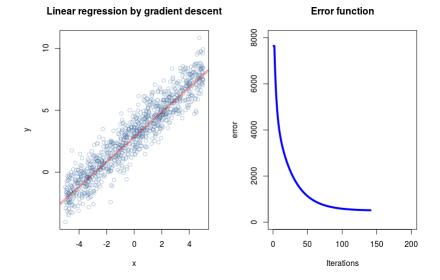


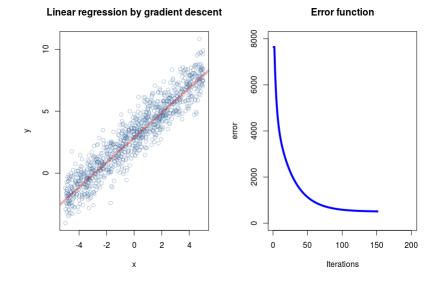


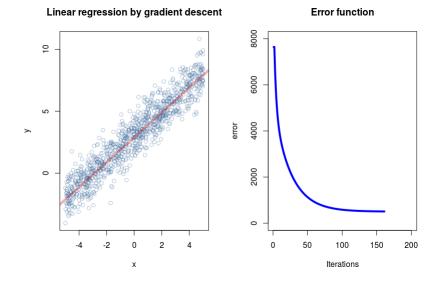


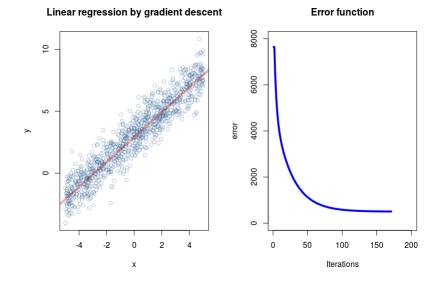


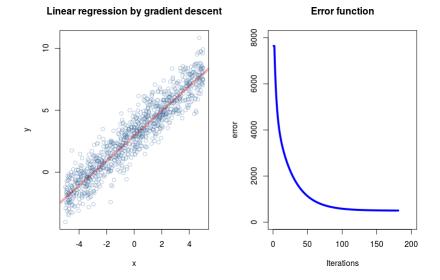


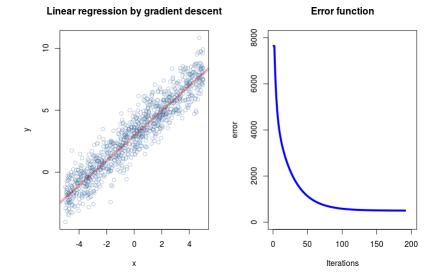


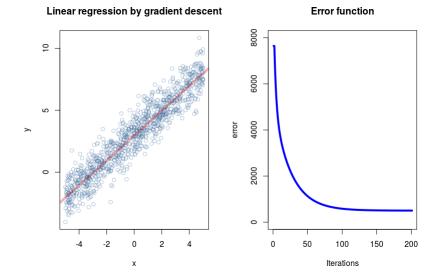












Finding the Minimum in Dimension One

Assume n = 1. Then, the error function E is

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Minimize E w.r.t. w_0 a w_1 :

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where $\bar{x} = \frac{1}{p} \sum_{k=1}^{p} x_k$ a $\bar{f} = \frac{1}{p} \sum_{k=1}^{p} f_k$

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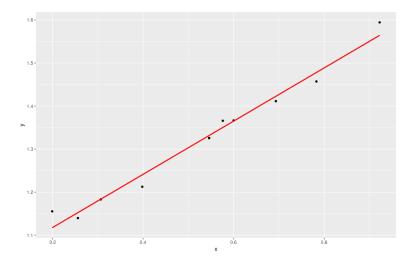
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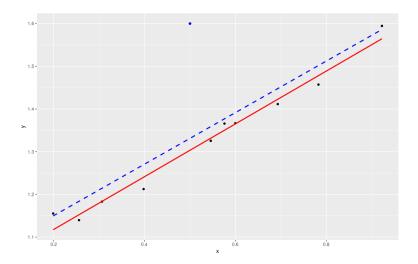
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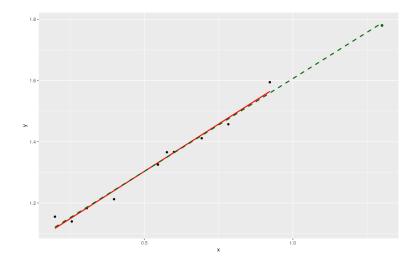
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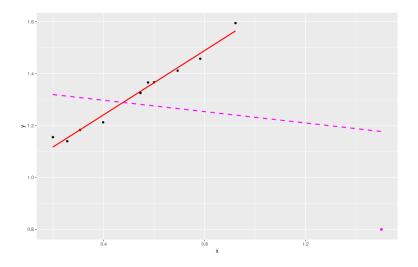
$$\frac{\partial E}{\partial w_1} = 0 \quad \Leftrightarrow \quad w_1 = \frac{\frac{1}{p} \sum_{k=1}^{p} (f_k - \bar{f})(x_k - \bar{x})}{\frac{1}{p} \sum_{k=1}^{p} (x_k - \bar{x})^2}$$

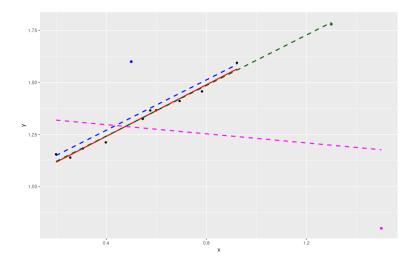
i.e. $w_1 = cov(f, x) / var(x)$









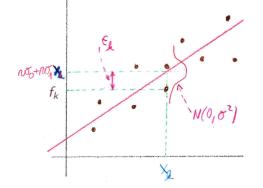


Maximum Likelihood vs Least Squares (Dim 1) Fix a training set $D = \{(x_1, f_1), (x_2, f_2), \dots, (x_p, f_p)\}$

Assume that each f_k has been generated randomly by

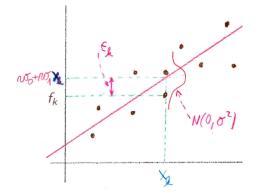
 $f_k = (\mathbf{w}_0 + \mathbf{w}_1 \cdot \mathbf{x}_k) + \epsilon_k$

where w_0, w_1 are **unknown weights**, and ϵ_k are independent, normally distributed noise values with mean 0 and some variance σ^2



How "probable" is it to generate the correct f_1, \ldots, f_p ?

Maximum Likelihood vs Least Squares (Dim 1)



How "probable" is it to generate the correct f_1, \ldots, f_p ?

The following conditions are equivalent:

- \blacktriangleright w₀, w₁ minimize the squared error E
- ▶ w_0, w_1 maximize the likelihood (i.e., the "probability") of generating the correct values f_1, \ldots, f_p using $f_k = (w_0 + w_1 \cdot x_k) + \epsilon_k$

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Linear models are parametric, i.e., they have a fixed form with a small number of parameters that need to be learned from data (as opposed, e.g., to decision trees where the structure is not fixed in advance).

