

# Classification of Tissues in Computed Tomography using Decision Trees

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## Motivation

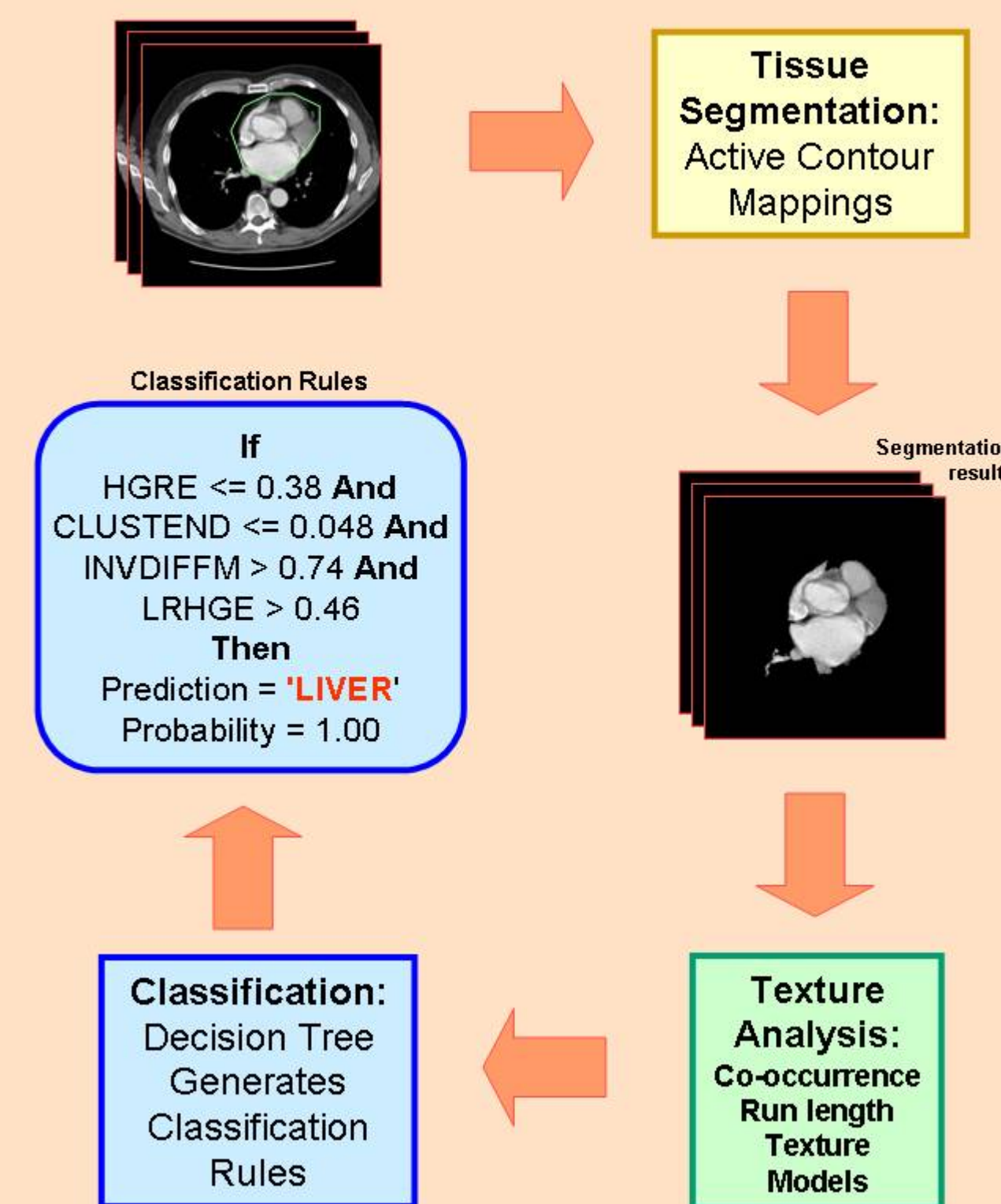
This project will demonstrate how co-occurrence and run-length texture information from computed tomography (CT) images can be used to automatically classify and annotate normal tissues from regions of interest of heart and great vessels, and liver, renal and splenic parenchyma.

Automatic classification and annotation of these images will save radiologists time and assist them in processing large volumes of patient data.

