

# Binary Image Analysis: Part 1

Readings: Chapter 3: 3.1, 3.4, 3.8

- thresholding grayscale images
- connected components labeling

# Binary Image Analysis

## Binary image analysis

- consists of a set of image analysis operations that are used to produce or process binary images, usually images of 0's and 1's.

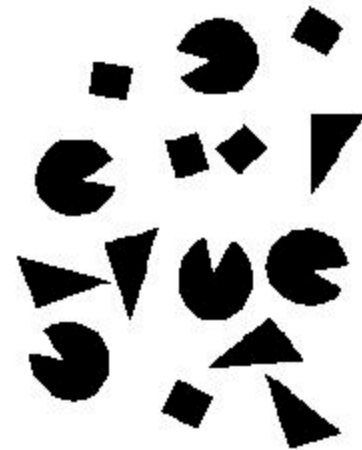
0 represents the background

1 represents the foreground

000	1	00	1	000	1	000	
000	1	1	1	1	000	1	000
000	1	00	1	000	1	000	

# Binary Image Analysis

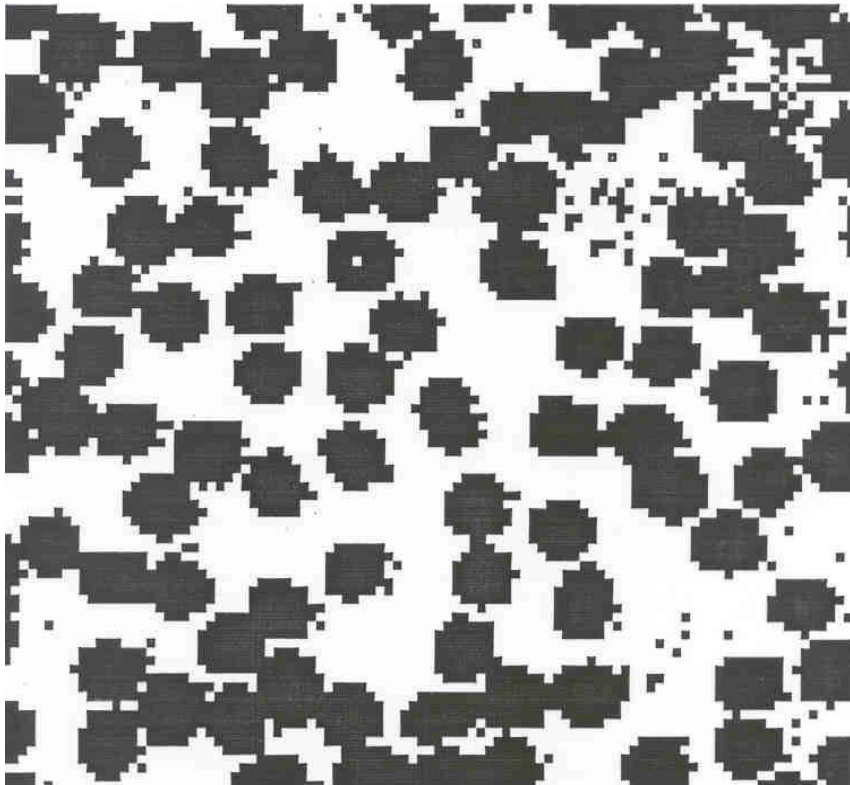
- is used in a number of practical applications, e.g.
  - part inspection
  - riveting
  - fish counting
  - document processing



# What kinds of operations?

- Separate objects from background and from one another
- Aggregate pixels for each object
- Compute features for each object

# Example: red blood cell image



- Many blood cells are separate objects
- Many touch – bad!
- Salt and pepper noise from thresholding
- How useable is this data?

# Results of analysis

- 63 separate objects detected
- Single cells have area about 50
- Noise spots
- Gobs of cells