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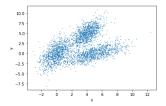
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- Linear models are prone to outliers.

Unsupervised Learning

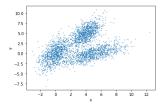
Clustering

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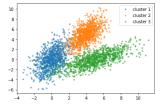
some notion of similarity. This means that the data distribution is *multimodal*,

10.0 7.5 5.0

2.5

i.e., contains several regions of higher probability mass.

We aim to group data into clusters of "similar" examples without using any additional information. (no supervision).



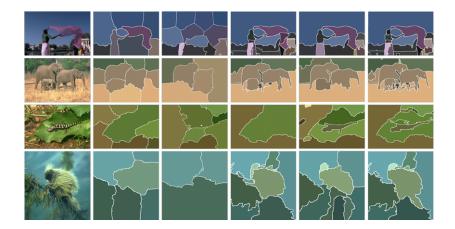
Motivation

...

Clustering is useful, e.g., in

- Customer segmentation based on their purchases.
- Data exploration identify patterns in data
- Semi-supervised learning cluster labeled examples with the unlabeled ones
- Search engines searching for images similar to a given image
- Image segmentation

Segmentation



Consider a dataset

 $D = \{\vec{x}_1, \ldots, \vec{x}_p\}$

Note that no target class/value is provided.

Clustering is a partition $\mathcal{U} = \{U_1, \ldots, U_K\}$ of D into K clusters.

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For concreteness:

- ▶ We stick with numerical features, which means that the dataset $D = {\vec{x_1}, ..., \vec{x_p}}$ contains vectors $\vec{x_i} \in \mathbb{R}^n$.
- Assume the Euclidean distance *d*.

Note that clustering may be based on completely different similarity/dissimilarity measures and non-numerical data.

K-Means Clustering

The K-means clustering model consists of

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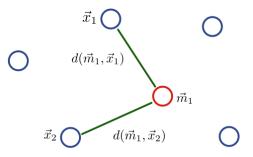
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How good is a given model?

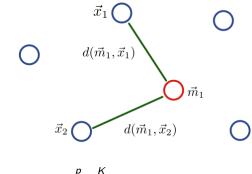
Error Function

Measure the distance of inputs \vec{x}_i to their cluster prototypes \vec{m}_i



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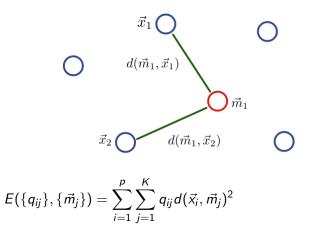
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$$E(\{q_{ij}\},\{\vec{m}_j\}) = \sum_{i=1}^{r} \sum_{j=1}^{N} q_{ij} d(\vec{x}_i,\vec{m}_j)^2$$

Error Function

Measure the distance of inputs \vec{x}_i to their cluster prototypes \vec{m}_j



We aim to *minimize* this error, i.e., to find proper positions of cluster prototypes and their assignment to minimize the total squared distance of examples to their prototypes.

K-means Clustering Complexity

The Problem *K*-means clustering problem (optimization): Given a set $D = {\vec{x_1}, ..., \vec{x_p}}$ where $\vec{x_k} \in \mathbb{R}^n$ for all k = 1, ..., pand an integer *K*, minimize

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The Problem K-means clustering problem (decision): Similar to the optimization variant except that given a constant $c \in \mathbb{R}$ we search for $\{q_{ij}\}, \{\vec{m}_j\}$ satisfying $E(\{q_{ij}\}, \{\vec{m}_j\}) \leq c$.

Theorem

The K-means clustering problem is NP-hard.

For details see Aloise et al. Clustering Large Graphs via the Singular Value Decomposition, Mach Learn (2009) 75: 245–248

Complexity of clustering for many other variants has been studied, see, e.g., Cluster Analysis and Mathematical Programming by Hansen & Jaumard

The Problem: Minimize

$$E(\{q_{ij}\},\{\vec{m}_j\}) = \sum_{i=1}^{p} \sum_{j=1}^{K} q_{ij} d(\vec{x}_i,\vec{m}_j)^2 \text{ w.r.t. } \{q_{ij}\},\{\vec{m}_j\}$$

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Note that

- ▶ If we fix $\{\vec{m}_j\}$, we can minimize $E(\{q_{ij}\}, \{\vec{m}_j\})$ by setting $q_{ij} = 1$ iff \vec{m}_j is the *closest prototype* to \vec{x}_i .
- If we fix {q_{ij}}, we can minimize E({q_{ij}}, {m_j}) by letting each m_j to minimize the total squared distance to its prototypes:

$$\sum_i q_{ij} d(\vec{x}_i, \vec{m}_j)^2$$

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Note that

- If we fix {m_j}, we can minimize E({q_{ij}}, {m_j}) by setting q_{ij} = 1 iff m_j is the *closest prototype* to x_j.
- If we fix {q_{ij}}, we can minimize E({q_{ij}}, {m_j}) by letting each m_j to minimize the total squared distance to its prototypes:

$$\sum_i q_{ij} d(\vec{x}_i, \vec{m}_j)^2$$

This is achieved by putting each prototype \vec{m}_j into the centroid of all inputs it represents:

$$\vec{m}_j = \frac{1}{\sum_{i=1}^p q_{ij}} \sum_{i=1}^p q_{ij} \vec{x}_i$$

Note that $\sum_{i=1}^{p} q_{ij}$ is the size of the cluster represented by $\vec{m_j}$.

Algorithm 1 K-means clustering

- 1: Initialize K cluster centers $\vec{m}_1, \vec{m}_2, \ldots, \vec{m}_K$ randomly
- 2: repeat
- 3: **for** each data point $\vec{x_i}$ **do**

4: Assign $\vec{x_i}$ to the nearest centroid, i.e., set $q_{ij} = 1$ for

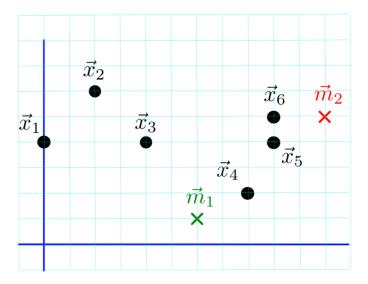
 $j = \arg\min_j d(\vec{x_i}, \vec{m_j})^2$

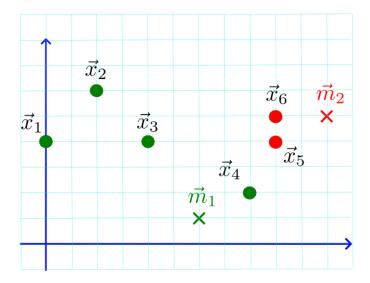
- 5: end for
- 6: **for** each cluster prototype \vec{m}_j **do**
- 7: Update \vec{m}_j to be the centroid of all points assigned to it

$$\vec{m}_j = \frac{1}{\sum_{i=1}^p q_{ij}} \sum_{i=1}^p q_{ij} \vec{x}_i$$

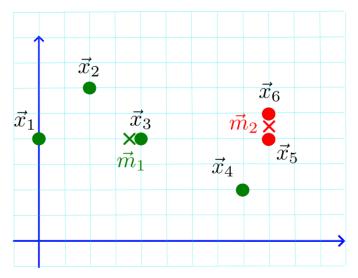
8: end for

9: until convergence

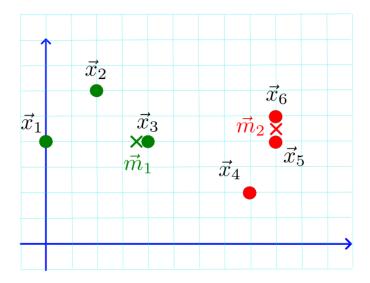




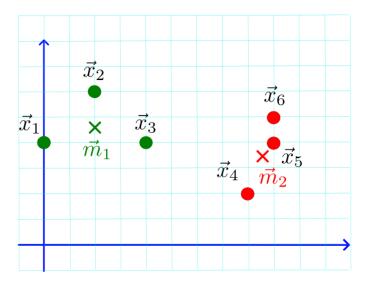
Lines 3-5: Assign examples to the prototypes.