## System Outline

- **System Diagram**
- **Segmentation**
- **Texture Models**
  - Co-occurrence matrix
  - Run-length encoding matrix
- **Classification**
  - CART Decision Tree Specifications
  - Important Features
  - Decision Rules
  - Model Accuracy for Training and Testing Data

## System Diagram



## Segmentation

**Data:** 344 DICOM images

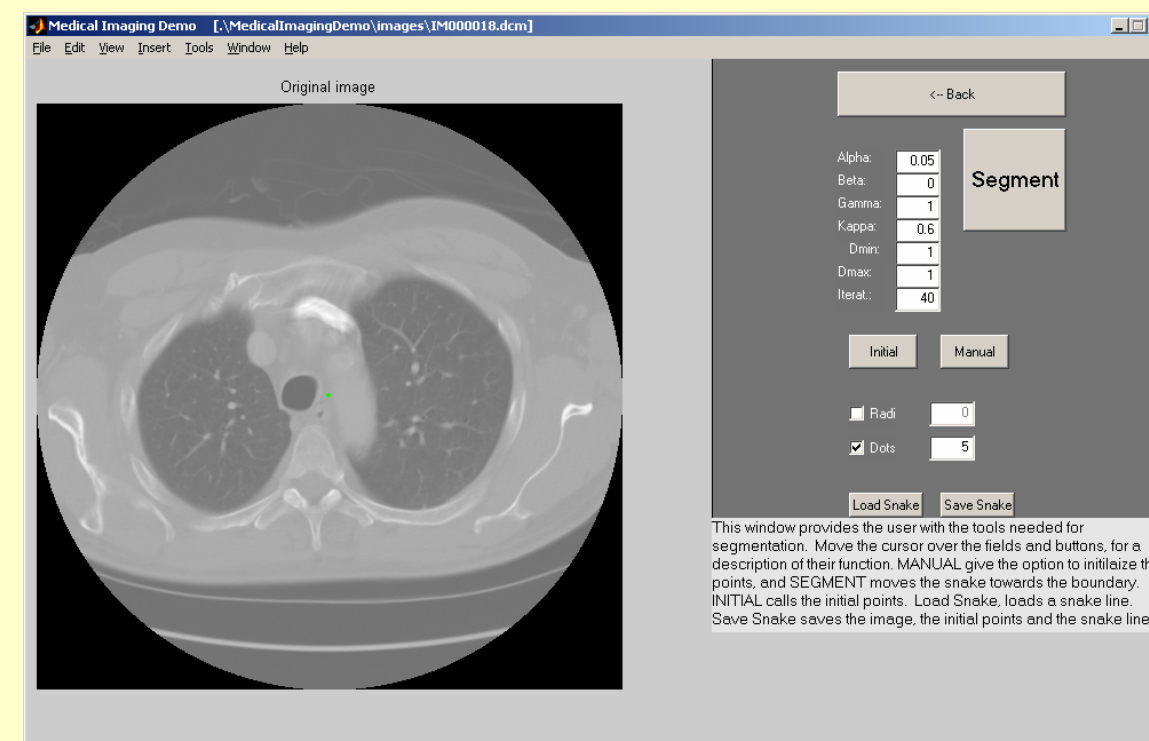
### Segmented organs:

liver, renal and splenic parenchyma, backbone, & heart and great vessels

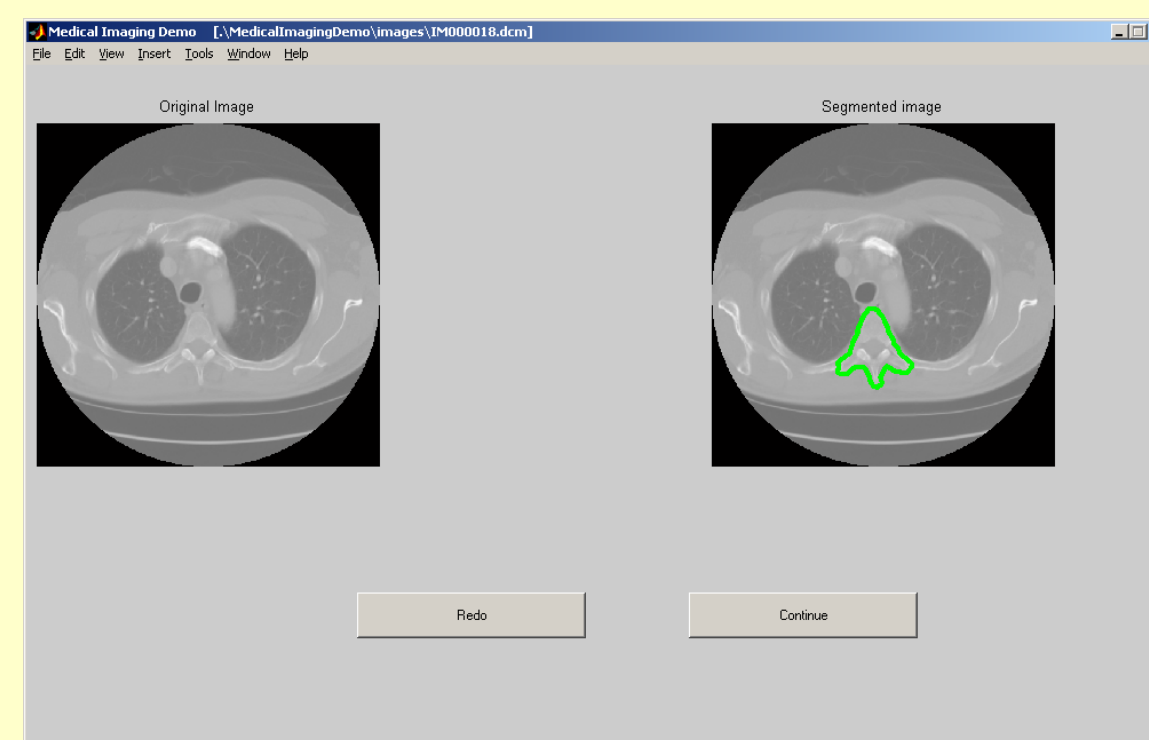
### Segmentation algorithm:

*Active Contour Mappings (Snakes)*

- A boundary-based segmentation algorithm
- Input: a number of initial points & five main parameters that influence the way the boundary is formed.



- The values of the five parameters simulate the action of two forces:
  - Internal: designed to keep the snake smooth during deformation.
  - External: designed to move the snake towards the boundary.
- Output: the curve evolves to match the nearest internal boundary, typically based on gradient intensity measures.



