



Texture-Based Image Retrieval for Computerized Tomography Databases

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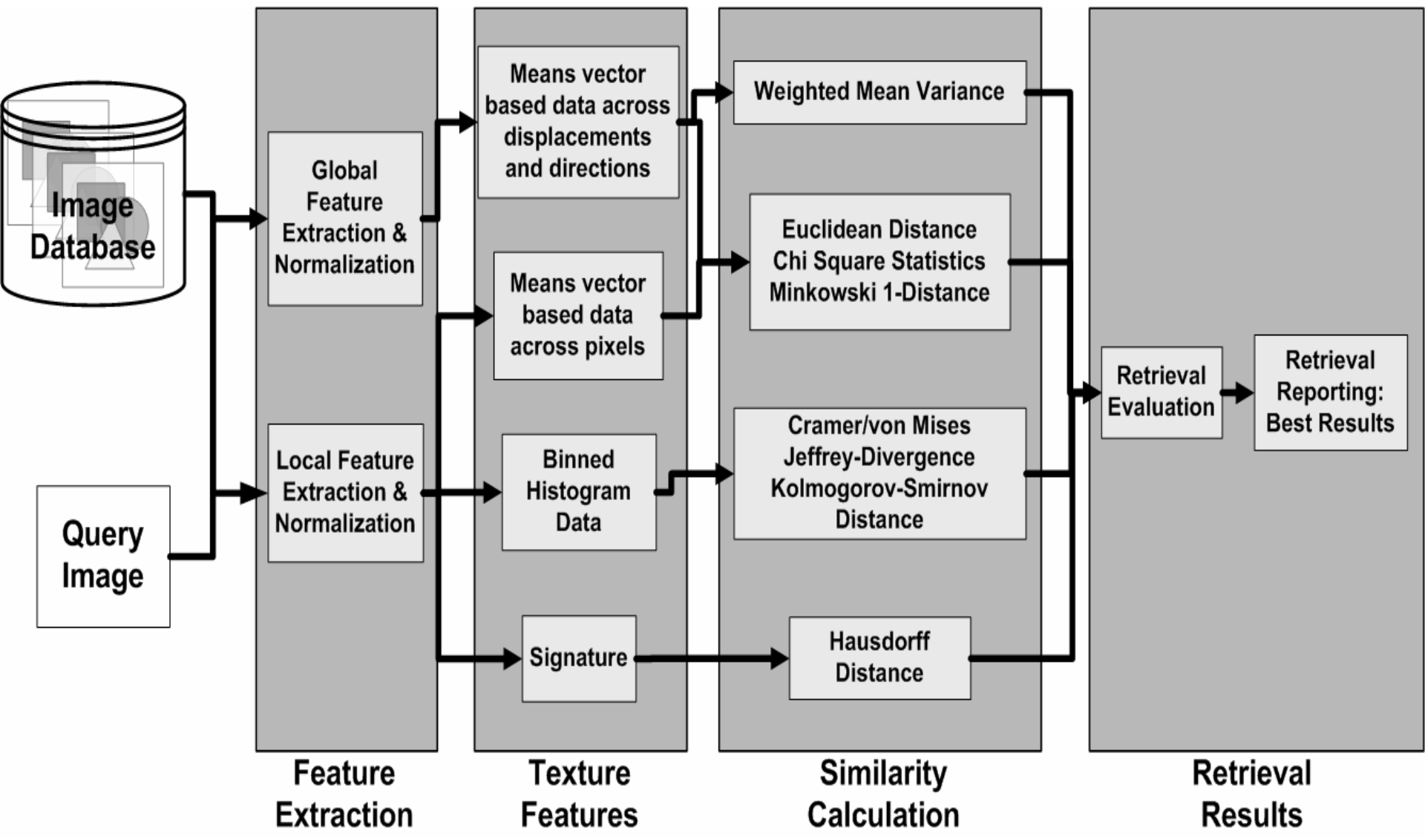
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- Motivation and Problem Statement
- Texture Feature Extraction
 - Global Features
 - Local Features
- Evaluation
- Texture Similarity Measures
- Performance Evaluation
- Experimental Results
- Conclusion
- Future Work