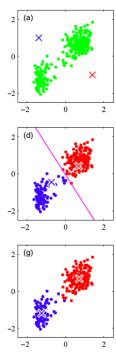
Lines 6-8: Move the prototypes to the centroids of their examples.

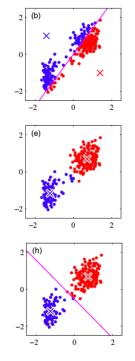


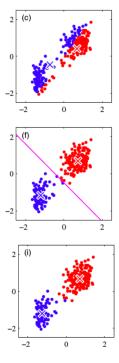
Lines 3-5: Assign examples to the prototypes.



Lines 6-8: Move the prototypes to the centroids of their examples.







Convergence of K-means Clustering

Every step of K-means reduces the error $E(\{q_{ij}\}, \{\vec{m}_j\})$:

- ▶ We always assign an input vector to the closest prototype.
- We always move the prototype to be "closest" to the input vectors it represents.

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Convergence can be tested by computing the error and checking whether it has not changed in the last step.

This will always happen after finitely many steps. There are only finitely many possible assignments to q_{ij} , and we always minimize the distance of inputs to their assigned centers.

Convergence of K-means Clustering

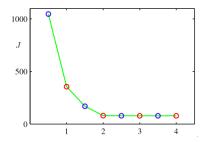
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Example error development during training. Blue circles mean reassignment, and red circles mean moving prototypes.



Setting K - the Elbow Method

K-means clustering minimizes the *inertia* measure:

$$E(\{q_{ij}\},\{\vec{m}_j\}) = \sum_{i=1}^{p} \sum_{j=1}^{k} q_{ij} d(\vec{x}_i,\vec{m}_j)^2$$

That is the sum of squared distances of all examples of D to the cluster prototypes.

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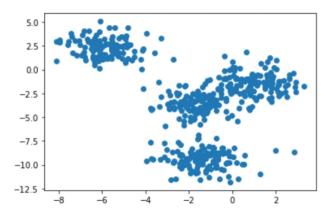
Note that the error does not consider the distance between the centers of the clusters.

Still, it is a valid measure that can be used to select the number of clusters.

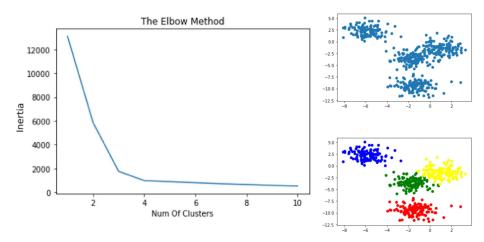
Elbow Method

The following method for setting up the hyperparameters can be used in general. Let us illustrate the elbow method on K-means clustering with the inertia measure.

Consider the following data:



Elbow Method



We could choose four clusters because adding more leads only to small decrements in the inertia.

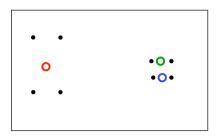
Bad Behavior

Minimizing $E(\{q_{ij}\}, \{\vec{m_j}\})$ starting from random positions of prototypes does not always produce "nice" results.

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Minimizing $E(\{q_{ij}\}, \{\vec{m}_j\})$ starting from random positions of prototypes does not always produce "nice" results.

Some runs correspond to apparently bad solutions to the clustering problem even though a better solution exists.



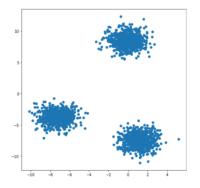
Possible solution: Start the algorithm several times with random initialization of the prototypes.

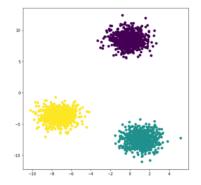
- Prototype initialization is a big issue in K-means. There are various strategies. For example:
 - Start with all centers in a single corner.
 - Include randomness in the setting of centers throughout the algorithm.
 - Initialize sequentially, always fit prototypes, and then choose a new one as far away from the others as possible.
 - Use hierarchical clustering (next slides) to find clusters and initialize K-means with their centroids.

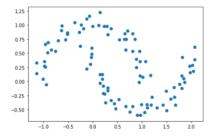
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- Empty clusters may occur need to resolve, e.g., by assigning the farthest point from any current prototype.

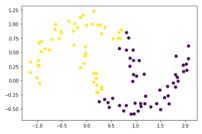
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- As the squared error is behind the basic method, outliers may strongly affect its behavior (as in the linear regression case).
- Other problematic properties of data include
 - non-convex clusters
 - clusters of different sizes
 - non-linearly separable clusters
 - overlapping clusters









Consider a dataset

$$D = \{\vec{x}_1, \ldots, \vec{x}_p\}$$

Here $\vec{x_i} \in \mathbb{R}^n$ for all i = 1, ..., p. Assume a distance d (e.g., Euclidean).

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- Incrementally build larger clusters by merging smaller clusters.

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Idea:

- Start by merging the closest examples (w.r.t. d)
- ▶ Incrementally build *larger clusters* by merging smaller clusters.

More concretely:

Maintain a set of clusters

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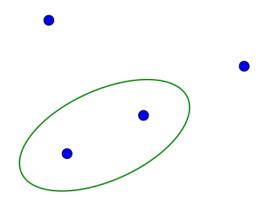
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How do we determine the closest clusters?

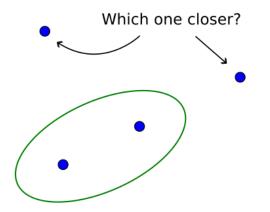
Closest Clusters

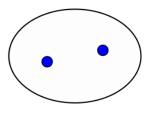


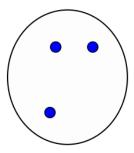
Closest Clusters

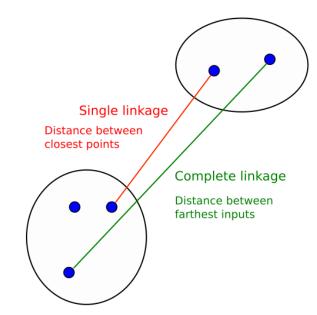


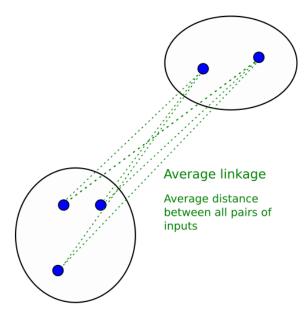
Closest Clusters



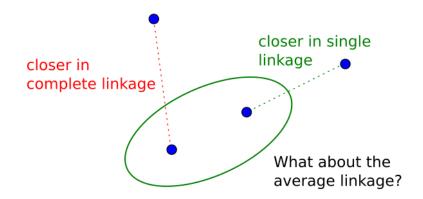








Which One is Closer?



