# Bayesian Classifiers and Probability Estimation

CSE 4308/5360: Artificial Intelligence I University of Texas at Arlington

#### Data Space

- Suppose that we have a classification problem
- The patterns for this problem come from some underlying space X.
- Note that we use the term "space".
- What is the difference between "space" and "set"?
  - Not much. Oftentimes "space" and "set" refer to the same thing.
- However, note the distinction between these terms:
  - Data space: the set of <u>all possible patterns</u> for a problem.
  - Data set: a specific set of examples that we are given.

- The space X can be discrete or continuous.
- The space X can be finite or infinite.
- Examples of discrete and finite spaces?

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- The space X can be finite or infinite.
- Examples of discrete and finite spaces?
- The restaurant waiting problem.
- The satellite image dataset.
  - Here, individual pixels of the image are classified.
  - Each pixel is represented as a 36-dimensional vector.
  - Each of the 36 values is an integer between 1 and 157.

• Examples of a discrete and infinite space?

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- The set of videos.
  - Each video is a sequence of images (frames).
  - Each image is a sequence of pixels.
  - Each pixel is a sequence of three integers, specifying the red, green, and blue component of the color.
  - Each of these three RGB values is a number between 0 and 255.
- Assuming that a video may contain any number of frames, the number of possible videos is infinite.

- The space of images is an interesting case.
- Suppose that each image is a color image of size 100x100 pixels.
  - This is tiny compared to the size of typical photos today.
- Then, we have a finite number of possible images.
- What is that number?

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- Why?

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  - This is tiny compared to the size of typical photos today.
- Then, we have a finite number of possible images.
- What is that number?
- $256^{30,000} = 2^{240,000}$
- Why? Because:
  - An image is defined by 30,000 numbers (10,000 pixels times 3 color values).
  - Each of those numbers has 256 possible values.
- So, technically the space of 100x100 images is discrete and finite, but practically you can treat it as discrete and infinite.

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- No!
- If the space is finite, it means it can only have a finite number of elements.
- Finite number of elements means finite (and thus discrete) number of possible values.

Any examples of continuous and infinite spaces?

- Any examples of continuous and infinite spaces?
- Any space where we represent data using continuous values.
- Examples of such continuous values:
  - Weight.
  - Height.
  - Temperature.
  - Distance.
- Example task: predict the gender of a chameleon based on its weight and length.

- Let X be the space of all possible patterns for some classification problem.
- Suppose that we have a function P(x | c) that produces the conditional probability of any x in X given any class label c.
- Suppose that we also know the prior probabilities
   P(c) of all classes c.
- Given this information, we can build the optimal (most accurate possible) classifier for our problem.
  - We can prove that no other classifier can do better.
- This optimal classifier is called the Bayes classifier.

- So, how do we define this optimal classifier? Let's call it B.
- B(x) = ???

Any ideas?

 First, for every class c, compute P(c | x) using Bayes rule.

$$P(c \mid x) = \frac{P(x \mid c) * P(c)}{P(x)}$$

- To compute the above, we need to compute P(x).
   How can we compute P(x)?
- Let C be the set of all possible classes.
- $P(x) = \sum_{c \in C} P(x \mid c) * P(c)$

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• Using  $P(c \mid x)$ , we can now define the optimal classifier:

$$B(x) = ???$$

Can anyone try to guess?

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$$P(x) = \sum_{c \in C} P(x \mid c) * P(c)$$

• Using  $P(c \mid x)$ , we can now define the optimal classifier:

$$B(x) = \underset{c \in C}{\operatorname{argmax}} P(c \mid x)$$

- What does this mean? What is  $\underset{c \in C}{\operatorname{argmax}} P(c \mid x)$ ?
- It is the class c that maximizes P(c | x).

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• Using  $P(c \mid x)$ , we can now define the optimal classifier:

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- B(x) is called the <u>Bayes Classifier</u>.
- It is the most accurate classifier you can possibly get.

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• Using  $P(c \mid x)$ , we can now define the optimal classifier:

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- B(x) is called the **Bayes Classifier**.
- Important note: the above formulas can also be applied when  $P(x \mid c)$  is a **probability density function**.

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## **Bayes Classifier Optimality**

$$B(x) = \underset{c \in C}{\operatorname{argmax}} P(c \mid x)$$

- Why is this a reasonable definition for B(x)?
- Why is it the best possible classifier?
- 555

## **Bayes Classifier Optimality**

$$B(x) = \underset{c \in C}{\operatorname{argmax}} P(c \mid x)$$

- Why is this a reasonable definition for B(x)?
- Why is it the best possible classifier?
- Because B(x) provides the answer that is most likely to be true.
- When we are not sure what the correct answer is, our best bet is the answer that is the most likely to be true.

$$B(x) = \underset{c \in C}{\operatorname{argmax}} P(c \mid x)$$

Will such a classifier always have perfect accuracy?

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- Will such a classifier always have perfect accuracy?
- No. Here is a toy example:
- We want our classifier B(x) to predict whether a temperature x came from Maine or from the Sahara desert.
- Consider B(90). A temperature of 90 is possible in both places.
- Whatever B(90) returns, it will be wrong in some cases.
  - If B(90) = Sahara, then B will be wrong in the few cases where this 90 was observed in Maine.
  - If B(90) = Maine, then B will be wrong in the many cases where this 90 was observed in Sahara.
- The Bayesian classifier B returns for 90 the most likely answer (Sahara), so as to be correct as frequently as possible.

$$B(x) = \underset{c \in C}{\operatorname{argmax}} P(c \mid x)$$

- Actually (though this is a side issue), to be entirely accurate, there is a case where B(90) would return Maine, even though a temperature of 90 is much more common in Sahara.
- What is that case?
- The case where the prior probability for Sahara is really really low.
  - Sufficiently low to compensate for the fact that temperatures of 90 are much more frequent there than in Maine.
- Remember,  $P(Sahara \mid x) = \frac{P(x \mid Sahara) * P(Sahara)}{P(x)}$
- If P(Sahara) is very low (if inputs x rarely come from Sahara), it drives P(Sahara | X) down as well.

- So, we know the formula for the optimal classifier for any classification problem.
- Why don't we always use the Bayes classifier?
  - Why are we going to study other classification methods in this class?
  - Why are people still trying to come up with new classification methods, if we already know that none of them can beat the Bayes classifier?

- So, we know the formula for the optimal classifier for any classification problem.
- Why don't we always use the Bayes classifier?
  - Why are we going to study other classification methods in this class?
  - Why are researchers still trying to come up with new classification methods, if we already know that none of them can beat the Bayes classifier?
- Because, sadly, the Bayes classifier has a catch.
  - To construct the Bayes classifier, we need to compute P(x | c),
     for every x and every c.
  - In most cases, we cannot compute  $P(x \mid c)$  precisely enough.

## Problems with Estimating Probabilities

- To show why we usually cannot estimate probabilities precisely enough, we can consider again the example of the space of 100x100 images.
  - In that case, x is a vector of 30,000 dimensions.
- Suppose we want B(x) to predict whether x is a photograph of Michael Jordan or Kobe Bryant.
- P(x | Jordan) can be represented as a joint distribution table of 30,000 variables, one for each dimension.
  - Each variable has 256 possible values.
  - We need to compute and store 256<sup>30,000</sup> numbers.
- We have neither enough storage to store such a table, nor enough training data to compute all these values.

- In typical pattern classification problems, our data is too complex to allow us to compute probability distributions precisely.
- So, what can we do?
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- In typical pattern classification problems, our data is too complex to allow us to compute probability distributions precisely.
- So, what can we do?
- We have two options.
- One is to not use a Bayes classifier.
- This is why other methods exist and are useful.
  - An example: neural networks (we will see them in more detail in a few weeks).
  - Other popular examples that we will not study: Boosting, support vector machines.