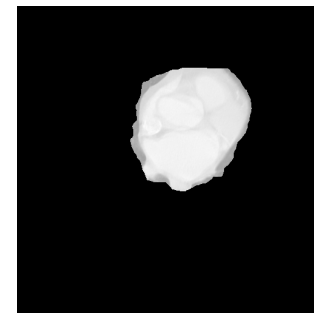
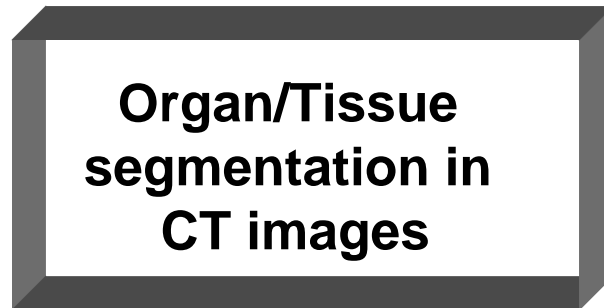
- Picture Archiving and Communications Systems (PACS) retrieve images simply by indices based on patient name, technique, or some-observer-coded text of diagnostic findings
- Textual approach, however, fails to fully account for quantitative and shape relationships of medically relevant structures within an image that are visible to a trained observer but not codable in conventional database terms.
- Each patient can have many CT images taken and time is too critical for doctors and radiologists to look through each image.
- There is a mass amount of visual medical data produced and it is important to develop applications and tools to assist and improve the process of analyzing visual medical data.

Methodology



- What are the best similarity measures for pixel and global-level data?
- The best similarity metric result for pixel-level would be compared with the best result from global-level data.
- At pixel-level, is vector-based, histogram-binned or texture signatures results better?
- Which similarity performed best for each individual organ?

Texture Feature Extraction



**Calculate texture descriptors
for each segmented image**

$[D_1, D_2, \dots, D_{21}]$

Data: 344 images of interests

Segmented organs: liver, kidneys, spleen,
backbone, & heart

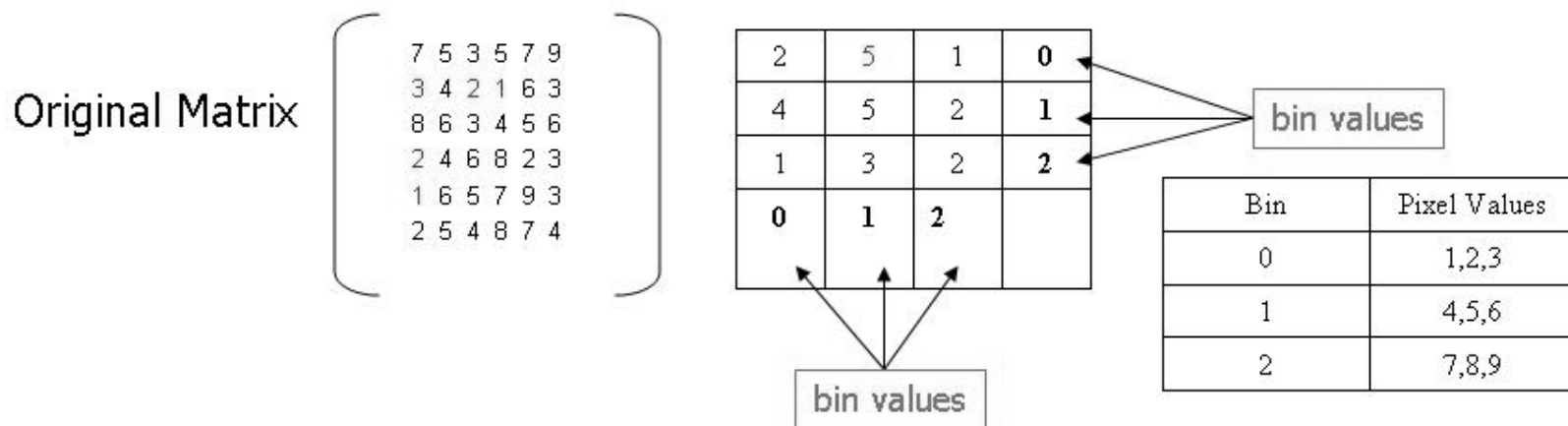
Segmentation algorithm: Active Contour Mappings
(Snakes)

2D Co-occurrence Matrix

- In order to quantify this spatial dependence of gray-level values, we calculate various textural features proposed by Haralick:
 - Entropy
 - Energy (Angular Second Moment)
 - Contrast
 - Homogeneity
 - SumMean (Mean)
 - Variance
 - Correlation
 - Maximum Probability
 - Inverse Difference Moment
 - Cluster Tendency