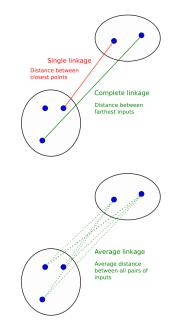
Consider two clusters $U_j, U_k \subseteq D$.

single_linkage (U_j, U_k) = min $\{d(\vec{x}, \vec{z}) \mid \vec{x} \in U_j, \vec{z} \in U_k\}$

 $\begin{aligned} & \text{complete_linkage}(U_j, U_k) \\ &= \max\{d(\vec{x}, \vec{z}) \mid \vec{x} \in U_j, \vec{z} \in U_k\} \end{aligned}$

$$egin{array}{l} \mathsf{average_linkage}(U_j, U_k) \ &= rac{1}{|U_j||U_k|} \sum_{ec{x} \in U_i} \sum_{ec{z} \in U_k} d(ec{x}, ec{z}) \end{array}$$

Each linkage can result in a different clustering.



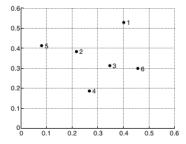
Agglomerative Hierarchical Clustering Algorithm

Maintain a set of clusters Initially, each $\vec{x_i}$ in its own cluster **repeat**

Pick two closest clusters

Using the distance measure d and single, average, or complete linkage. Merge them into a new cluster until only one cluster is left

Example

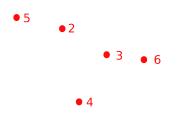


Point	x Coordinate	y Coordinate
p1	0.40	0.53
p2	0.22	0.38
p3	0.35	0.32
p4	0.26	0.19
p5	0.08	0.41
p6	0.45	0.30

	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

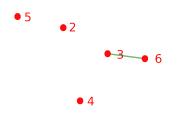
	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

•1



	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

•1

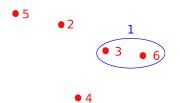


d(3,6) = 0.11

which is the minimum distance between points.

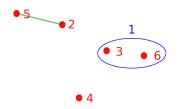
	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
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•1



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p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

•1

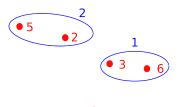


d(2,5) = 0.14

which is the second smallest distance.

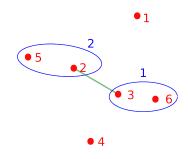
	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

•1



• 4

	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00



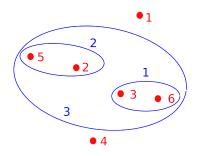
d(2,3) = 0.15 = $\min\{d(2,3), d(2,6), d(5,3), d(5,6)\}$

which is smaller than

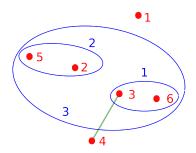
$$d(1,2) = 0.24,$$

 $d(1,3) = 0.22,$
 $d(4,2) = 0.2,$
 $d(4,3) = 0.16,$
 $d(4,1) = 0.37$
the min. distances of points
in all other pairs of clusters.

	p1	p2	p3	p4	$\mathbf{p5}$	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00



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p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
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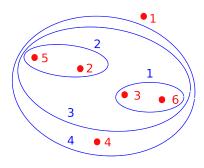


d(4,3) = 0.15= min{d(4,3), d(4,5), d(4,2), d(4,6)}

which is smaller than d(1,3) = 0.22, the distance of 1 to the cluster 3.

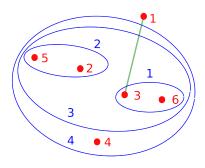
Example - Single Linkage

	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
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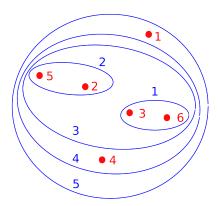
Example - Single Linkage

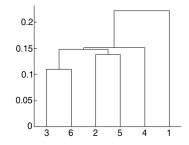
	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
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p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00



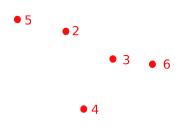
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p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

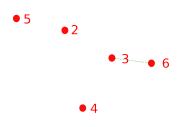




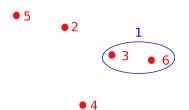
	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
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p3	0.22	0.15	0.00	0.16	0.28	0.11
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p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00



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p2	0.24	0.00	0.15	0.20	0.14	0.25
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p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

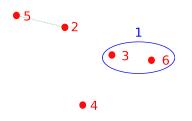


	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00



	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

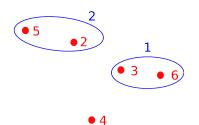
•1



d(2,5) = 0.14

which is second smallest distance.

	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00



	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

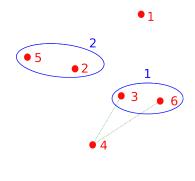
The average distance between 4 and both points of $\{3,6\}$ is

$$\frac{1}{2}(d(4,3)+d(4,6))=0.19$$

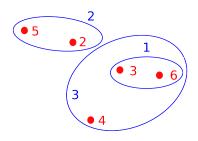
which is smaller than the average distance between all points of clusters 1, 2:

$$\frac{d(5,2) + d(5,3) + d(2,3) + d(2,6)}{4}$$

(equal to 0.205), and the average distance of 1 to any cluster.

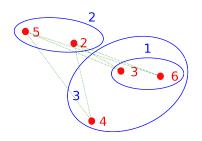


	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00



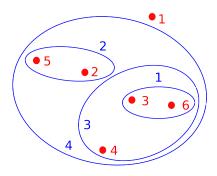
	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

•1

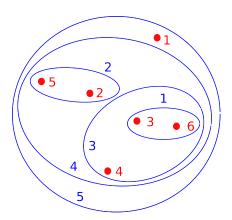


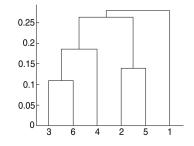
The average distance between clusters 2, 3 is 0.26 which is smaller than the average distance of 1 to any of the two clusters 1, 2 (the average distances are 0.273 and 0.29).

	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

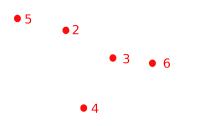


	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00



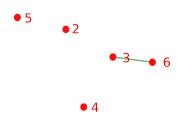


	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00



	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

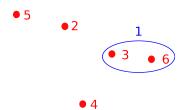
•1



d(3,6) = 0.11

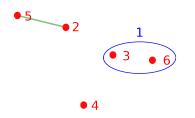
which is the minimum distance between points.