## Texture Models

### What is Texture?

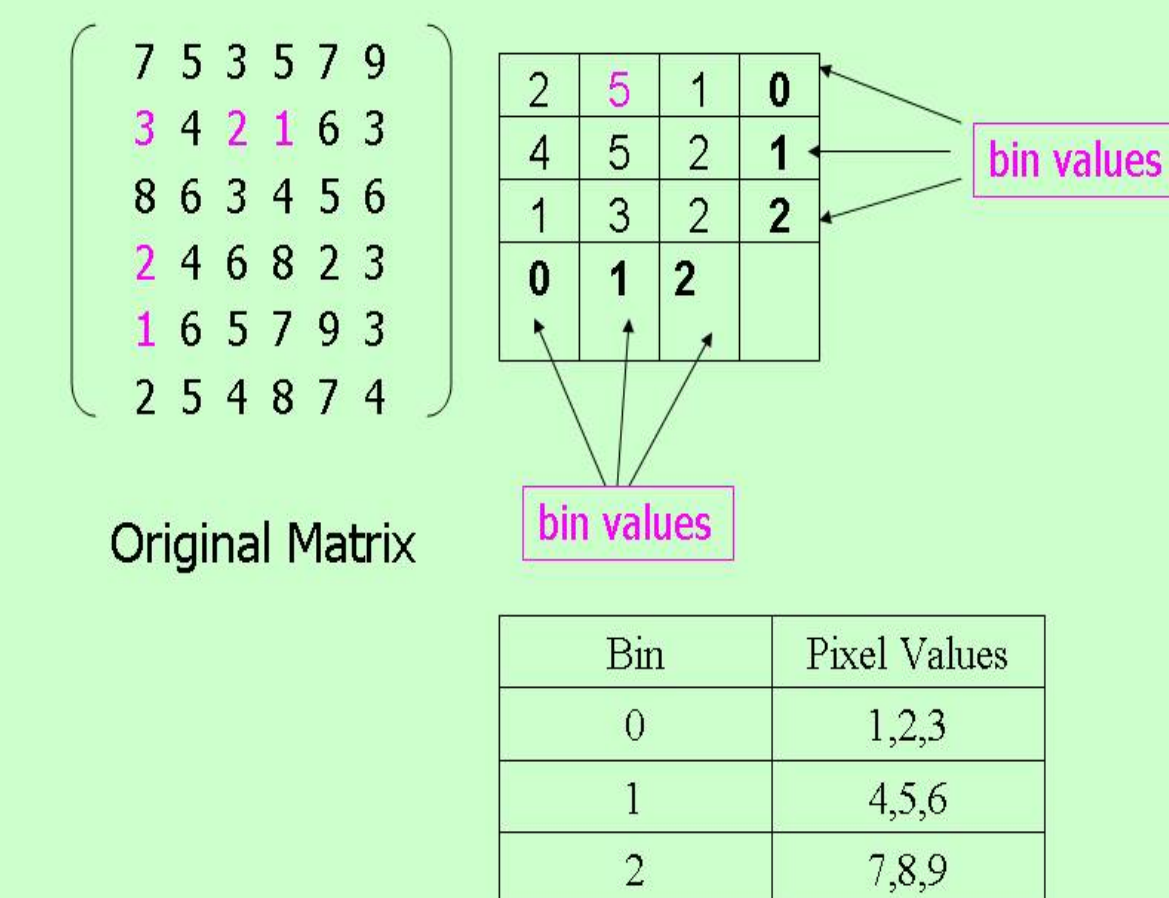
- a measure of the variation of the intensity of a surface, quantifying properties such as smoothness, coarseness, and regularity
- a connected set of pixels satisfying a given gray level property which occurs repeatedly in an image

### Texture Models:

- Co-occurrence Matrices
- Run-Length Matrices

### Definition of Co-occurrence Matrix:

- Co-occurrence captures the spatial dependence of gray-level values within an image.
- A 2D co-occurrence matrix, P, is an n x n matrix, where n is the number of gray-levels within an image.
- The matrix acts as an accumulator so that P[i,j] counts the number of pixel pairs having the intensities i and j.



Bin	Pixel Values
0	1,2,3
1	4,5,6
2	7,8,9

In order to quantify this spatial dependence of gray-level values, we calculate various **Co-occurrence Matrix features**:

Entropy	Energy (Angular Second Moment)
Correlation	SumMean (Mean)
Contrast	Maximum Probability
Homogeneity	Inverse Difference Moment
Variance	Cluster Tendency

**Run-Length descriptors** capture the coarseness of the texture in a specific direction.

The run-length matrix p(i,j) is defined by specifying the direction and then counting the occurrence of runs for each gray level and length in this direction.

- (i) Dimension corresponds to the gray level (bin values) and has a length equal to the maximum gray level (bin values) n.
- (j) Dimension corresponds to the run length and has length equal to the maximum run length (bin values).