- The second option is to use a pseudo-Bayes classifier, and estimate <u>approximate</u> probabilities P(x | c).
- What is approximate?
  - An approximate estimate is an estimate that is not expected to be 100% correct.
  - An approximate method for estimating probabilities is a method that produces approximate estimates of probability distributions.
- Approximate methods are designed to require reasonable memory and reasonable amounts of training data, so that we can actually use them in practice.

- We will see several examples of such approximate methods, but you have already seen two approaches (and two associated programming assignments):
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- We will see several examples of such approximate methods, but you have already seen two approaches (and two associated programming assignments):
- Bayesian networks is one approach for simplifying the representation of the joint probability distribution.
  - Of course, Bayesian networks may be exact in some cases, but typically the variables have dependencies in the real world that the network topology ignores.
- Decision trees and random forests are another approach.

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- What is the output of a decision tree on some input x?
- $\underset{c \in C}{\operatorname{argmax}} P(c \mid x)$ , based on the P(c, x) stored on the leaf.
- What is the output of a decision forest on some input x?

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- What is the output of a decision tree on some input x?
- $\underset{c \in C}{\operatorname{argmax}} P(c \mid x)$ , based on the P(c, x) stored on the leaf.
- What is the output of a decision forest on some input x?
- argmax P(c | x), based on the average of P(c | x) values
   c∈C
   we get from each tree.

- The Bayesian classifier outputs  $\underset{c \in C}{\operatorname{argmax}} P(c \mid x)$
- Decision trees and forests also output  $\underset{c \in C}{\operatorname{argmax}} P(c \mid x)$
- So, are decision trees and forests Bayes classifiers?
  - Which would mean that no other classifier can do better!

- The Bayesian classifier outputs  $\underset{c \in C}{\operatorname{argmax}} P(c \mid x)$
- Decision trees and forests also output  $\underset{c \in C}{\operatorname{argmax}} P(c \mid x)$
- So, are decision trees and forests Bayes classifiers?
  - Which would mean that no other classifier can do better!
- Theoretically, they are Bayes classifiers, in the (usually unrealistic)
  case that the probability distributions stored in the leaves are
  accurate.
- I call them "pseudo-Bayes" classifiers, because they look like Bayes classifiers, but use inaccurate probabilities.

## Bayes and "pseudo-Bayes" Classifiers

- This approach is very common in classification:
  - Estimate probability distributions  $P(x \mid c)$ , using an approximate method.
  - Use the Bayes classifier approach and output, given x,

$$\operatorname*{argmax} P(c \mid x)$$

- The resulting classifier looks like a Bayes classifier, but is not a true Bayes classifier.
  - It is not the most accurate classifier, whereas a true Bayes classifier has the best possible accuracy.
- The true Bayes classifier uses the true (and usually impossible to compute) probabilities P(x | c).

## **Approximate Probability Estimation**

- We are going to look at some popular approximate methods for estimating probability distributions.
- Histograms.
- Gaussians.
- Mixtures of Gaussians.

We start with histograms.

## Example Application: Skin Detection

- In skin detection (at least in our version of the problem), the input x is the color of a pixel.
- The output is whether that pixel belongs to the skin of a human or not.
  - So, we have two classes: skin and non-skin.
- Application: detection of skin regions in images and video.
- Why would skin detection be useful?

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- Application: detection of skin regions in images and video.
- Why would skin detection be useful?
  - It is very useful for detecting hands and faces.
  - It is used a lot in computer vision systems for person detection, gesture recognition, and human motion analysis.

## **Examples of Skin Detection**

Input Image



Output Image



- The classifier is applied individually on each pixel of the input image.
- In the output:
  - White pixels are pixels classified as "skin".
  - Black pixels are pixels classified as "not skin".

## **Examples of Skin Detection**

Input Image



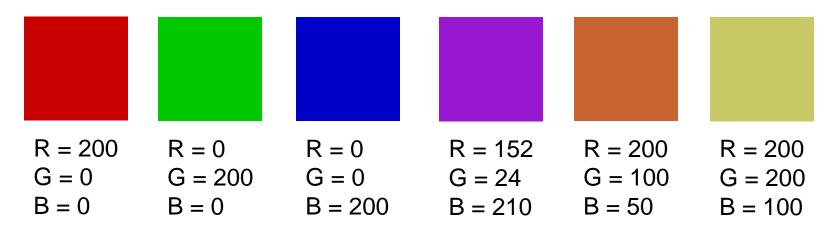
**Output Image** 



- The classifier is applied individually on each pixel of the input image.
- In the output:
  - White pixels are pixels classified as "skin".
  - Black pixels are pixels classified as "not skin".

#### Building a Skin Detector

- We want to classify each pixel of an image, as skin or non-skin.
- What are the attributes (features) of each pixel?
- Three integers: R, G, B. Each is between 0 and 255.
  - The red, green, and blue values of the color of the pixel.
- Here are some example RGB values and their associated colors:



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- If we want to use a pseudo-Bayes classifier, which probability distributions do we need to estimate?
  - P(skin | R, G, B)
  - P(not skin | R, G, B)
- To compute the above probability distributions, we first need to compute:
  - P(R, G, B | skin)
  - $P(R, G, B \mid not skin)$
  - P(skin)
  - P(not skin)

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  - P(R, G, B | not skin)
  - P(skin)
  - P(not skin)
- To compute these quantities, we need training data.
  - We need lots of pixels, for which we know both the color and whether they were skin or non-skin.
- P(skin) is a single number.
  - How can we compute it?

- We need to compute:
  - $P(R, G, B \mid skin)$
  - P(R, G, B | not skin)
  - P(skin)
  - P(not skin)
- To compute these quantities, we need training data.
  - We need lots of pixels, for which we know both the color and whether they were skin or non-skin.
- P(skin) is a single number.
  - We can simply set it equal to the percentage of skin pixels in our training data.
- P(not skin) is just 1 P(skin).

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- How about P(R, G, B | skin) and P(R, G, B | not skin)?
  - How many numbers do we need to compute for them?
- How many possible combinations of values do we have for R, G, B?
  - $-256^3 = 16,777,216$  combinations.
- So, we need to estimate about 17 million probability values for P(R, G, B | skin)
- Plus, we need an additional 17 million values for P(R, G, B | not skin)

- So, in total we need to estimate about 34 million numbers.
- How do we estimate each of them?
- For example, how do we estimate P(152, 24, 210 | skin)?

- So, in total we need to estimate about 34 million numbers.
- How do we estimate each of them?
- For example, how do we estimate P(152, 24, 210 | skin)?
- We need to go through our training data.
  - Count the number of all skin pixels whose color is (152,24,210).
- Divide that number by the total number of skin pixels in our training data.
- The result is P(152, 24, 210 | skin).

How much training data do we need?

- How much training data do we need?
- Lots, in order to have an accurate estimate for each color value.
- Even though estimating 34 million values is not an utterly hopeless task, it still requires a lot of effort in collecting data.
- Someone would need to label hundreds of millions of pixels as skin or non skin.
- While doable (at least by a big company), it would be a very time-consuming and expensive undertaking.

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- Do we need to handle that many values?

- Our problem is caused by the fact that we have to many possible RGB values.
- Do we need to handle that many values?
  - Is P(152, 24, 210 | skin) going to be drastically different than P(153, 24, 210 | skin)?
  - The difference in the two colors is barely noticeable to a human.
- We can group similar colors together.
- A histogram is an array (one-dimensional or multidimensional), where, at each position, we store the frequency of occurrence of a certain range of values.

- For example, if we computed P(R, G, B | skin) for every combination, the result would be a histogram.
  - More specifically, it would be a three-dimensional 256x256x256 histogram.
  - Histogram[R][G][B] = frequency of occurrence of that color in skin pixels.
- However, a histogram allows us to group similar values together.
- For example, we can represent the P(R, G, B | skin) distribution as a 32x32x32 histogram.
  - To find the histogram position corresponding to an R, G, B combination, just divide R, G, B by 8, and take the floor.