	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00



	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

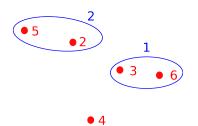
•1



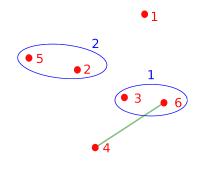
d(2,5) = 0.14

which is the second smallest distance.

	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00



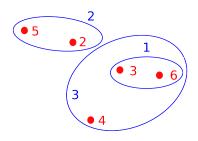
	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00



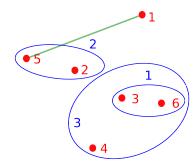
 $d(4,6) = 0.22 = \max\{d(4,3), d(4,6)\}$

which is smaller than d(4,5) = 0.29, d(1,5) = 0.34, d(1,6) = 0.23, d(5,6) = 0.39, d(4,1) = 0.37the max distances of points in all other pairs of clusters.

	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00



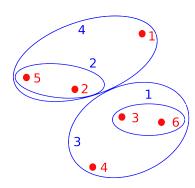
	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00



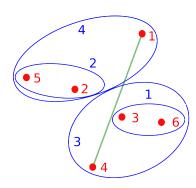
$$d(1,5) = 0.34$$

which is smaller than d(1, 4) = 0.37, d(5, 6) = 0.39, which are the maximum distances of points in all other pairs of clusters.

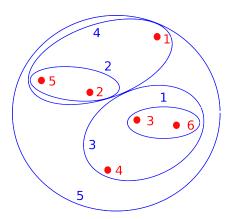
	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00

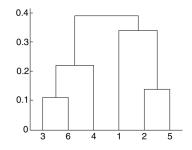


	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00



	p1	p2	p3	p4	p5	p6
p1	0.00	0.24	0.22	0.37	0.34	0.23
p2	0.24	0.00	0.15	0.20	0.14	0.25
p3	0.22	0.15	0.00	0.16	0.28	0.11
p4	0.37	0.20	0.16	0.00	0.29	0.22
p5	0.34	0.14	0.28	0.29	0.00	0.39
p6	0.23	0.25	0.11	0.22	0.39	0.00



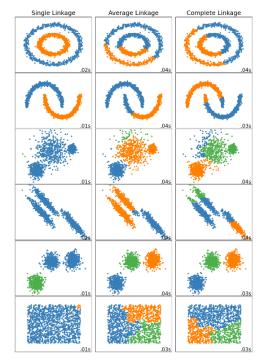


Properties of Agglomerative Hierarchical Clustering

- Provides hierarchy of clusters different cut levels provide different levels of coarseness of clusters
- Compared with k-means, it does not depend on the initialization and may provide better clusters than k-means.

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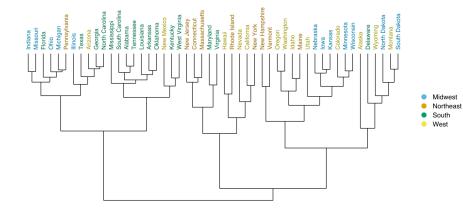
- Provides hierarchy of clusters different cut levels provide different levels of coarseness of clusters
- Compared with k-means, it does not depend on the initialization and may provide better clusters than k-means.
- Lack of global objective function
 - The agglomerative hierarchical clustering uses local criteria to decide which clusters to merge.
- Agglomerative clustering has a "rich get richer" behavior that leads to uneven cluster sizes
- Merging decision cannot be undone bad for noisy data
- Computationally expensive.

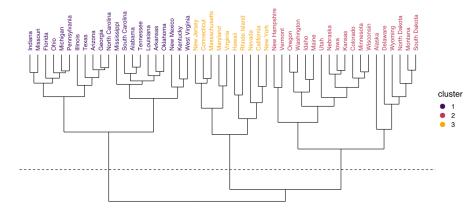


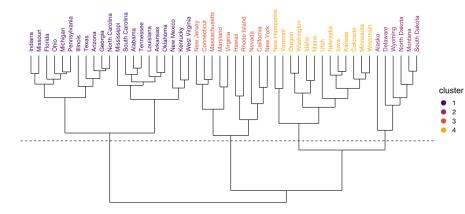
# A tibble: 5	50 × 20								
state	homeo1	multi…2	income	med_i…³	poverty	fed_s4	smoke	murder	robbery
<chr></chr>	<dbl></dbl>								
1 Alabama	71.1	15.5	22984	42081	17.1	11.7	24.8	8.2	141.
2 Alaska	64.7	24.6	30726	66521	9.5	16.8	25	4.8	80.9
3 Arizona	67.4	20.7	25680	50448	15.3	9.85	20.4	7.5	144.
4 Arkansas	67.7	15.2	21274	39267	18	9.61	23.5	6.7	91.1
5 Californ…	57.4	30.7	29188	60883	13.7	8.89	15.2	6.9	176.
6 Colorado	67.6	25.6	30151	56456	12.2	9.15	19.9	3.7	84.6
7 Connecti…	69.2	34.6	36775	67740	9.2	14.8	16.5	2.9	113
8 Delaware	73.6	17.7	29007	57599	11	8.89	20.7	4.4	155.
9 Florida	69.7	30	26551	47661	13.8	9.62	21.6	5	169.
10 Georgia	67.2	20.5	25134	49347	15.7	8.88	22.2	6.2	155.
# with 40 more rows, 10 more variables: agg_assault <dbl>, larceny <dbl>,</dbl></dbl>									
<pre># motor_theft <dbl>, soc_sec <dbl>, nuclear <dbl>, coal <dbl>,</dbl></dbl></dbl></dbl></pre>									
<pre># tr_deaths <dbl>, tr_deaths_no_alc <dbl>, unempl <dbl>, popdens2010 <dbl>,</dbl></dbl></dbl></dbl></pre>									

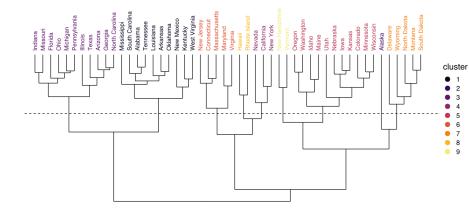
and abbreviated variable names 'homeownership, 'multiunit, 'med_income,

4fed_spend









Cluster Validation

Cluster Validity

For supervised classification (= we have class labels) we have a variety of measures to evaluate how good our model is: Accuracy, Precision, Recall, F_1 , etc.

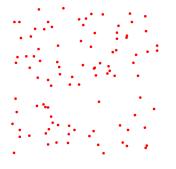
Cluster Validity

For supervised classification (= we have class labels) we have a variety of measures to evaluate how good our model is: Accuracy, Precision, Recall, F_1 , etc.

For cluster analysis (=unsupervised learning), the analogous question is:

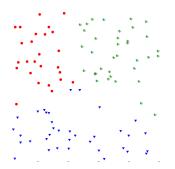
How to evaluate the "goodness" of the resulting clusters?

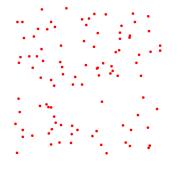
Keep in mind that the dataset can be large and high-dimensional. Visualization might be difficult. Random points:



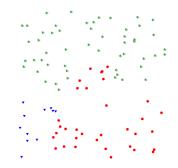
Random points:







Hierarchical



1. Determining the **clustering tendency** of a set of data, i.e., distinguishing whether non-random structure exists in the data (e.g., to avoid overfitting).