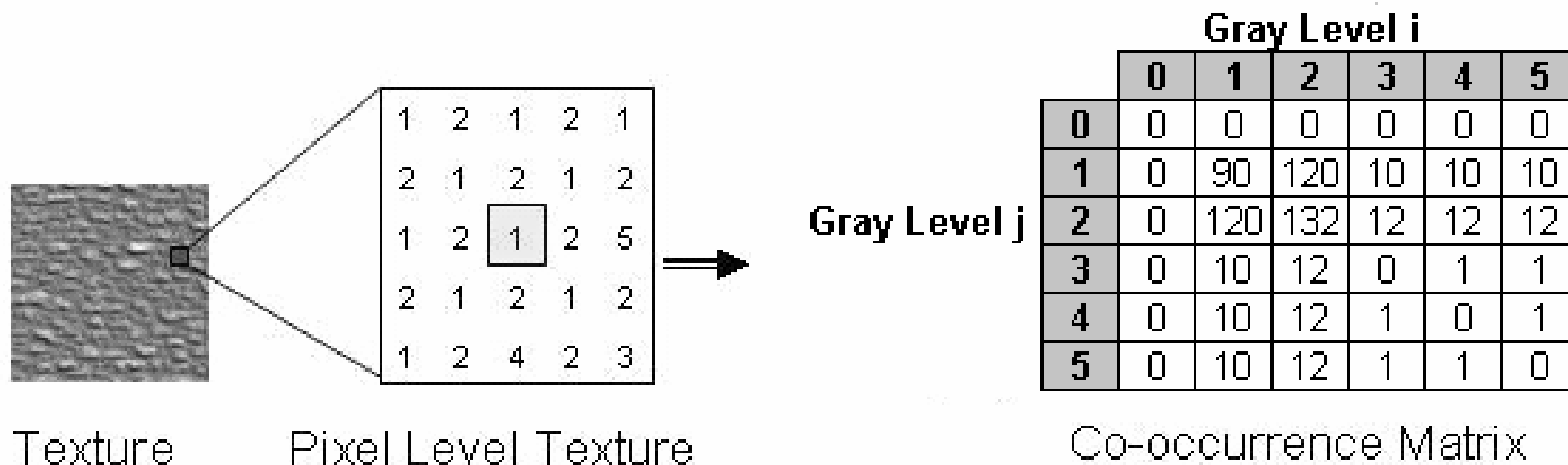
- For global-level, the normalized co-occurrence texture descriptors were calculated in four directions and five distances by pixel pairs generating twenty different matrices per segmented slice. The ten Haralick features are calculated for each of the twenty matrices, thus twenty values for entropy, energy, etc. The twenty values were then averaged to have a single value for each of the ten Haralick texture features per slice

The co-occurrence matrix would look like the following:



Pixel-Level Texture

The local texture descriptors were calculated with a 5-by-5 neighborhood pixel pair comparison in eight directions within the region, taking into account every pixel within the region, generating one matrix per 5x5 neighborhood region, and thus pixel-level, to capture information at a local level.



- Means Vector-based Data
 - Consists of the average of the normalized pixel-level data for each region such that the texture representation of that corresponding region is a vector instead of a set of vectors given by the pixels' vector representation within that region
- Binned-Histogram Data
 - Consists of texture values grouped within 256 equal-width bins
- Signature-based Data
 - Consists of clusters representing feature values that are similar
 - A k-d tree algorithm is used to generate the clusters using two stopping criteria:
 - 1) minimum variance
 - 2) minimum cluster size

Evaluation

- The **precision** is calculated as the number of relevant retrieved images divided by the total number of retrieved images in return to the query.

$$\text{precision} = \frac{\text{\# of relevant items retrieved}}{\text{\# of items retrieved}}$$

- The **recall** is calculated as the number of relevant retrieved images divided by the total number of relevant images within the entire database. A retrieved image is 'relevant' if belongs to the same anatomical region as the query.

$$\text{recall} = \frac{\text{\# of relevant items retrieved}}{\text{total \# of relevant items}}$$

GLOBAL

Vector-Based

- Euclidean Distance
- χ^2 Statistics
- Minkowski-1 Distance

PIXEL-LEVEL

Vector-Based

- Euclidean Distance
- χ^2 Statistics
- Minkowski-1 Distance
- Weighted Mean Variance