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- Suppose that we represent P(R, G, B | skin) as a 32x32x32 histogram.
  - To find the histogram position corresponding to an R, G, B combination, just divide R, G, B by 8, and take the floor.
- Then, what histogram position corresponds to RGB value (152, 24, 210)?
- floor(152/8, 24/8, 210/8) = (19, 3, 26).
- In this case, each position in the histogram corresponds to 8x8x8 = 512 distinct RGB combinations.
- Each position in the histogram is called a <u>bin</u>, because it counts the frequency of multiple values.

## **How Many Bins?**

- How do we decide the size of the histogram?
  - Why 32x32x32?
  - Why not 16x16x16, or 8x8x8, or 64x64x64?

#### **How Many Bins?**

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- Overall, we have a tradeoff:
  - Larger histograms require more training data.
  - If we do have sufficient training data, larger histograms give us more information compared to smaller histograms.
  - If we have insufficient training data, then larger histograms give us less reliable information than smaller histograms.
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  - If we have insufficient training data, then larger histograms give us less reliable information than smaller histograms.
- How can we choose the size of a histogram in practice?
  - Just try different sizes, see which one is the most accurate in classifying test examples.

## Limitations of Histograms

- For skin detection, histograms are a reasonable choice.
- How about the satellite image dataset?
  - There, each pattern has 36 dimensions (i.e., 36 attributes).
  - Each attribute is an integer between 1 and 157.
- What histogram size would make sense here?

## Limitations of Histograms

- For skin detection, histograms are a reasonable choice.
- How about the satellite image dataset?
  - There, each pattern has 36 dimensions (i.e., 36 attributes).
  - Each attribute is an integer between 1 and 157.
- What histogram size would make sense here?
- Even if we discretize each attribute to just two values, we still need to compute 2<sup>36</sup> values, which is about 69 billion values.
- We have 4,435 training examples, so clearly we do not have enough data to estimate that many values.

- The naive Bayes classifier is a method that makes the (typically unrealistic) assumption that the different attributes are independent of each other.
  - The naïve Bayes classifier can be combined with pretty much any probability estimation method, including histograms.
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     we can compute 36 one-dimensional histograms.
- Why?

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$$- P(X_1, X_2, ..., X_{36} \mid c) = ???$$

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     we can compute 36 one-dimensional histograms.
- Why? Because of independence. We can compute the probability distribution separately for each dimension.
  - $P(X_1, X_2, ..., X_{36} | c) = P(X_1 | c) * P(X_2 | c) * ... * P(X_{36} | c).$

#### The Naïve Bayes Classifier

- Suppose that build these 36 one-dimensional histograms.
- Suppose that we treat each value (from 1 to 157) separately, so each histogram has 157 bins.
- How many numbers do we need to compute in order to compute our  $P(X_1, X_2, ..., X_{36} \mid c)$  distribution?

#### The Naïve Bayes Classifier

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- Suppose that we treat each value (from 1 to 157) separately, so each histogram has 157 bins.
- How many numbers do we need to compute in order to compute our  $P(X_1, X_2, ..., X_{36} \mid c)$  distribution?
- We need 36 histograms (one for each dimension).
  - -36\*157 = 5,652 values.
  - Much better than 69 billion values for 2<sup>36</sup> bins.
- We compute  $P(X_1, X_2, ..., X_{36} \mid c)$  for six different classes c, so overall we compute 36\*157\*6 = 33,912 values.

#### Gaussians

- A popular way to estimate <u>probability density</u>
   functions is to model them as Gaussians.
  - These Gaussian densities are also called normal distributions.
- In one dimension, a normal distribution is defined as:

$$N(x) = \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{(x-\mu)^2}{2\sigma^2}}$$

 To define a Gaussian, what parameters do we need to specify?

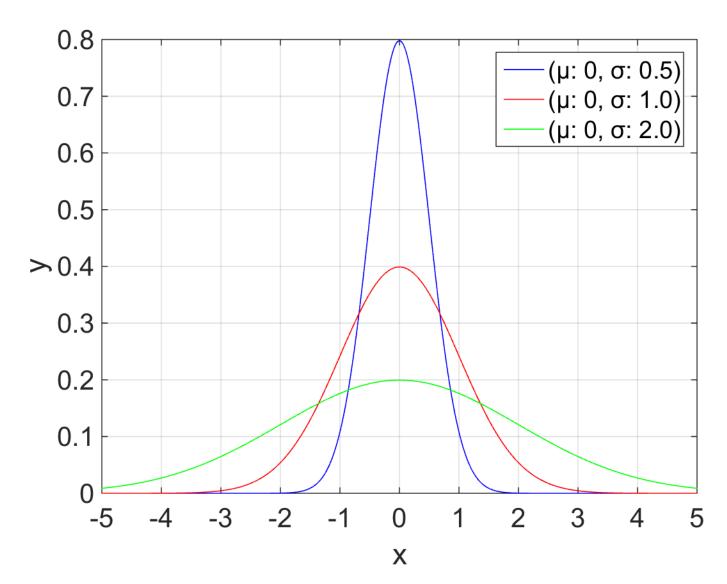
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- To define a Gaussian, what parameters do we need to specify? Just two parameters:
  - $-\mu$ , which is the mean (average) of the distribution.
  - $-\sigma$ , which is the standard deviation of the distribution.
  - Note:  $\sigma^2$  is called the **variance** of the distribution.

#### **Examples of Gaussians**

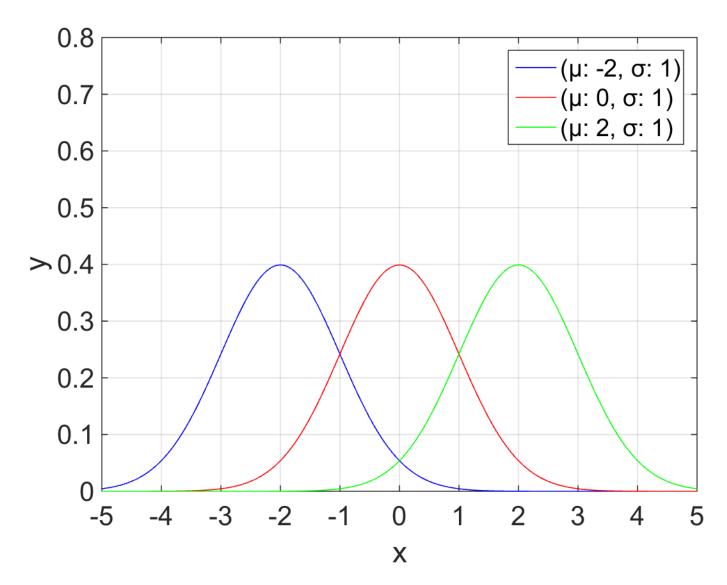


Increasing the standard deviation makes the values more spread out.

Decreasing the std makes the distribution more peaky.

The integral is always equal to 1.

#### **Examples of Gaussians**



Changing the mean moves the distribution to the left or to the right.

