CSE 4309 – Machine Learning
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Example Application: Skin Detection

- Goal: find skin pixels in the image.
- In the output:
 - White pixels are pixels classified as "skin".
 - Black pixels are pixels classified as "not skin".
- This is an opportunity to talk about images.
- We will use images as data in several cases this semester.

Input Image



Example Output Image



Pixel-Based Skin Detection

- In pixel-based skin detection, each pixel is classified as skin or nonskin, based on its color.
- No other information is used.
 - Each pixel is classified independently of any other pixel.
- So, the input space is the space of 3D vectors (r, g, b), such that r, g, b are integers between 0 and 255.
- The output space is binary ("skin" or "non skin").

Input Image



Output Image



Example Application: Skin Detection

Why would skin detection be useful?

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- 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.
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Building a Skin Detector

- We want to classify each pixel of an image, as skin or non-skin.
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Building a Skin Detector

- We want to classify each pixel of an image, as skin or non-skin.
- What is the input to the classifier?
- Three integers: R, G, B. Each is between 0 and 255.
 - The red, green, and blue values of the color of the pixel.
- If we want to use a Bayes classifier, which probability distributions do we need to estimate?

- 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:
 - $p(R, G, B \mid skin)$
 - $p(R, G, B \mid not skin)$
 - p(skin)
 - p(not skin)

- We need to compute:
 - $-p(R, G, B \mid skin)$
 - $p(R, G, B \mid not skin)$
 - 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:
 - $-p(R, G, B \mid skin)$
 - $p(R, G, B \mid not skin)$
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- 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 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)

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- How do we estimate each of them?
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- 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?

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- 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 billions 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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- 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 (a 3D array of size 256x256x256).
 - 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.

- Suppose that we represent p(R, G, B | skin) as a 32x32x32 histogram.
 - Thus, the histogram is a 3D array of size 32x32x32.
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 - Thus, the histogram is a 3D array of size 32x32x32.
 - 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).
- So, to look up the histogram value for RGB color (152, 24, 210),
 we look at position [19][3][26] of the histogram 3D array.
- In this case, each position in the histogram corresponds to 8x8x8 = 512 distinct RGB combinations.
- Each position in the histogram is called a **bin**, because it counts the frequency of multiple values.

How Many Bins?

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 - Why 32x32x32?
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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.
- How can we choose the size of a histogram in practice?

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- How can we choose the size of a histogram in practice?
 - Just try different sizes, see which one is the most accurate.

The Statlog Dataset

- Another dataset that we will use several times in this course, is the UCI Statlog dataset (we also call it the *Satellite* dataset).
- Input: a 36-dimensional vector, describing a pixel in an image taken by a satellite.
 - The value in each dimension is an integer between 1 and 157.
- Why 36 dimensions?
 - To describe each pixel, four basic colors are used, instead of the standard three colors (r, g, b) we are used to.
 - To classify a pixel, information is used from its 8 neighboring pixels. So, overall, 9 pixels x 4 colors = 36 values.
- Output: type of soil shown on the picture.

1: red soil

2: cotton crop

3: grey soil

4: damp grey soil

5: soil with vegetation stubble

7: very damp grey soil

Limitations of Histograms

- For skin detection, histograms are a reasonable choice.
- How about the satellite image dataset?
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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).
- What histogram size would make sense here?
- Even if we discretize each attribute to just two values, we still need to compute 2³⁶ 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.

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 we can compute 36 one-dimensional histograms.
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- Using the naïve Bayes approach, what histograms do we compute for the satellite image data?
 - Instead of needing to compute a 36-dimensional histogram,
 we can compute 36 one-dimensional histograms.
- Why? Because of independence. We can compute the probability distribution separately for each dimension.

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- The naive Bayes classifier assumes that the different dimensions of an input vector are independent of each other given the class.
- Using the naïve Bayes approach, what histograms do we compute for the satellite image data?
 - Instead of needing to compute a 36-dimensional histogram,
 we can compute 36 one-dimensional histograms.
- Why? Because of independence. We can compute the probability distribution separately for each dimension.

$$- p(X_1, X_2, ..., X_{36} | C_k) = p_1(X_1 | C_k) * p_2(X_2 | C_k) * ... * p_{36}(X_{36} | C_k)$$

- 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 $p(X_1, X_2, ..., X_{36} \mid C_k)$ distribution?

- 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 $p(X_1, X_2, ..., X_{36} \mid C_k)$ distribution?
- We need 36 histograms (one for each dimension).
 - -36*157 = 5,652 values.
 - Much better than 69 billion values for 2³⁶ bins.
- We compute $p(X_1, X_2, ..., X_{36} | C_k)$ for six different classes c, so overall we compute 36*157*6 = 33,912 values.