Binned-Histogram

- Cramer/von Mises
- Jeffrey-Divergence
- Kolmogorov-Smirnov

Signature-based

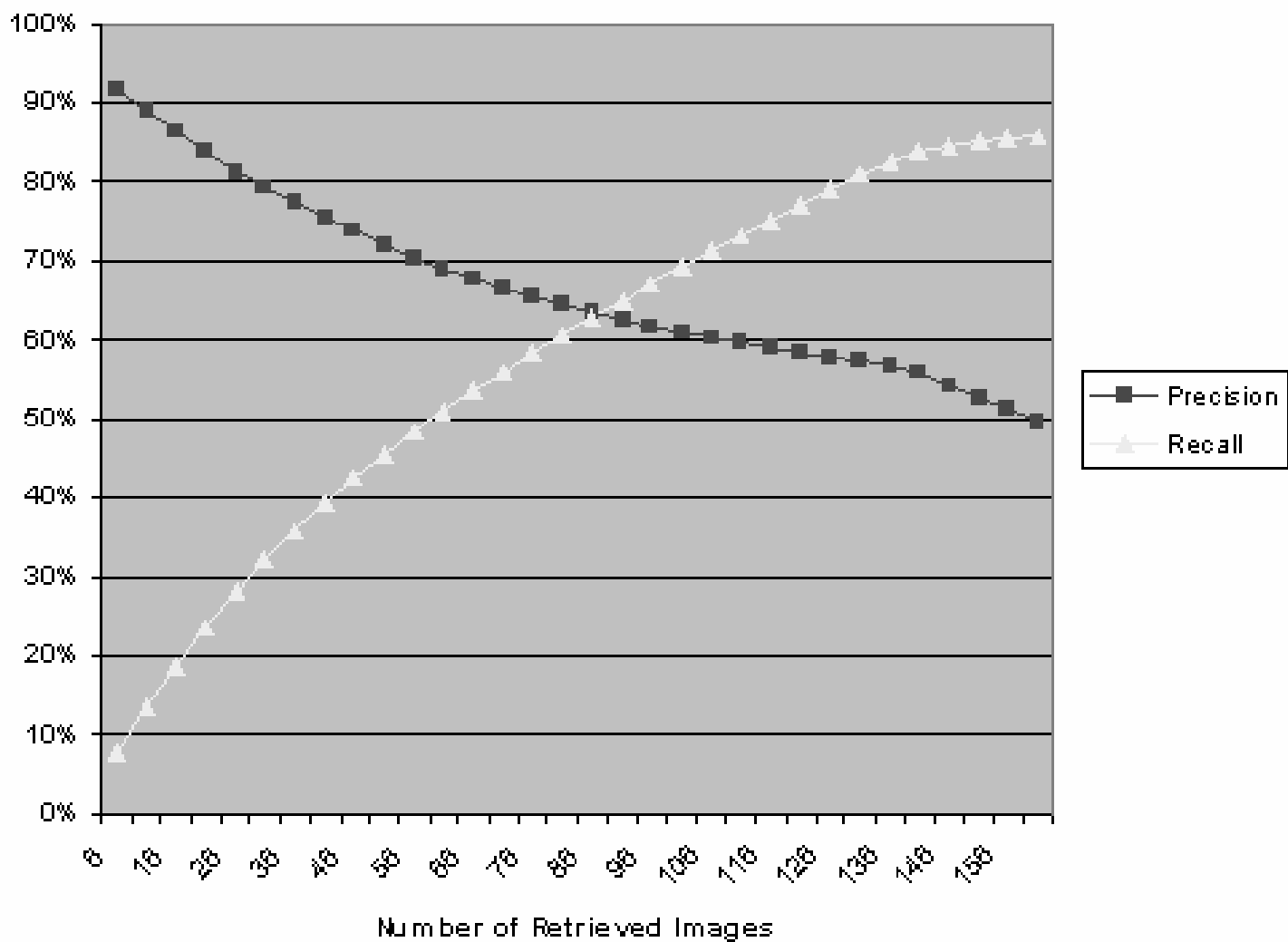
- Hausdorff Distance

Performance Evaluation

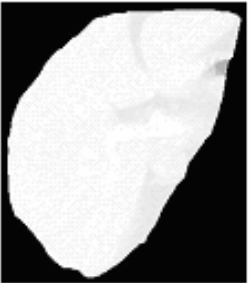
GLOBAL LEVEL		Backbone	Heart	Kidney	Liver	Spleen	OVERALL
VECTOR BASED PRECISION	Euclidean Distance	100%	90.38%	93.83%	67.82%	62.08%	87.74%
	Chi Square Statistics	100%	90.71%	93.83%	62.93%	57.50%	86.43%
	Minkowski 1 Distance	100%	90.06%	92.90%	68.97%	62.50%	87.79%