#### Estimating a Gaussian

In one dimension, a Gaussian is defined like this:

$$N(x) = \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{(x-\mu)^2}{2\sigma^2}}$$

- Given a set of n real numbers  $x_1, ..., x_n$ , we can easily find the best-fitting Gaussian for that data.
- The mean μ is simply the average of those numbers:

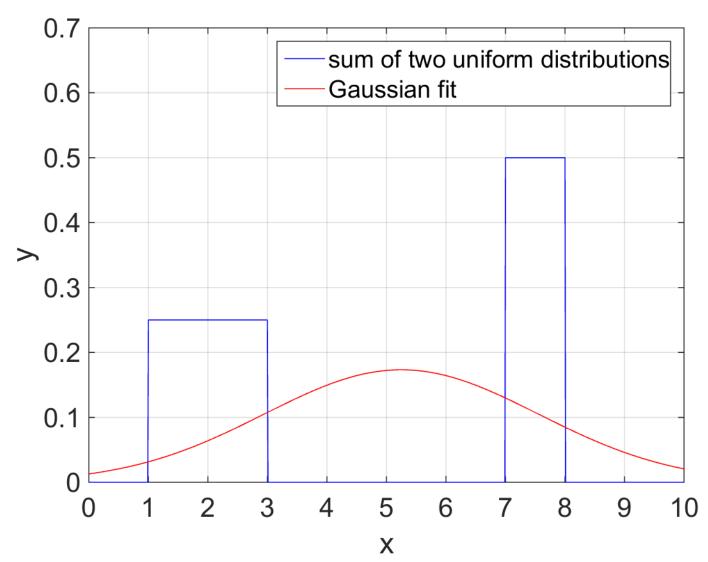
$$\mu = \frac{1}{n} \sum_{i=1}^{n} x_i$$

The standard deviation σ is computed as:

$$\sigma = \sqrt{\frac{1}{n-1} \sum_{i=1}^{n} (x_i - \mu)^2}$$

#### Estimating a Gaussian

- Fitting a Gaussian to data does not guarantee that the resulting Gaussian will be an accurate distribution for the data.
- The data may have a distribution that is very different from a Gaussian.
- This also happens when fitting a line to data.
  - We can estimate the parameters for the best-fitting line.
  - Still, the data itself may not look at all like a line.

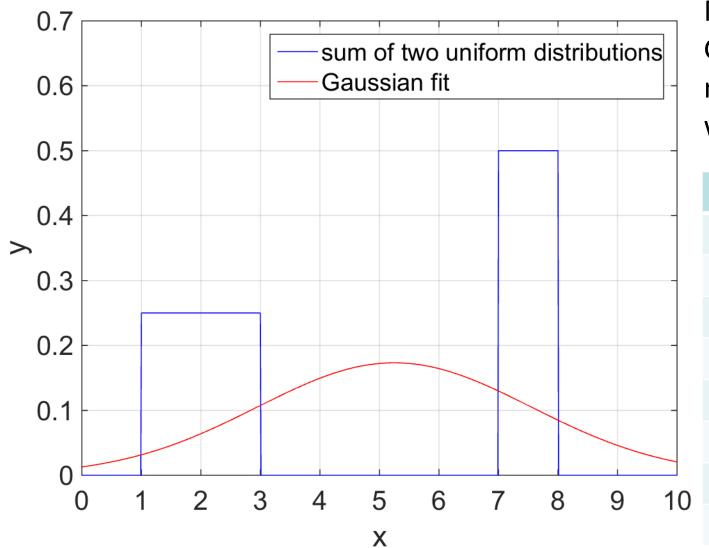


The blue curve is a density function F such that:

- F(x) = 0.25for  $1 \le x \le 3$ .
- F(x) = 0.5 for  $7 \le x \le 8$ .

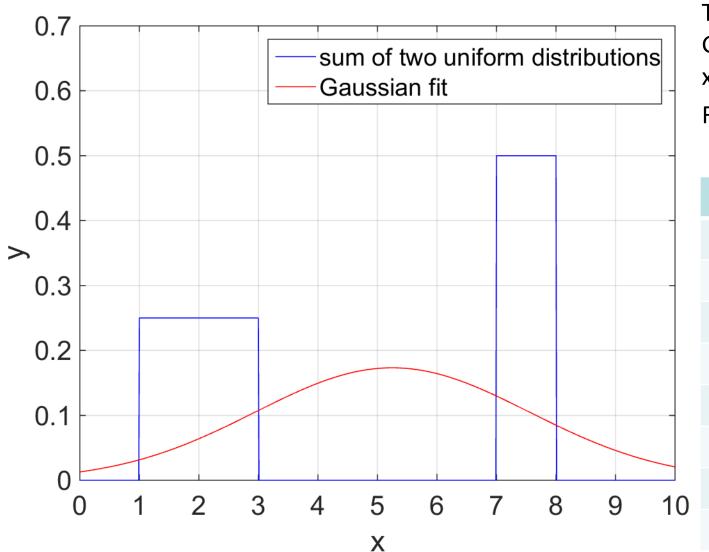
The red curve is the Gaussian fit G to data

10 generated using F.



Note that the Gaussian does not fit the data well.

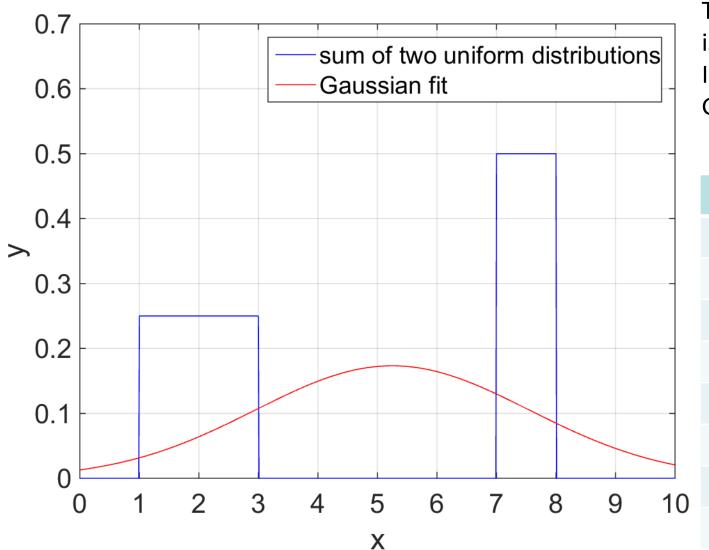
X	F(x)	G(x)
1	0.25	0.031
2	0.25	0.064
3	0.25	0.107
4	0	0.149
5	0	0.172
6	0	0.164
7	0.5	0.130
8	0.5	0.085



The peak value of G is 0.173, for x=5.25.

F(5.25) = 0!!!

X	F(x)	G(x)
1	0.25	0.031
2	0.25	0.064
3	0.25	0.107
4	0	0.149
5	0	0.172
6	0	0.164
7	0.5	0.130
8	0.5	0.085



The peak value of F is 0.5, for  $7 \le x \le 8$ . In that range,  $G(x) \le 0.13$ .

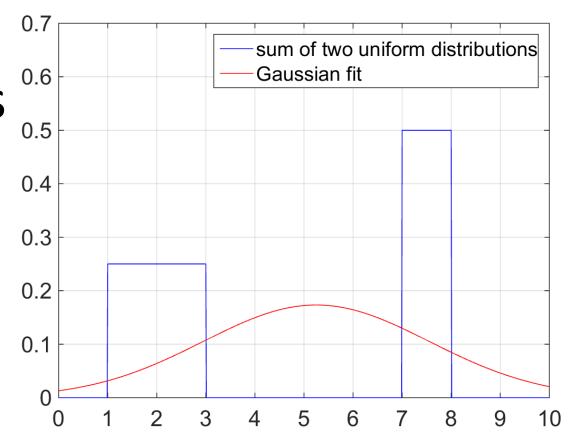
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6	0	0.164
7	0.5	0.130
8	0.5	0.085

#### Naïve Bayes with 1D Gaussians

- Suppose the patterns come from a d-dimensional space:
  - Examples: the pendigits, satellite, and yeast datasets.
- Let dim(x, i) be a function that returns the value of a pattern x in the i-th dimension.
  - For example, if  $x = (v_1, ..., v_d)$ , then dim(x, i) returns  $v_i$ .
- For each dimension i, we can use a Gaussian to model the distribution  $P_i(v_i \mid c)$  of the data in that dimension, given their class.
- For example for the pendigits dataset, we would get 160 Gaussians:
  - 16 dimensions \* 10 classes.
- Then, we can use the naïve Bayes approach (i.e., assume pairwise independence of all dimensions), to define P(x | c) as:

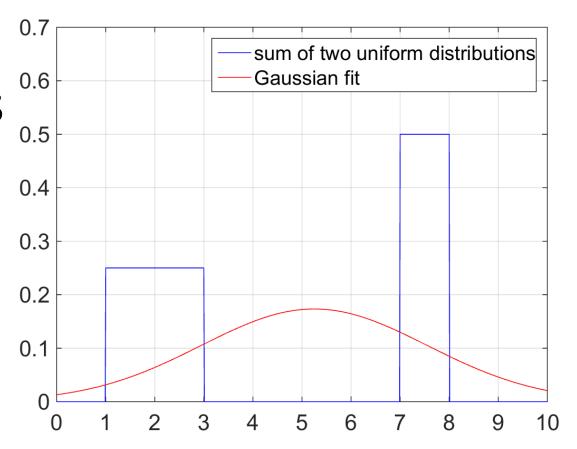
$$P(x \mid c) = \prod_{i=1}^{a} P_i(\dim(x, i) \mid c)$$

# Mixtures of Gaussians



- This figure shows our previous example, where we fitted a Gaussian into some data, and the fit was poor.
- Overall, Gaussians have attractive properties:
  - They require learning only two numbers ( $\mu$  and  $\sigma$ ), and thus require few training data to estimate those numbers.
- However, for some data, Gaussians are just not good fits.

# Mixtures of Gaussians



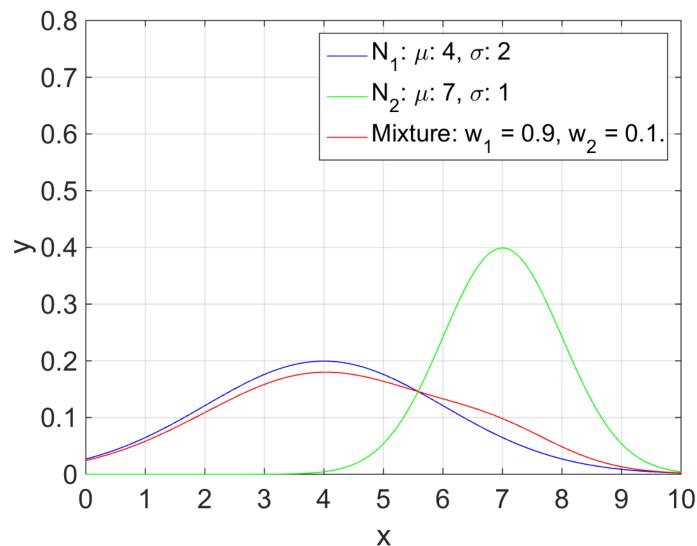
- Mixtures of Gaussians are oftentimes a better solution.
  - They are defined in the next slide.
- They still require relatively few parameters to estimate, and thus can be learned from relatively small amounts of data.
- They can fit pretty well actual distributions of data.

#### Mixtures of Gaussians

- Suppose we have k normal (i.e., Gaussian) distributions N<sub>i</sub>.
- Each  $N_i$  has its own mean  $\mu_i$  and std  $\sigma_i$ .
- Using these k Gaussians, we can define a <u>Gaussian</u> <u>mixture</u> M as follows:

$$M(x) = \sum_{i=1}^{k} w_i N_i(x)$$

- Each w<sub>i</sub> is a weight, specifying the relative importance of Gaussian N<sub>i</sub> in the mixture.
  - Weights w<sub>i</sub> are real numbers between 0 and 1.



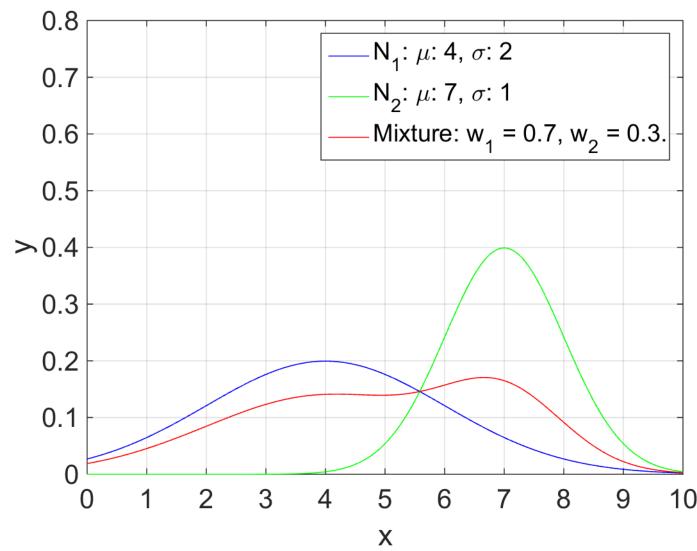
The blue and green curves show two Gaussians.

The red curve shows a mixture of those Gaussians.

$$w_1 = 0.9$$
.

$$w_2 = 0.1$$
.

The mixture looks a lot like  $N_1$ , but is influenced a little by  $N_2$  as well.



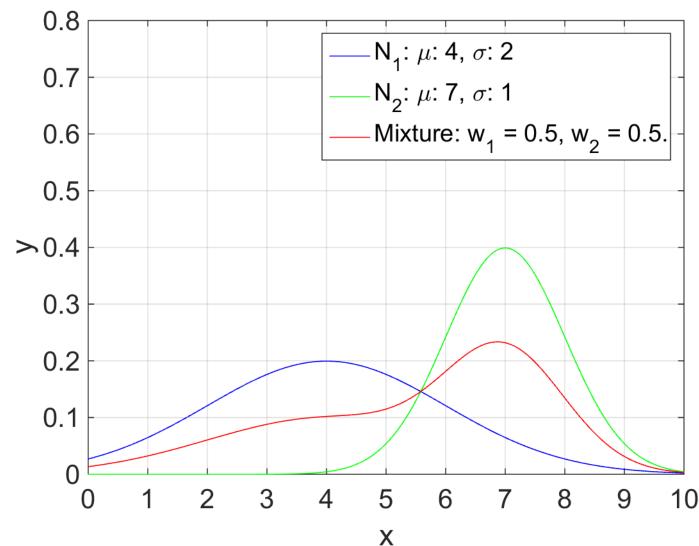
The blue and green curves show two Gaussians.

The red curve shows a mixture of those Gaussians.

$$w_1 = 0.7$$
.

$$w_2 = 0.3$$
.

The mixture looks less like N<sub>1</sub> compared to the previous example, and is influenced more by N<sub>2</sub>.



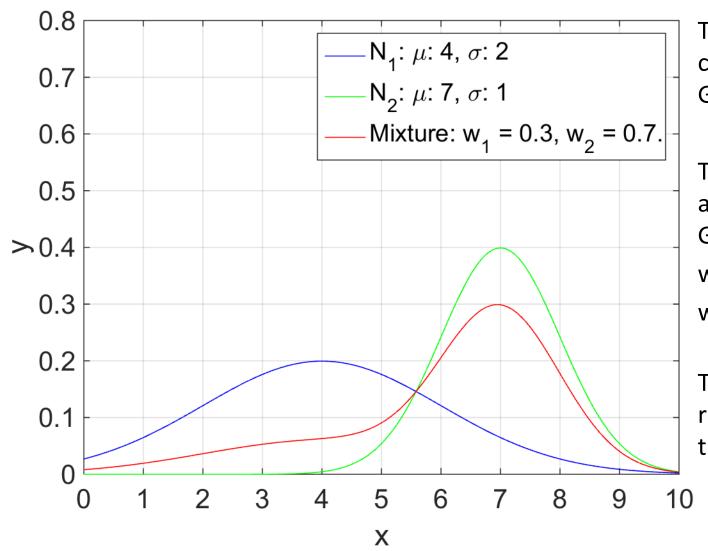
The blue and green curves show two Gaussians.