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- 4. Compare clusterings to determine which is better.
- 5. Determining the 'correct' number of clusters.

For 2, 3, and 4, we can further distinguish whether we want to evaluate the entire clustering or just individual clusters.

Numerical measures applied to judge various aspects of cluster validity are classified into the following three types.

- Internal Index: Used to measure the goodness of a clustering structure without respect to external information.
- External Index: Used to measure the extent to which cluster labels match externally supplied class labels.
- Relative Index: Used to compare two different clusterings or clusters.

Internal Index

Consider a dataset

 $D = \{\vec{x}_1, \ldots, \vec{x}_p\}$

Assume that a clustering algorithm produced a partition $\mathcal{U} = \{U_1, \dots, U_K\}$ of D into K clusters.

No other information has been provided.

We aim to measure the clustering's "niceness" (??)

Internal Index

Consider a dataset

 $D = \{\vec{x}_1, \ldots, \vec{x}_p\}$

Assume that a clustering algorithm produced a partition $\mathcal{U} = \{U_1, \dots, U_K\}$ of D into K clusters.

No other information has been provided.

We aim to measure the clustering's "niceness" (??)

Assume that we have a distance measure d measuring how far apart the objects being clustered.

For concreteness:

- ▶ We stick with numerical features, which means that the dataset $D = {\vec{x_1}, ..., \vec{x_p}}$ contains vectors $\vec{x_i} \in \mathbb{R}^n$.
- Assume the Euclidean distance *d*.

Note that the validity measures may be based on completely different similarity/dissimilarity measures and non-numerical data.

Consider a dataset $D = \{\vec{x}_1, \dots, \vec{x}_p\}$ and its clustering $\mathcal{U} = \{U_1, \dots, U_K\}.$

Let us utilize the concept of distance to cluster prototypes and consider the distance between prototypes.

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To measure the dissimilarity of examples, we use the notion of *proximity* defined on pairs of vectors \vec{x}, \vec{z} :

 $proximity(\vec{x}, \vec{z})$

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Let us utilize the concept of distance to cluster prototypes and consider the distance between prototypes.

To measure the dissimilarity of examples, we use the notion of *proximity* defined on pairs of vectors \vec{x}, \vec{z} :

 $proximity(\vec{x}, \vec{z})$

The proximity might be, e.g.,

- the distance $d(\vec{x}, \vec{z})$,
- the square of the distance, that is $d(\vec{x}, \vec{z})^2$,
- > any other notion of dissimilarity based on the application.

Consider a dataset $D = \{\vec{x}_1, \dots, \vec{x}_p\}$ and its clustering $\mathcal{U} = \{U_1, \dots, U_K\}.$

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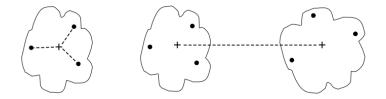
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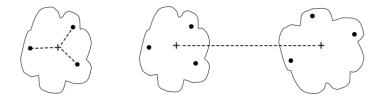
any other notion of dissimilarity based on the application.
 We consider the notions of *cohesion* (proximity of examples within clusters) and *separation* (proximity of clusters).



Prototype-based cohesion = the similarity of examples within a given cluster to a prototype of the cluster (e.g., centroid). Given a cluster $U_i \in U$ and its prototype $\vec{m_i} \in \mathbb{R}^n$,

$$cohesion(U_j) = \sum_{\vec{x} \in U_j} proximity(\vec{x}, \vec{m}_j)$$

Note that the prototype **does not** have to be an element of U_j . Intuitively, cohesion is the proximity of cluster's examples and a point somewhere "between" all examples of the cluster.



Prototype-based separation = dissimilarity of prototypes of different clusters.

Given a cluster $U_j \in U$, its prototype $\vec{m}_j \in \mathbb{R}^n$, and a prototype of all examples $\vec{m} \in \mathbb{R}^n$ (e.g. the centroid of all examples)

separation
$$(U_j) = proximity(\vec{m}_j, \vec{m})$$

Intuitively, separation is the proximity of the cluster's examples to the dataset's center.

Summarize the prototype-based cohesion and separation as follows:

$$egin{aligned} \mathsf{cohesion}(\mathcal{U}) &= \sum_{j=1}^{K} \mathit{cohesion}(U_j) \ &= \sum_{j=1}^{K} \sum_{ec{x} \in U_j} \mathit{proximity}(ec{x},ec{m}_j) \end{aligned}$$

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If $proximity(\vec{x}, \vec{z})$ is defined as $d(\vec{x}, \vec{z})^2$ then the cohesion is the inertia.

There is an interesting relationship between the above measures and the squared distances to the prototype of the whole dataset \vec{m} .

Consider a dataset $D = \{\vec{x}_1, \dots, \vec{x}_p\}$ and its clustering $\mathcal{U} = \{U_1, \dots, U_K\}$ of D.

Consider *proximity* $(\vec{x}, \vec{z}) = d(\vec{x}, \vec{z})^2$ and all prototypes to be centroids.

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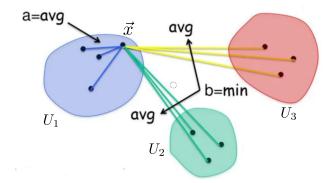
$$\mathsf{TSS} = \sum_{i=1}^{p} \mathsf{proximity}(\vec{x_i}, \vec{m}) = \sum_{i=1}^{p} d(\vec{x_i}, \vec{m})^2$$

The following holds:

$$\mathsf{TSS} = \mathsf{cohesion}(\mathcal{U}) + \mathsf{separation}(\mathcal{U})$$

Note that TSS is determined by D.

Silhouette score can be used to measure both qualities of clustering from the point of view of individual examples and from the point of view of the overall clustering.



silhouette
$$(\vec{x}) = \frac{b-a}{\max\{a, b\}}$$

Consider a clustering $\mathcal{U} = \{U_1, \ldots, U_k\}$ and $\vec{x} \in U_j$.

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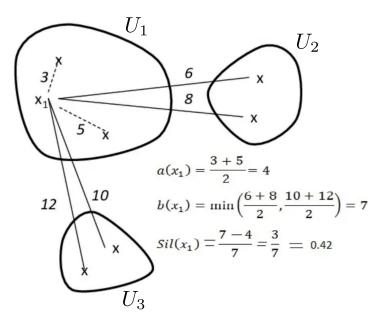
$$a(\vec{x}) = \frac{1}{|U_j| - 1} \sum_{\vec{z} \in U_j \smallsetminus \{\vec{x}\}} d(\vec{x}, \vec{z})$$

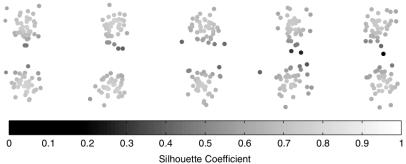
$$b(\vec{x}) = \min_{k \neq j} \frac{1}{|U_k|} \sum_{\vec{z} \in U_k} d(\vec{x}, \vec{z})$$

If $|U_j| > 1$ we define

$$silhouette(ec{x}) = rac{b(ec{x}) - a(ec{x})}{\max\{a(ec{x}), b(ec{x})\}}$$

Else, we define *silhouette*(\vec{x}) = 0.