PIXEL LEVEL		Backbone	Heart	Kidney	Liver	Spleen	OVERALL
VECTOR-BASED PRECISION	Euclidean Distance	100%	75.96%	85.80%	59.77%	46.67%	81.16%
	Chi Square Statistics	100%	81.09%	87.65%	60.06%	47.50%	82.37%
	Minkowski 1 Distance	100%	74.36%	85.19%	59.48%	48.75%	81.01%
	Weighted-Mean-Variance	100%	87.18%	91.67%	58.91%	53.75%	84.45%
BINNED HISTOGRAM PRECISION	Cramer/von Mises	100%	88.78%	83.64%	64.08%	51.25%	84.01%
	Jeffrey-Divergence	100%	91.67%	95.99%	77.87%	75.83%	91.57%
	Kolmogorov-Smirnov Distance	100%	89.10%	89.81%	69.83%	60.00%	87.02%
SIGNATURE-BASED PRECISION	Hausdorff 10% v 20% cs	100%	81.09%	86.42%	57.76%	42.08%	81.16%

Jeffery Divergence

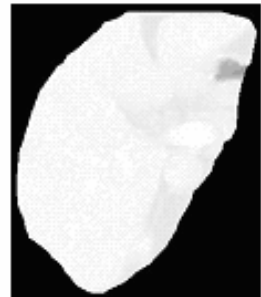


QUERY IMAGE



1_liv_60_3pix.dcm

JEFFREY-DIVERGENCE



1_liv_61_3pix.dcm
1st Match



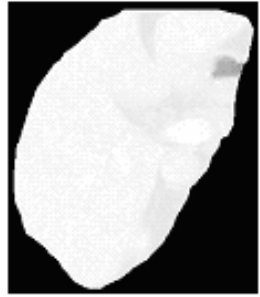
1_liv_55_3pix.dcm
2nd Match



1_liv_57_3pix.dcm
3rd Match



1_liv_59_3pix.cm
4th Match



1_liv_51_3pix.dcm
5th Match

Distance: 6463.600569 Distance: 7189.011701 Distance: 10529.67283 Distance: 14027.54196 Distance: 17401.42262

- All eight similarity measures at both levels gave an overall precision over 80% for the number (k) of most similar images retrieved equal to 6.
- At the global level, there was not much difference in the overall accuracy among the three similarity metrics, but the Minkowski and Euclidean distance performed better for liver and spleen than the Chi-square statistics metric.
- At the pixel level, the retrieval precision was in general higher for the binned-histogram data and reached a value of 91.57% for the Jeffrey-divergence making this metric to outperform all the other similarity metrics.

- Comparing the metrics with respect to the granularity of the feature data, the local features overall perform better by about 4%.
- Even though there is not a high difference in the overall performance of the two levels of descriptors, the performance is 10% to 20% better for liver and spleen when using pixel-level descriptors.
- Furthermore, comparing the best similarity metrics per organ at the pixel level, we notice that Jeffrey divergence performs the best with respect to each individual organ: backbone (100%), heart (89.7%), kidneys (96%), liver (77.87%) and spleen (75.83%).

- We would like to experiment our system with patches of ‘pure’ tissues delineated by radiologists; the current implementation used the segmented images produced by the snake algorithm.
- We plan to investigate the effect of the window size for calculating the pixel level texture and explore other similarity measures.
- As a long term goal, we will be exploring the integration of the CBIR system in the standard DICOM Query/Retrieve mechanisms in order to allow texture-based retrieval for the daily medical work flow.