The red curve shows a mixture of those Gaussians.

$$W_1 = 0.5.$$

$$w_2 = 0.5$$
.

At each point x, the value of the mixture is the average of  $N_1(x)$  and  $N_2(x)$ .



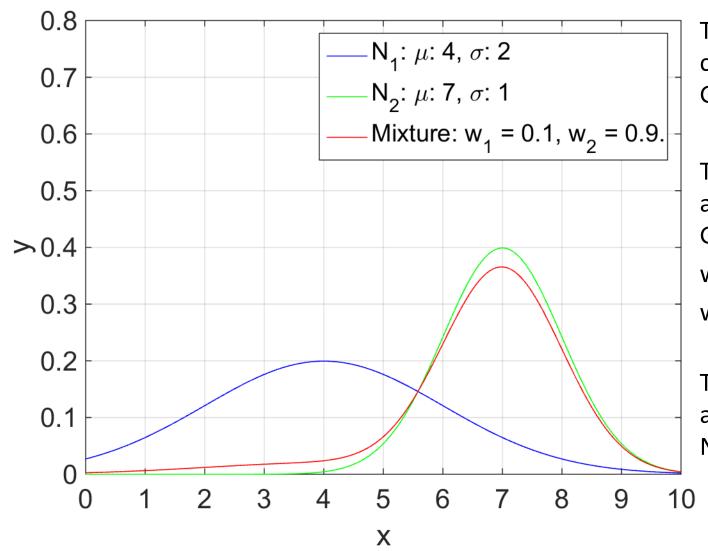
The blue and green curves show two Gaussians.

The red curve shows a mixture of those Gaussians.

$$w_1 = 0.3$$
.

$$w_2 = 0.7.$$

The mixture now resembles  $N_2$  more than  $N_1$ .



The blue and green curves show two Gaussians.

The red curve shows a mixture of those Gaussians.

$$W_1 = 0.1.$$

$$w_2 = 0.9$$
.

The mixture now is almost identical to  $N_2(x)$ .

- Suppose we are given training data  $x_1, x_2, ..., x_n$ .
- Suppose all x<sub>i</sub> belong to the same class c.
- How can we fit a mixture of Gaussians to this data?
- This will be the topic of the next few slides.
- We will learn a very popular machine learning algorithm, called the EM algorithm.
  - EM stands for **Expectation-Maximization**.
- Step 0 of the EM algorithm: pick k manually.
  - Decide how many Gaussians the mixture should have.
  - Any approach for choosing k automatically is beyond the scope of this class.

- Suppose we are given training data  $x_1, x_2, ..., x_n$ .
- Suppose all x<sub>i</sub> belong to the same class c.
- We want to model P(x | c) as a mixture of Gaussians.
- Given k, how many parameters do we need to estimate in order to fully define the mixture?
- Remember, a mixture M of k Gaussians is defined as:

$$M(x) = \sum_{i=1}^{k} w_i N_i(x) = \sum_{i=1}^{k} \left[ w_i \frac{1}{\sigma_i \sqrt{2\pi}} e^{-\frac{(x - \mu_i)^2}{2\sigma_i^2}} \right]$$

- For each N<sub>i</sub>, we need to estimate three numbers:
  - $w_i$ ,  $\mu_i$ ,  $\sigma_i$ .
- So, in total, we need to estimate 3\*k numbers.

- Suppose we are given training data  $x_1, x_2, ..., x_n$ .
- A mixture M of k Gaussians is defined as:

$$M(x) = \sum_{i=1}^{k} w_i N_i(x) = \sum_{i=1}^{k} \left[ w_i \frac{1}{\sigma_i \sqrt{2\pi}} e^{-\frac{(x - \mu_i)^2}{2\sigma_i^2}} \right]$$

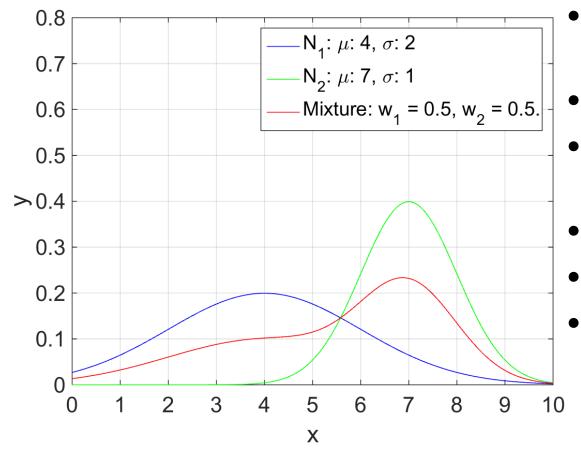
- For each  $N_i$ , we need to estimate  $w_i$ ,  $\mu_i$ ,  $\sigma_i$ .
- Suppose that we knew for each  $x_j$ , that it belongs to one and only one of the k Gaussians.
- Then, learning the mixture would be a piece of cake:
- For each Gaussian N<sub>i</sub>:
  - Estimate  $\mu_i$ ,  $\sigma_i$  based on the examples that belong to it.
  - Set w<sub>i</sub> equal to the fraction of examples that belong to N<sub>i</sub>.

- Suppose we are given training data  $x_1, x_2, ..., x_n$ .
- A mixture M of k Gaussians is defined as:

$$M(x) = \sum_{i=1}^{k} w_i N_i(x) = \sum_{i=1}^{k} \left[ w_i \frac{1}{\sigma_i \sqrt{2\pi}} e^{-\frac{(x-\mu_i)^2}{2\sigma_i^2}} \right]$$

- For each  $N_i$ , we need to estimate  $w_i$ ,  $\mu_i$ ,  $\sigma_i$ .
- However, we have no idea which mixture each x<sub>i</sub> belongs to.
- If we knew  $\mu_i$  and  $\sigma_i$  for each  $N_i$ , we could **probabilistically** assign each  $x_i$  to a component.
  - "Probabilistically" means that we would not make a hard assignment, but we would partially assign  $x_j$  to different components, with each assignment weighted proportionally to the density value  $N_i(x_i)$ .

#### Example of Partial Assignments



- Using our previous example of a mixture:
- Suppose  $x_{i} = 6.5$ .
- How do we assign 6.5 to the two Gaussians?
- $N_1(6.5) = 0.0913$ .
- $N_2(6.5) = 0.3521$ .
- So:
  - 6.5 belongs to  $N_1$  by  $\frac{0.0913}{0.0913 + 0.3521} = 20.6\%.$
  - 6.5 belongs to  $N_2$  by  $\frac{0.3521}{0.0913 + 0.3521} = 79.4\%.$

#### The Chicken-and-Egg Problem

- To recap, fitting a mixture of Gaussians to data involves estimating, for each  $N_i$ , values  $w_i$ ,  $\mu_i$ ,  $\sigma_i$ .
- If we could assign each  $x_j$  to one of the Gaussians, we could compute easily  $w_i$ ,  $\mu_i$ ,  $\sigma_i$ .
  - Even if we probabilistically assign  $x_j$  to multiple Gaussians, we can still easily  $w_i$ ,  $\mu_i$ ,  $\sigma_i$ , by adapting our previous formulas. We will see the adapted formulas in a few slides.
- If we knew  $\mu_i$ ,  $\sigma_i$  and  $w_i$ , we could assign (at least probabilistically)  $x_i$ 's to Gaussians.
- So, this is a chicken-and-egg problem.
  - If we knew one piece, we could compute the other.
  - But, we know neither. So, what do we do?

#### On Chicken-and-Egg Problems

- Such chicken-and-egg problems occur frequently in AI.
- Surprisingly (at least to people new in AI), we can easily solve such chicken-and-egg problems.
- Overall, chicken and egg problems in AI look like this:
  - We need to know A to estimate B.
  - We need to know B to compute A.
- There is a fairly standard recipe for solving these problems.
- Any guesses?