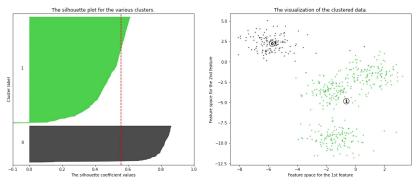
Silhouette for Clusters and Clusterings

We have defined the silhouette for a single $\vec{x} \in D$.

To obtain the silhouette score for a whole cluster U_j or for D we summarize using simple averaging:

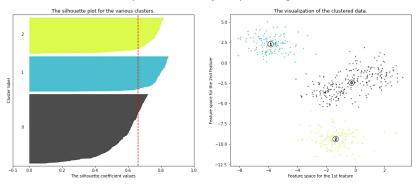
$$silhouette(U_j) = \frac{1}{|U_j|} \sum_{\vec{x} \in U_j} silhouette(\vec{x})$$

$$\textit{silhouette}(D) = rac{1}{|D|} \sum_{\vec{x} \in D} \textit{silhouette}(\vec{x})$$



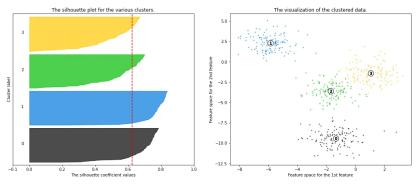
Silhouette analysis for KMeans clustering on sample data with n_clusters = 2

The colored graphs on the left are silhouette scores of the individual elements of clusters.



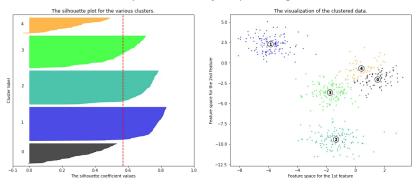
Silhouette analysis for KMeans clustering on sample data with n_clusters = 3

The colored graphs on the left are silhouette scores of the individual elements of clusters.



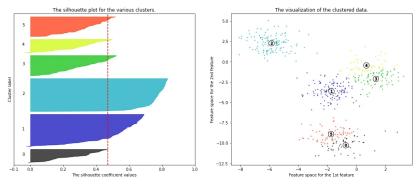
Silhouette analysis for KMeans clustering on sample data with n_clusters = 4

The colored graphs on the left are silhouette scores of the individual elements of clusters.



Silhouette analysis for KMeans clustering on sample data with n_clusters = 5

The colored graphs on the left are silhouette scores of the individual elements of clusters.



Silhouette analysis for KMeans clustering on sample data with n_clusters = 6

The colored graphs on the left are silhouette scores of the individual elements of clusters.

External Index

Consider a *supervised learning* dataset

$$D = \{ (\vec{x}_1, c_1), \dots, (\vec{x}_p, c_p) \}$$

Here $c_i \in C$ is a class of $\vec{x_i}$.

Assume that a clustering algorithm produced a partition $U = \{U_1, \ldots, U_K\}$ of D into K clusters.

We measure how the clustering conforms with the given classes.

Purity

Consider the clustering to be a classification model.

Define a classifier $h: D \to C$ such that given $\vec{x_i} \in U_i \in U$

 $h(\vec{x}_i)$ = the most frequent class in U_i

Now we can measure the Accuracy of h.

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Accuracy of *h* is called *purity*.

Intuitively, it is the proportion of majority class elements in clusters.

Is it a good measure?

Probably not; many clusters lead to high purity (each element in its own cluster means purity = 1).

Given $\vec{x_i}$, denote by $\mathcal{U}(\vec{x_i})$ the cluster $U_j \in \mathcal{U}$ containing $\vec{x_i}$.

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Distinguish the following types of *pairs* of examples:

TP = number of examples of the same class and the same cluster

$$\mathsf{TP} = |\{(i,j) \mid \mathcal{U}(\vec{x}_i) = \mathcal{U}(\vec{x}_j) \land c_i = c_j)\}$$

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► TN = number of examples of different classes and different clusters $TN = |\{(i,j) \mid U(\vec{x}_i) \neq U(\vec{x}_j) \land c_i \neq c_j)\}$

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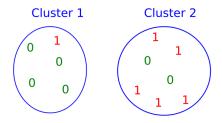
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Now, we may apply all the measures from the supervised model.

Example



$$TP = \binom{4}{2} + \binom{5}{2} + \binom{2}{2}$$

= 6 + 10 + 1 = 17
$$TN = 4 * 5 + 1 * 2 = 22$$

$$FP = 1 * 4 + 5 * 2 = 14$$

$$FN = 1 * 5 + 4 * 2 = 13$$

		Cluster	
		same	diff
Class	same	TP=17	FN=13
	diff	FP=14	TN=22

Rand Index

Accuracy (in this area known as *Rand index*) is

$$\mathsf{RandInd} = \mathsf{Accuracy} = \frac{\mathsf{TP} + \mathsf{TN}}{\mathsf{TP} + \mathsf{TN} + \mathsf{FP} + \mathsf{FN}}$$

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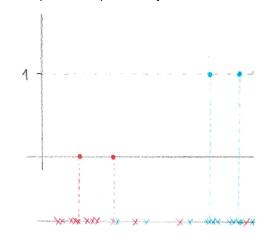
Here, note that the Rand index considers the purity and the number of clusters.

Note that the Rand index can be used to compare two clusterings: Simply consider class labels to be indicators of clusters.

Similarly, we may compute the other measures such as Precision, Recall, and F_1 with all their benefits and limitations.

What about classification using regression?

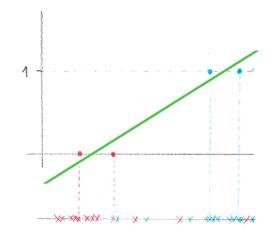
Binary classification: Desired outputs 0 and 1 ... we want to capture the probability distribution of the classes



What about classification using regression?

Binary classification: Desired outputs 0 and 1

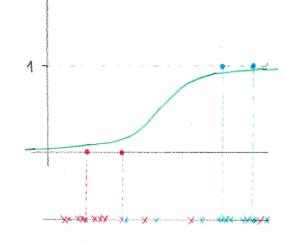
... we want to capture the probability distribution of the classes



... does not capture the probability well (it is not probability at all)

What about classification using regression?

Binary classification: Desired outputs 0 and 1 ... we want to capture the probability distribution of the classes



... logistic sigmoid $\frac{1}{1+e^{-(\vec{w}\cdot\vec{x})}}$ is much better!

Logistic regression model $h[\vec{w}]$ is determined by a vector of weights $\vec{w} = (w_0, w_1, \dots, w_n) \in \mathbb{R}^{n+1}$ as follows:

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Given
$$\vec{x} = (x_1, \dots, x_n) \in \mathbb{R}^n$$
,
 $h[\vec{w}](\vec{x}) := \frac{1}{1 + e^{-(w_0 + \sum_{k=1}^n w_k x_k)}} = \frac{1}{1 + e^{-\vec{w} \cdot \vec{\mathbf{x}}}}$

Here

$$\mathbf{\tilde{x}} = (x_0, x_1, \dots, x_n)$$
 where $x_0 = 1$

is the *augmented feature vector*.