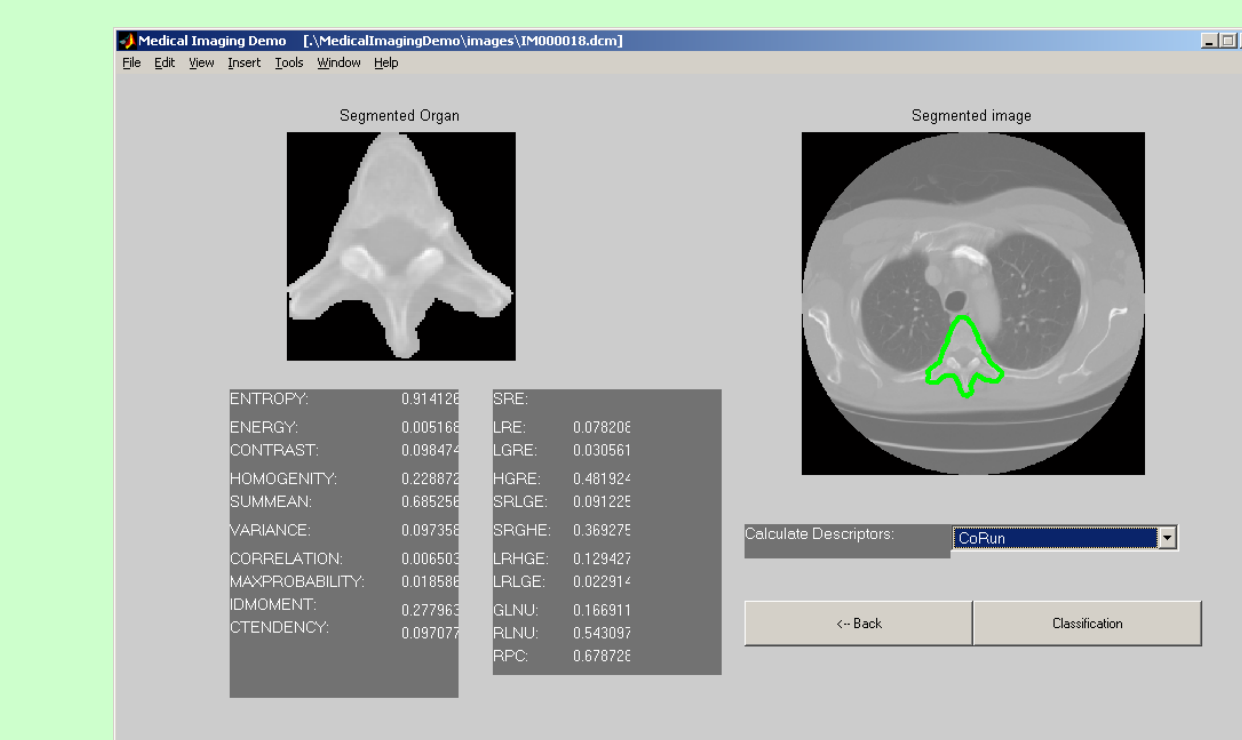
i \ j	1	2	3	4	5	6
1	1	8	0	0	0	0
2	2	4	1	0	0	0
3	4	1	0	0	0	0

Eleven **Run-Length texture descriptors** are calculated to capture the texture properties and differentiate among different textures.

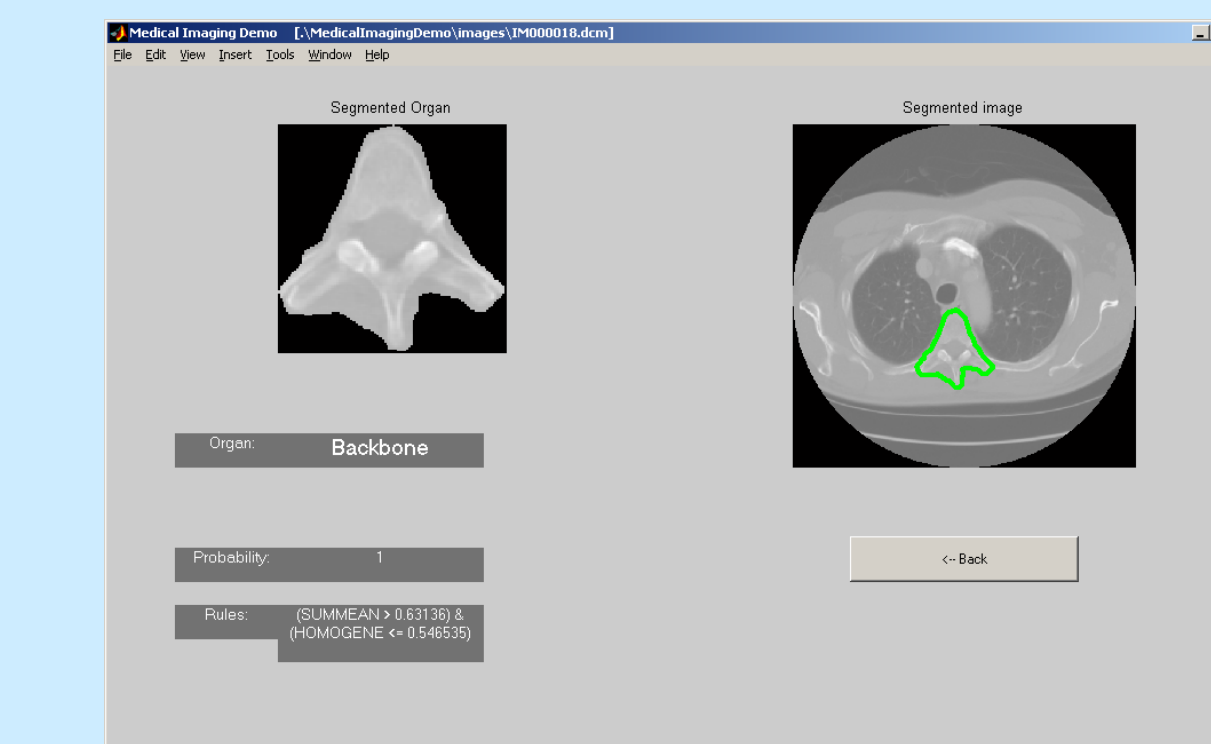
Short Run Emphasis (SRE)	Long Run Emphasis (LRE)
High Gray-level Run Emphasis (HGRE)	Low Gray-level Run Emphasis (LGRE)
Short Run Low Gray-level Emphasis (SRLGE)	Short Run High Gray-level Emphasis (SRHGE)
Long Run Low Gray-level Emphasis (LRLGE)	Long Run High Gray-level Emphasis (LRHGE)
Gray-level Non-uniformity (GLNU)	Run Length Non-uniformity (RLNU)
Run Percentage (RPC)	