#### On Chicken-and-Egg Problems

- Such chicken-and-egg problems occur frequently in AI.
- Surprisingly (at least to people new in AI), we can easily solve such chicken-and-egg problems.
- Overall, chicken and egg problems in AI look like this:
  - We need to know A to estimate B.
  - We need to know B to compute A.
- There is a fairly standard recipe for solving these problems.
- Start by giving to A values chosen randomly (or perhaps nonrandomly, but still in an uninformed way, since we do not know the correct values).
- Repeat this loop:
  - Given our current values for A, estimate B.
  - Given our current values of B, estimate A.
  - If the new values of A and B are very close to the old values, break.

#### The EM Algorithm - Overview

- We use this approach to fit mixtures of Gaussians to data.
- This algorithm, that fits mixtures of Gaussians to data, is called the EM algorithm (Expectation-Maximization algorithm).
- Remember, we choose k (the number of Gaussians in the mixture) manually, so we don't have to estimate that.
- To initialize the EM algorithm, we initialize each  $\mu_i$ ,  $\sigma_i$ , and  $w_i$ . Values  $w_i$  are set to 1/k. We can initialize  $\mu_i$ ,  $\sigma_i$  in different ways:
  - Giving random values to each  $\mu_i$ .
  - Uniformly spacing the values given to each  $\mu_i$ .
  - Giving random values to each  $\sigma_i$ .
  - Setting each  $\sigma_i$  to 1 initially.
- Then, we iteratively perform two steps.
  - The **E-step**.
  - The M-step.

#### The E-Step

- E-step. Given our **current estimates** for  $\mu_i$ ,  $\sigma_i$ , and  $w_i$ :
  - We compute, for each i and j, the probability  $p_{ij} = P(N_i \mid x_j)$ : the probability that  $x_i$  was generated by Gaussian  $N_i$ .
  - How? Using Bayes rule.

$$p_{ij} = P(N_i|x_j) = \frac{P(x_j|N_i) * P(N_i)}{P(x_j)} = \frac{N_i(x_j) * w_i}{P(x_j)}$$

$$N_i(x_j) = \frac{1}{\sigma_i \sqrt{2\pi}} e^{-\frac{(x-\mu_i)^2}{2\sigma_i^2}}$$

$$P(x_j) = \sum_{i'=1}^{\kappa} (w_{i'}N_{i'}(x_j))$$

# The M-Step: Updating $\mu_i$ and $\sigma_i$

- M-step. Given our current estimates of p<sub>ii</sub>, for each i, j:
  - We compute  $\mu_i$  and  $\sigma_i$  for each  $N_i$ , as follows:

$$\mu_i = \frac{\sum_{j=1}^{n} [p_{ij} x_j]}{\sum_{j=1}^{n} p_{ij}}$$

$$\sigma_{i} = \sqrt{\frac{\sum_{j=1}^{n} [p_{ij}(x_{j} - \mu_{j})^{2}]}{\sum_{j=1}^{n} p_{ij}}}$$

 To understand these formulas, it helps to compare them to the standard formulas for fitting a Gaussian to data:

$$\mu = \frac{1}{n} \sum_{1}^{n} x_j$$

$$\sigma = \sqrt{\frac{1}{n-1} \sum_{j=1}^{n} (x_j - \mu)^2}$$

# The M-Step: Updating $\mu_i$ and $\sigma_i$

$$\mu_i = \frac{\sum_{j=1}^n [p_{ij} x_j]}{\sum_{j=1}^n p_{ij}}$$

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 To understand these formulas, it helps to compare them to the standard formulas for fitting a Gaussian to data:

$$\mu = \frac{1}{n} \sum_{1}^{n} x_j$$

$$\sigma = \sqrt{\frac{1}{n-1} \sum_{j=1}^{n} (x_j - \mu)^2}$$

- Why do we take <u>weighted</u> averages at the M-step?
- Because each  $x_i$  is probabilistically assigned to multiple Gaussians.
- We use  $p_{ij} = P(N_i|x_j)$  as weight of the assignment of  $x_j$  to  $N_i$ .

## The M-Step: Updating w<sub>i</sub>

$$w_{i} = \frac{\sum_{j=1}^{n} p_{ij}}{\sum_{i=1}^{k} \left[\sum_{j=1}^{n} p_{ij}\right]}$$

- At the M-step, in addition to updating  $\mu_i$  and  $\sigma_i$ , we also need to update  $w_i$ , which is the weight of the i-th Gaussian in the mixture.
- The formula shown above is used for the update of w<sub>i</sub>.
  - We sum up the weights of all objects for the i-th Gaussian.
  - We divide that sum by the sum of weights of all objects for all Gaussians.
  - The division ensures that  $\sum_{i=1}^k w_i = 1$ .

## The EM Steps: Summary

• E-step: Given current estimates for each  $\mu_i$ ,  $\sigma_i$ , and  $w_i$ , update  $p_{ii}$ :

$$p_{ij} = \frac{N_i(x_j) * w_i}{P(x_j)}$$

• M-step: Given our current estimates for each  $p_{ij}$ , update  $\mu_i$ ,  $\sigma_i$  and  $w_i$ :

$$\mu_i = \frac{\sum_{j=1}^{n} [p_{ij} x_j]}{\sum_{j=1}^{n} p_{ij}}$$

$$\sigma_{i} = \sqrt{\frac{\sum_{j=1}^{n} [p_{ij} (x_{j} - \mu_{j})^{2}]}{\sum_{j=1}^{n} p_{ij}}}$$

$$w_{i} = \frac{\sum_{j=1}^{n} p_{ij}}{\sum_{i=1}^{k} \left[\sum_{j=1}^{n} p_{ij}\right]}$$

#### The EM Algorithm - Termination

The log likelihood of the training data is defined as:

$$L(x_1, ..., x_n) = \sum_{j=1}^{n} \log_2(M(x_j))$$

As a reminder, M is the Gaussian mixture, defined as:

$$M(x) = \sum_{i=1}^{k} w_i N_i(x) = \sum_{i=1}^{k} \left[ w_i \frac{1}{\sigma_i \sqrt{2\pi}} e^{-\frac{(x-\mu_i)^2}{2\sigma_i^2}} \right]$$

- One can prove that, after each iteration of the E-step and the Mstep, this log likelihood increases or stays the same.
- We check how much the log likelihood changes at each iteration.
- When the change is below some threshold, we stop.

### The EM Algorithm: Summary

#### • Initialization:

- Initialize each  $\mu_i$  and  $\sigma_i$  using your favorite approach (e.g., set each  $\mu_i$  to a random value, and set each  $\sigma_i$  to 1).
- last\_log\_likelihood = -infinity.

#### Main loop:

- E-step:
  - Given our current estimates for each  $\mu_i$  and  $\sigma_i$ , update each  $p_{ii}$ .
- M-step:
  - Given our current estimates for each  $p_{ii}$ , update each  $\mu_i$  and  $\sigma_i$ .
- log\_likelihood =  $L(x_1, ..., x_n)$ .
- if (log\_likelihood last\_log\_likelihood) < threshold, break.</li>
- last\_log\_likelihood = log\_likelihood

### The EM Algorithm: Limitations

- When we fit a Gaussian to data, we always get the same result.
- We can also prove that the result that we get is the best possible result.
  - There is no other Gaussian giving a higher log likelihood to the data,
     than the one that we compute as described in these slides.
- When we fit a **mixture of Gaussians** to the same data, do we always end up with the same result?

### The EM Algorithm: Limitations

- When we fit a Gaussian to data, we always get the same result.
- We can also prove that the result that we get is the best possible result.
  - There is no other Gaussian giving a higher log likelihood to the data,
     than the one that we compute as described in these slides.
- When we fit a mixture of Gaussians to the same data, we (sadly) do not always get the same result.
- The EM algorithm is a greedy algorithm.
- The result depends on the initialization values.
- We may have bad luck with the initial values, and end up with a bad fit.
- There is no good way to know if our result is good or bad, or if better results are possible.