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GLOBAL

Vector-Based

- Euclidean Distance

$$d_A(H, K) = \sqrt{(h - k)^T A (h - k)}$$

where $A = [a_{ij}]$

- C^2 Statistics

$$d_{c^2}(H, K) = \sum_i \frac{(h_i - m_i)^2}{m_i}$$

where $m_i = \frac{h_i + k_i}{2}$

- Minkowski-1 Distance

$$d_{L_r}(H, K) = \left(\sum_i |h_i - k_i|^r \right)^{\frac{1}{r}}$$

PIXEL-LEVEL

Vector-Based

- Euclidean Distance

$$d_A(H, K) = \sqrt{(h - k)^T A (h - k)}$$

where $A = [a_{ij}]$

- C^2 Statistics

$$d_{c^2}(H, K) = \sum_i \frac{(h_i - m_i)^2}{m_i}$$

where $m_i = \frac{h_i + k_i}{2}$

- Minkowski-1 Distance

$$d_{L_r}(H, K) = \left(\sum_i |h_i - k_i|^r \right)^{\frac{1}{r}}$$

- Weighted Mean Variance

$$d_{wmv}(H, K) = \sum_i \frac{|\mathbf{m}_i(H) - \mathbf{m}_i(K)|}{|\mathbf{s}(\mathbf{m}_i)|} + \frac{|\mathbf{s}_i(H) - \mathbf{s}_i(K)|}{|\mathbf{s}(\mathbf{s}_i)|}$$

PIXEL-LEVEL

Binned-Histogram

- Cramer/von Mises

$$d_{cvm}(H, K) = \sum_i \sum_j (F^i(j; H) - F^i(j; K))^2$$

- Jeffrey-Divergence

$$d_{JD}(H, K) = \sum_i \sum_j \left(f(j; H) \log \frac{f(j; H)}{m_j} + f(j; K) \log \frac{f(j; K)}{m_j} \right)$$

$$\text{where } m_j = \frac{f(j; H) + f(j; K)}{2}$$

- Kolomogorov-Smirnov

$$d_{KS}(H, K) = \sum_i \max_j \left(\left| F^i(j; H) - F^i(j; K) \right| \right)$$

PIXEL-LEVEL

Signature-Based

- Hausdorff Distance

$$d_{HD}(H, K) = \max_{h \in H} (\min_{k \in K} (\|h - k\|))$$

Haralick Texture Features

Feature	Formula	What is measured?
Entropy	$-\sum_i^M \sum_j^N P[i, j] \log P[i, j]$	Measures the randomness of a gray-level distribution. The Entropy is expected to be high if the gray levels are distributed randomly throughout the image.
Energy (Angular Second Moment)	$\sum_i^M \sum_j^N P^2[i, j]$	Measures the number of repeated pairs. The Energy is expected to be high if the occurrence of repeated pixel pairs is high.
Contrast	$\sum_i^M \sum_j^N (i - j)^2 P[i, j]$	Measures the local contrast of an image. The Contrast is expected to be low if the gray levels of each pixel pair are similar.
Homogeneity	$\sum_i^M \sum_j^N \frac{P[i, j]}{1 + i - j }$	Measures the local homogeneity of a pixel pair. The Homogeneity is expected to be large if the gray levels of each pixel pair are similar.
SumMean (Mean)	$\frac{1}{2} \sum_i^M \sum_j^N (iP[i, j] + jP[i, j])$	Provides the mean of the gray levels in the image. The SumMean is expected to be large if the sum of the gray levels of the image is high.
Variance	$\frac{1}{2} \sum_i^M \sum_j^N ((i - m)^2 P[i, j] + (j - m)^2 P[i, j])$	Variance tells us how spread out the distribution of gray-levels is. The Variance is expected to be large if the gray levels of the image are spread out greatly.
Correlation	$\sum_i^M \sum_j^N \frac{(i - m)(j - m)P[i, j]}{s^2}$	Provides a correlation between the two pixels in the pixel pair. The Correlation is expected to be high if the gray-levels of the pixel pairs are highly correlated.
Maximum Probability (MP)	$\text{Max}_{i, j}^{M, N} P[i, j]$	Results in the pixel pair that is most predominant in the image. The MP is expected to be high if the occurrence of the most predominant pixel pair is high.
Inverse Difference Moment (IDM)	$\sum_i^M \sum_j^N \frac{P[i, j]}{ i - j ^k} \quad i \neq j$	Inverse Difference Moment tells us about the smoothness of the image, like homogeneity. The IDM is expected to be high if the gray levels of the pixel pairs are similar.
Cluster Tendency	$\sum_i^M \sum_j^N (i + j - 2m)^k P[i, j]$	Measures the grouping of pixels that have similar gray-level values.