Introduction to Image Description

Alexandre Xavier Falcão

Institute of Computing - UNICAMP

afalcao@ic.unicamp.br

Alexandre Xavier Falcão MO445(MC940) - Image Analysis

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How can we extract and combine simple image descriptors?

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The subsequent lectures will focus on popular texture descriptors: HoG, BoVW, and CNN.

The histogram h(i) of a grayscale image $\hat{I} = (D_I, I)$ is defined as

$$h(i) = \sum_{\forall p \in D_I} \delta(I(p) - i),$$

$$\delta(I(p) - i) = \begin{cases} 1, & \text{when } i = I(p), \\ 0, & \text{otherwise.} \end{cases}$$

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For color images $\hat{l} = (D_I, \mathbf{I})$, where $\mathbf{I}(p) = (l_1(p), l_2(p), l_3(p))$ in some color space (e.g., RGB, YCbCr, Lab), this definition would lead to a sparse and, in this case, likely ineffective feature vector $\mathbf{x}(s) = h$, where $s = \hat{l}$ and $x_i(s) = h(i)$.

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The problem is addressed by dividing each axis of the color space into fixed intervals, called bins. For a 64-bin histogram of a 24-bit-RGB image, $I_1 = R$, $I_2 = G$, and $I_3 = B$, the histogram *h* is



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where $V(p) \in [0, 63]$. It is also common to create normalized histograms by setting $h(i) \leftarrow \frac{h(i)}{|D_i|}$, i = 1, 2, ..., 64.

The BIC descriptor consists of three components.

- A simple and yet effective pixel classification algorithm into image regions defined as either border (high frequency) or interior (low frequency).
- A compact region representation based on color histograms.
- A logarithmic distance function to compare histograms from two images.

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- Once V(p) is computed for each pixel p ∈ D_I, a pixel p is classified as follows.

$$L(p) = \begin{cases} 1, & \text{when } \exists q \in \mathcal{A}_1(p) \mid V(q) \neq V(p), \text{ and} \\ 0, & \text{otherwise.} \end{cases}$$

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The normalized color histograms h₀ (interior) and h₁ (border) of each region are computed and then quantized from 0 to 255 by setting h₀(i) ← 255h₀(i) and h₁(i) ← 255h₁(i).

Assuming the L1 metric, the logarithmic distance (log2) is encoded in the histograms by mapping h_b(i), b = {0,1} from [0,255] to [0,9] (4 bits per bin) as follows.

$$h_b(i) \leftarrow \begin{cases} 0 & \text{if } h_b(i) = 0, \\ 1 & \text{if } h_b(i) < 1, \\ 2 & \text{if } h_b(i) < 2, \\ 3 & \text{if } h_b(i) < 4, \\ 4 & \text{if } h_b(i) < 8, \\ 5 & \text{if } h_b(i) < 16, \\ 6 & \text{if } h_b(i) < 32, \\ 7 & \text{if } h_b(i) < 128, \\ 9 & \text{otherwise.} \end{cases}$$

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Finally, the histograms h₀ and h₁ are concatenated into a single histogram x.

Texture: Local Binary Patterns (LBP)

For a given grayscale image $\hat{I} = (D_I, I)$ and adjacency set $\mathcal{A}_{\sqrt{2}}(p) = \{q_1, q_2, \dots, q_8\}$ for $p \in D_I$.

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- The histogram of the map *B* can be used as LBP feature vector.
- Alternatively, D_I can be divided into cells of N × N pixels, one LBP histogram can be extracted per cells, and the histograms concatenated into a single feature vector per image.

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- Some of them treat rotation in the distance function and others incorporate rotation invariance in the feature vector.
- The problem is also not critical, when the images are aligned.
- The extension to color images can simply concatenate the histograms from each band.

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The fractal dimension of a 2D point set S (contour, skeleton) by Minkowski-Bouligand is a number $F \in [0, 2]$,

$$F = 2 - \lim_{r \to 0} \frac{\ln(A(r))}{\ln(r)},$$

where A(r) is the number of propagated points (area) when S is dilated by a disk of radius r.

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- The fractal dimension represents the self-similarity of *S* when *r* tends to zero.
- Note that A can be obtained from the cumulative histogram of the Euclidean distance map of S upto the distance r.

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It is known, for instance, that the fractal dimension of a koch star (on the left) is $F \approx 1.26$ [4].



One can then fit a line to the logarithmic curve of the cumulative histogram of the EDT (on the right) and use the slope m of the line to estimate $F = 2 - m \approx 1.23$.

By fitting a polynomial curve (on the left) and computing its first derivative, the resulting curve F (on the right) is a feature vector of the shape, called multiscale fractal dimension.



Note that its maximum value (on the right) is ≈ 1.25 for some value $\ln(r) \in [3.5, 4]$.

Shape: Point/segment saliences

The dilation of a contour S by a disk of small radius r (e.g., r = 10) shows that the outside area $A_{out}(p)$ of the influence zone of a point $p \in S$ is higher than its inside area $A_{in}(p)$, when p is convex, and the other way around when it is concave [5].



Such areas come from the root histogram of the EDT, which can be normalized for the purpose of shape description.

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By considering only the salience points $p \in S$, a point-salience feature vector can encode the respective positive (convex) and negative (concave) areas.



Shape: Point/segment saliences

Similar idea works for a segment-salience feature vector, when replacing points by contour segments around the salience points.



Note that, in any case, the distance function must account for possible shape rotations.

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- Let $\{D_1, D_2, \dots, D_k\}$ be a set of descriptors such that $D_i = (v_i, d_i), i = 1, 2, \dots, k$, consists of
 - an algorithm v_i that extracts feature vectors v_i(s) and v_i(t) from samples s and t, and
 - a distance function d_i that assigns a dissimilarity value $d_i(s, t)$ in the feature space between samples s and t (e.g., $||v_i(t) - v_i(s)||$).

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- The distance functions d_i, i = 1, 2, ..., k, can be combined into a single distance function d using, for instance, Genetic Programming (GP) [1].
- The resulting descriptor *D* is called a composite descriptor.

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Illustration of a composite descriptor D^* with the GP combiner C (one may use any other optimization technique).



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- Each candidate solution is an individual of a population, as represented by a data structure (e.g., tree, list, stack) whose nodes are mathematical operations, rather than a sequence of numbers, such as in genetic algorithms.

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- GP is an Artificial Intelligence technique based on biological principles of heritage and evolution.
- Each candidate solution is an individual of a population, as represented by a data structure (e.g., tree, list, stack) whose nodes are mathematical operations, rather than a sequence of numbers, such as in genetic algorithms.
- From some initial random population, the most promising individuals pass through genetic transformations (e.g., mutations) that make the population more diverse and suitable to solve the problem.

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Example of individual, where the distances d_i , i = 1, 2, ..., k, are the terminal nodes of a binary tree and the remaining nodes are other mathematical operations.



In addition to the mathematical operations (see examples in [6]),

- the reproduction selects the most effective individuals to the next population,
- the crossover exchanges subtrees between selected individuals to increase diversity, generating new trees (sons), and
- the mutation replaces a subtree of a selected individual by another subtree randomly chosen.

The individuals are assessed by a fitness function, which can be the accuracy of classification in a validation set.

The algorithm can be sketched as follows.

- 1. Generate an initial random population (first generation).
- 2. For each generation from a given maximum number do.
- 3. Evaluate each individual by the fitness function.
- 4. Select a number of the most effective ones.
- 5. Generate the next population by reproduction, crossover, and mutation of the selected individuals.
- 6. Select the best individual as the final solution.

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