### Texture feature extraction:

For each segmented organ image we calculate 21 features derived from the co-occurrence and run-length matrices to capture the texture properties and differentiate among different textures.



<b>Algorithm:</b>	CART Decision Tree
<b>Output:</b>	Decision Rules
<b>Advantages:</b>	Automatic & efficient processing for: <ul style="list-style-type: none"> <li>- Classification</li> <li>- Annotation</li> </ul> Good to excellent predictive accuracy



## Specifications

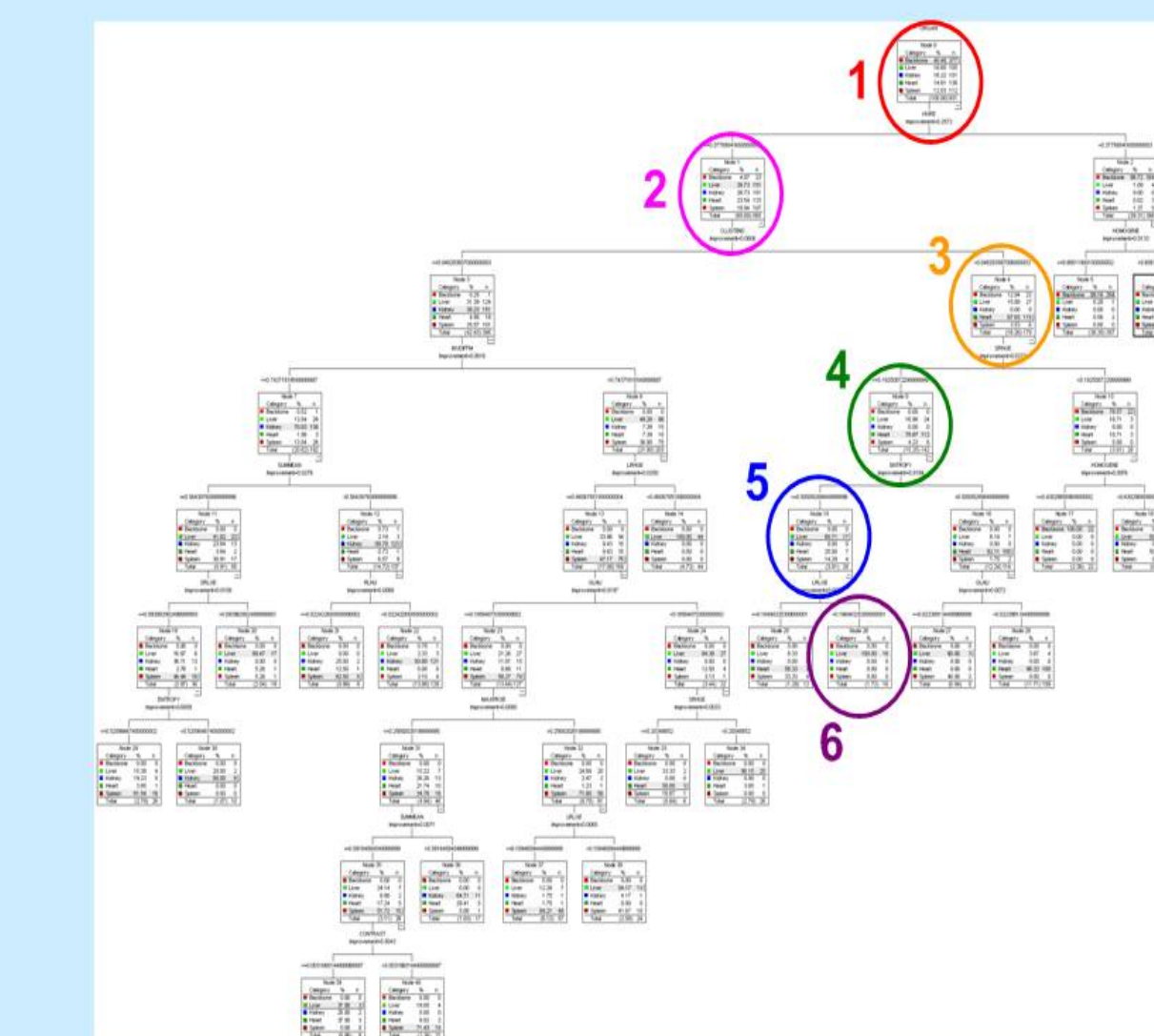
Dataset: divided into 66% training, 34% testing  
 CART algorithm  
 Cross-validation folds = 10  
 Maximum Tree Depth = 20  
 Parent Node (Minimum Number of Cases) = 28  
 Child Node (Minimum Number of Cases) = 5  
 Minimum Change in Impurity = 0.0001  
 Impurity Measure = Gini  
 Minimum Risk Pruning