### Mixtures of Gaussians - Recap

- Mixtures of Gaussians are widely used.
- Why? Because with the right parameters, they can fit very well various types of data.
  - Actually, they can fit almost anything, as long as k is large enough (so that the mixture contains sufficiently many Gaussians).
- The EM algorithm is widely used to fit mixtures of Gaussians to data.

#### Multidimensional Gaussians

- So far we have discussed Gaussians (and mixtures) for the case where our training examples  $x_1, x_2, ..., x_n$  are real numbers.
- What if each x<sub>i</sub> is a vector?
  - Let D be the dimensionality of the vector.
  - Then, we can write  $x_j$  as  $(x_{j,1}, x_{j,2}, ..., x_{j,D})$ , where each  $x_{j,d}$  is a real number.
- We can define Gaussians for vector spaces as well.
- To fit a Gaussian to vectors, we must compute two things:
  - The mean (which is also a D-dimensional vector).
  - The covariance matrix (which is a DxD matrix).

#### Multidimensional Gaussians - Mean

- Let  $x_1, x_2, ..., x_n$  be D-dimensional vectors.
- $x_i = (x_{i,1}, x_{i,2}, ..., x_{i,D})$ , where each  $x_{i,d}$  is a real number.
- Then, the mean  $\mu = (\mu_1, ..., \mu_D)$  is computed as:

$$\mu = \frac{1}{n} \sum_{1}^{n} x_j$$

• Therefore,  $\mu_d = \frac{1}{n} \sum_{1}^{n} x_{j,d}$ 

## Multidimensional Gaussians – Covariance Matrix

- Let  $x_1, x_2, ..., x_n$  be D-dimensional vectors.
- $x_j = (x_{j,1}, x_{j,2}, ..., x_{j,D})$ , where each  $x_{j,d}$  is a real number.
- Let  $\Sigma$  be the covariance matrix. Its size is DxD.
- Let  $\sigma_{r,c}$  be the value of  $\Sigma$  at row r, column c.

$$\sigma_{r,c} = \sqrt{\frac{1}{n-1} \sum_{j=1}^{n} (x_{j,r} - \mu_r)(x_{j,c} - \mu_c)}$$

## Multidimensional Gaussians – Evaluation

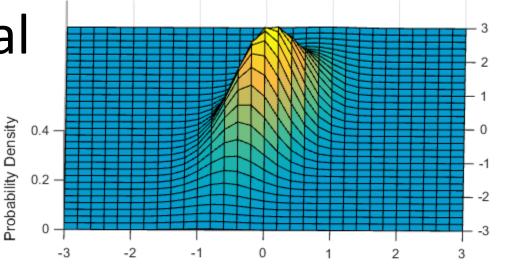
- Let  $v = (v_1, v_2, ..., v_D)$  be a D-dimensional vector.
- Let N be a D-dimensional Gaussian with mean  $\mu$  and covariance matrix  $\Sigma$ .
- Let  $\sigma_{r,c}$  be the value of  $\Sigma$  at row r, column c.
- Then, the density N(v) of the Gaussian at point v is:

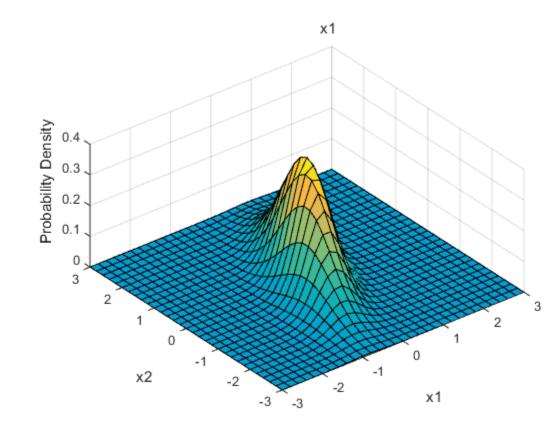
$$N(v) = \frac{1}{\sqrt{(2\pi)^D |\Sigma|}} \exp\left(-\frac{1}{2} (x - \mu)^T \Sigma^{-1} (x - \mu)\right)$$

- $|\Sigma|$  is the determinant of  $\Sigma$ .
- $\Sigma^{-1}$  is the matrix inverse of  $\Sigma$ .
- $(x \mu)^{\mathrm{T}}$  is a 1xD row vector,  $(x \mu)$  is a Dx1 column vector.

# A 2-Dimensional Example

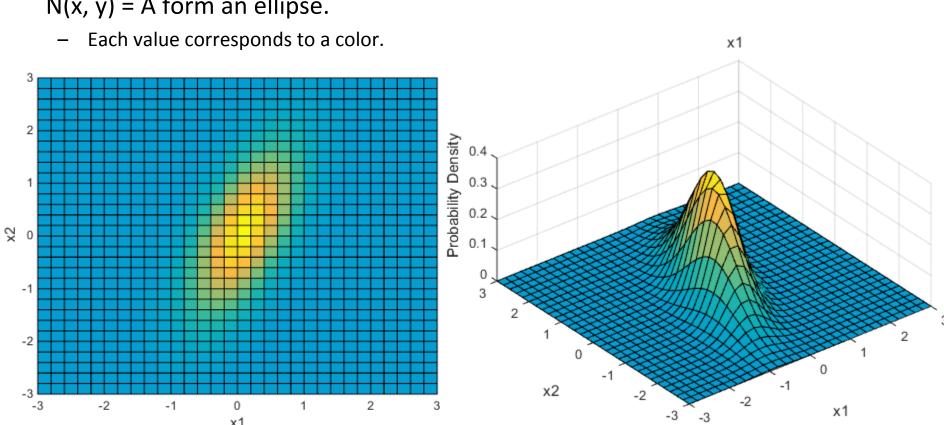
- Here you see (from different points of view) a visualization of a two dimensional Gaussian.
  - Axes: x1, x2, value.
- Its peak value is on the mean, which is (0,0).
- It has a ridge directed (in the top figure) from the bottom left to the top right.

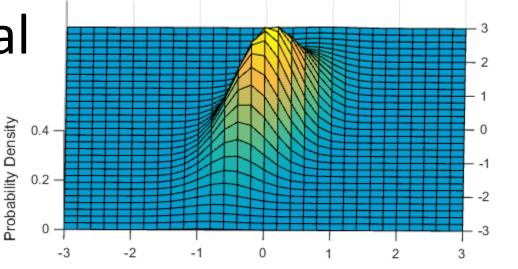




# A 2-Dimensional Example

 The view from the top shows that, for any value A, the set of points (x, y) such that N(x, y) = A form an ellipse.





# Multidimensional Gaussians – Training

- Let N be a D-dimensional Gaussian with mean  $\mu$  and covariance matrix  $\Sigma$ .
- How many parameters do we need to specify N?
  - The mean  $\mu$  is defined by D numbers.
  - The covariance matrix  $\Sigma$  requires  $D^2$  numbers  $\sigma_{r.c}$ .
  - Strictly speaking,  $\Sigma$  is symmetric,  $\sigma_{r,c} = \sigma_{c,r}$ .
  - So, we need roughly  $D^2/2$  parameters.
- The number of parameters is quadratic to D.
- The number of training data we need for reliable estimation is also quadratic to D.

### Gaussians: Recap

- 1-dimensional Gaussians are easy to estimate from relatively few examples.
  - They are specified using only two parameters,  $\mu$  and  $\sigma$ .
- D-dimensional Gaussians are specified using O(D²) parameters.
- Gaussians take a specific shape, which may not fit well the actual distribution of the data.
- Mixtures of Gaussians can take a wide range of shapes, and fit a wide range of actual distributions.
  - Mixtures are fitted to data using the EM algorithm.
  - The EM algorithm can be used for both one-dimensional and multi-dimensional mixtures.