The model gives probability $h[\vec{w}](\vec{x})$ of the class 1 given an input \vec{x} . But why do we model such probability using $1/(1 + e^{-\vec{w}\cdot\tilde{x}})$??

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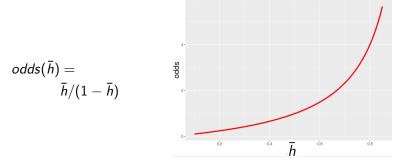
Denote by \overline{h} the probability $P(Y = 1 | X = \overline{x})$, i.e., the "true" probability of the class 1 given features \overline{x} .

The probability \bar{h} cannot be easily modeled using a linear function (the probabilities are between 0 and 1).

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What about odds of the class 1?

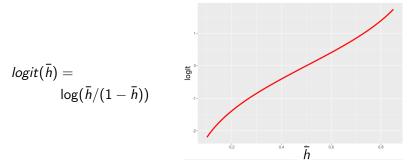


Better, at least it is unbounded on one side ...

The model gives probability $h[\vec{w}](\vec{x})$ of the class 1 given an input \vec{x} . But why do we model such probability using $1/(1 + e^{-\vec{w}\cdot\tilde{x}})$? Denote by \bar{h} the probability $P(X - 1 | X - \vec{x})$ i.e. the "true"

Denote by \overline{h} the probability $P(Y = 1 | X = \overline{x})$, i.e., the "true" probability of the class 1 given features \overline{x} .

What about log odds (aka logit) of the class 1?



Looks almost linear, at least for probabilities not too close to 0 or 1 ...

Assume that \overline{h} is the actual probability of the class 1 for an "object" with features $\vec{x} \in \mathbb{R}^n$. Put

 $\log(ar{h}/(1-ar{h})) = ec{w}\cdot \widetilde{\mathbf{x}}$

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and

$$ar{h} = rac{1}{1+e^{-ec{w}\cdot\widetilde{\mathbf{x}}}} = h[ec{w}](ec{x})$$

If we model log odds using a linear function, the probability is obtained by applying the logistic sigmoid on the result of the linear function.

► Given a set *D* of training samples:

$$D = \{ (\vec{x_1}, c_1), (\vec{x_2}, c_2), \dots, (\vec{x_p}, c_p) \}$$

Here $\vec{x}_k = (x_{k1} \dots, x_{kn}) \in \mathbb{R}^n$ and $c_k \in \{0, 1\}$.

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Recall that $h[\vec{w}](\vec{x}_k) = 1 / (1 + e^{-\vec{w} \cdot \tilde{\mathbf{x}}_k})$ where $\tilde{\mathbf{x}}_k = (x_{k0}, x_{k1} \dots, x_{kn})$, here $x_{k0} = 1$

Our goal: Find \vec{w} such that for every k = 1, ..., p we have that $h[\vec{w}](\vec{x}_k) \approx c_k$

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Binary Cross-entropy:

$$E(\vec{w}) = -\sum_{k=1}^{p} c_k \log(h[\vec{w}](\vec{x}_k)) + (1 - c_k) \log(1 - h[\vec{w}](\vec{x}_k))$$

Gradient of the Error Function

Consider the gradient of the error function:

$$\nabla E(\vec{w}) = \left(\frac{\partial E}{\partial w_0}(\vec{w}), \dots, \frac{\partial E}{\partial w_n}(\vec{w})\right) = \sum_{k=1}^p \left(\frac{h[\vec{w}](\vec{x}_k) - c_k}{\vec{x}_k}\right)$$

Fact 1

If $\nabla E(\vec{w}) = \vec{0} = (0, ..., 0)$, then \vec{w} is a global minimum of E. This follows from the fact that E is convex.

Using the squared error with the logistic sigmoid would lead to a non-convex error with several minima!

Gradient Descent:

• Weights $\vec{w}^{(0)}$ are initialized randomly close to $\vec{0}$.

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Gradient Descent:

 Weights w⁽⁰⁾ are initialized randomly close to 0.
 In (t + 1)-th step, w^(t+1) is computed as follows: w^(t+1) = w^(t) - ε · ∇E(w^(t)) = w^(t) - ε · ∑^p_{k=1} (h[w^(t)](x_k) - c_k) · x_k

Here 0 < $\varepsilon \leq$ 1 is the learning rate.

Note that the algorithm is almost similar to the batch perceptron algorithm!

Gradient Descent:

• Weights $\vec{w}^{(0)}$ are initialized randomly close to $\vec{0}$.

• In (t+1)-th step, $\vec{w}^{(t+1)}$ is computed as follows:

$$\vec{w}^{(t+1)} = \vec{w}^{(t)} - \varepsilon \cdot \nabla E(\vec{w}^{(t)})$$

$$= \vec{w}^{(t)} - \varepsilon \cdot \sum_{k=1}^{p} \left(h[\vec{w}^{(t)}](\vec{x}_{k}) - c_{k} \right) \cdot \tilde{\mathbf{x}}_{k}$$

Here 0 $< \varepsilon \leq 1$ is the learning rate.

Note that the algorithm is almost similar to the batch perceptron algorithm!

Proposition

For sufficiently small $\varepsilon > 0$, the sequence $\vec{w}^{(0)}, \vec{w}^{(1)}, \vec{w}^{(2)}, \ldots$ converges (in a component-wise manner) to the global minimum of the error function E.

Logistic Regression - Using the Trained Model

We have already trained our logistic regression model, i.e., we have a vector of weights $\vec{w} = (w_0, w_1, \dots, w_n)$.

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$$h[\vec{w}](\vec{x}) = rac{1}{1 + e^{-\left(w_0 + \sum_{k=1}^n w_k x_k
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To decide whether a given \vec{x} belongs to the class 1 we use $h[\vec{w}]$ as a Bayes classifier: Assign \vec{x} to the class 1 iff $h[\vec{w}](\vec{x}) \ge 1/2$. Other thresholds can also be used depending on the application and properties of the model. In such a case, given a threshold $\xi \in [0, 1]$, assign \vec{x} to the class 1 iff $h[\vec{w}](\vec{x}) \ge \xi$.

Maximum Likelihood vs Cross-entropy (Dim 1) Fix a training set $D = \{(x_1, c_1), (x_2, c_2), \dots, (x_p, c_p)\}$

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$$h[w_0, w_1](x_k) = \frac{1}{1 + e^{-(w_0 + w_1 \cdot x_k)}}$$

and 0 otherwise.

Here w_0, w_1 are unknown weights.

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The following conditions are equivalent:

• w_0, w_1 minimize the binary cross-entropy E

▶ w_0, w_1 maximize the likelihood (i.e., the "probability") of generating the correct values c_1, \ldots, c_p using the above described Bernoulli trials (i.e., that $c'_k = c_k$ for all $k = 1, \ldots, p$)

Note that the above equivalence is a property of the cross-entropy and is not dependent on the "implementation" of $h[w_0, w_1](x_k)$ using the logistic sigmoid.