## Resulting Tree

Total number of nodes 41  
 Total number of levels 8  
 Total number of terminal nodes 21

## Resulting Rules

Total number of rules 21



## Classification

### Examples of Decision Tree Rules:

- **IF** (HGRE <= 0.38) & (CLUSTEND <= 0.05) & (INVDIFFM <= 0.74) & (SUMMEAN > 0.56) & (RLNU > 0.02)  
**THEN** Prediction = 'Kidney', Probability = 0.94
- **IF** (HGRE <= 0.38) & (CLUSTEND > 0.05) & (SRHGE <= 0.19) & (ENTROPY <= 0.51) & (LRLGE > 0.16)  
**THEN** Prediction = 'Liver', Probability = 1.00
- **IF** (HGRE <= 0.38) & (CLUSTEND > 0.05) & (SRHGE <= 0.19) & (ENTROPY > 0.51) & (GLNU > 0.02)  
**THEN** Prediction = 'Heart', Probability = 0.96

## Most important features

The most important determining features for classification are located in the nodes at the top of the tree.

- HGRE (High Gray-level Run Emphasis)
- CLUSTEND (Cluster Tendency)
- HOMOGENE (Homogeneity)
- INVDIFFM (Inverse Difference Moment)
- SRHGE (Short Run High Gray-level Emphasis)

## Accuracy measures

$$\text{sensitivity} = \frac{\text{true positives}}{\text{total positives}}$$

$$\text{specificity} = \frac{\text{true negatives}}{\text{total negatives}}$$

$$\text{precision} = \frac{\text{true positives}}{\text{true positives} + \text{false positives}}$$

$$\text{accuracy} = \frac{\text{true positives} + \text{true negatives}}{\text{total samples}}$$

Example: A *true\_positive* occurs when the classification system correctly classifies a heart image as a heart image.

Example: A *true\_negative* occurs when the system recognizes that a liver image is not a heart image.

Example: A *false\_positive* occurs when the system classifies a non-heart image as a heart image.

## Summary

The results show that using only 21 texture descriptors calculated from Hounsfield unit data, it is possible to automatically classify regions of interest representing different organs or tissues in CT images.

Furthermore, the results lead us to the conclusion that the incorporation of some other texture models into our proposed approach will increase the performance of the classifier, and will also extend the classification functionality to other organs.

## References

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