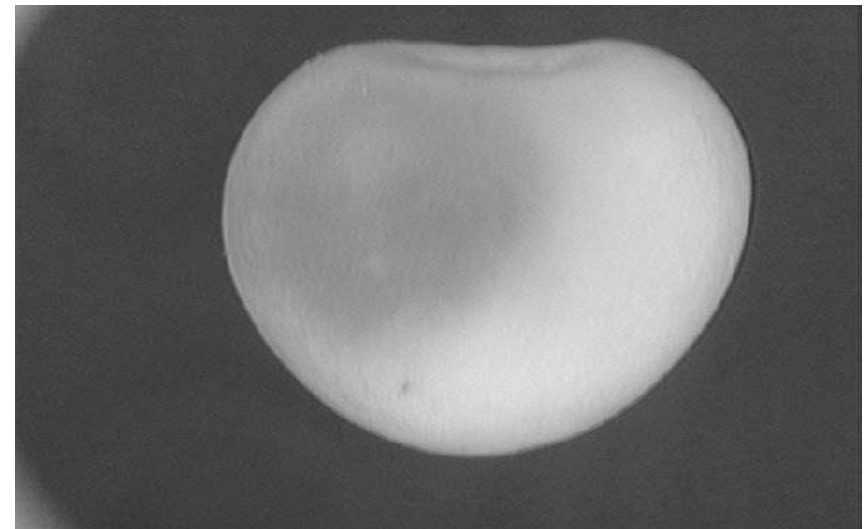
Object	Area	Centroid	Bounding Box	
1	383	( 8.8 , 20)	[1 22 1 39]	
2	83	( 5.8 , 50)	[1 11 42 55]	
3	11	( 1.5 , 57)	[1 2 55 60]	
4	1	( 1 , 62)	[1 1 62 62]	
5	1048	( 19 , 75)	[1 40 35 100]	gobs
32	45	( 43 , 32)	[40 46 28 35]	cell
33	11	( 44 , 1e+02)	[41 47 98 100]	
34	52	( 45 , 87)	[42 48 83 91]	cell
35	54	( 48 , 53)	[44 52 49 57]	cell
60	44	( 88 , 78)	[85 90 74 82]	
61	1	( 85 , 94)	[85 85 94 94]	
62	8	( 90 , 2.5)	[89 90 1 4]	
63	1	( 90 , 6)	[90 90 6 6]	

# Useful Operations

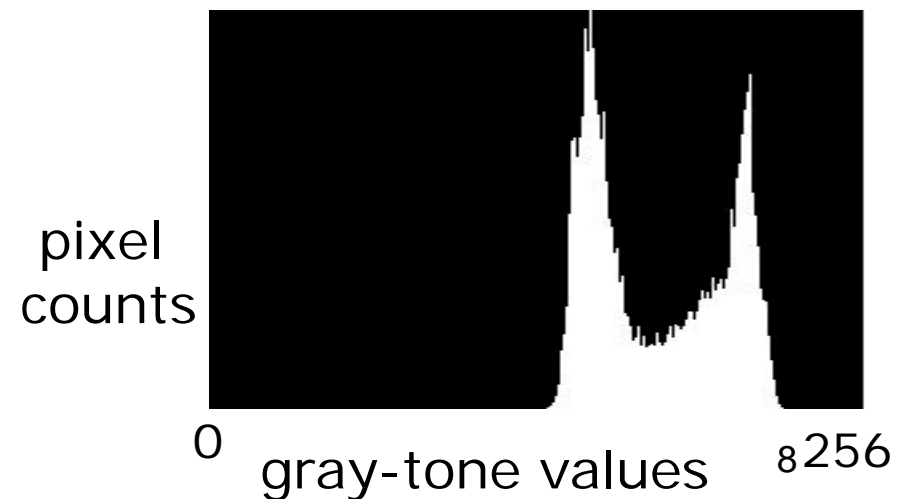
1. Thresholding a gray-tone image
2. Determining good thresholds
3. Connected components analysis
4. Binary mathematical morphology
5. All sorts of feature extractors  
(area, centroid, circularity, ...)

# Thresholding

- Background is black
- Healthy cherry is bright
- Bruise is medium dark
- Histogram shows two cherry regions (black background has been removed)



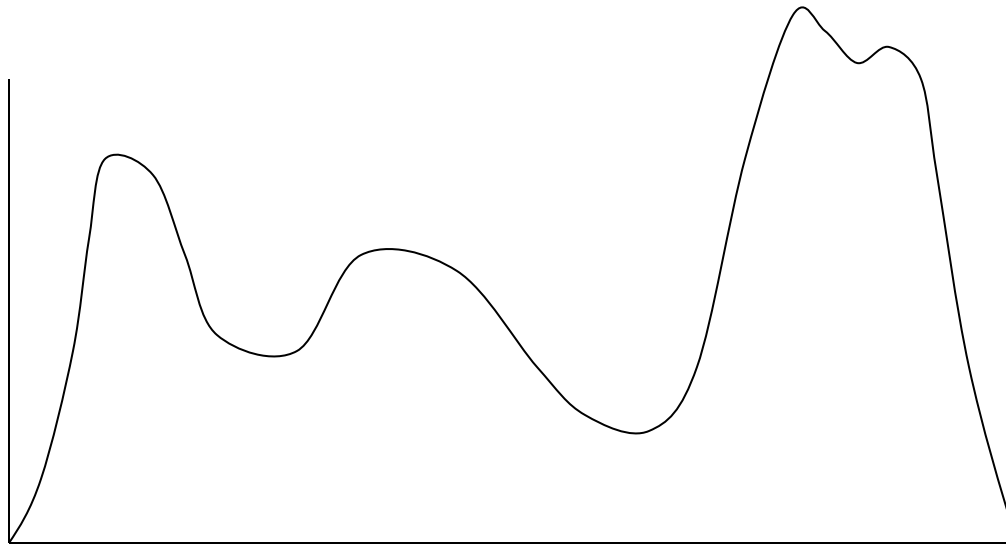
This is abstract.  
How are histograms represented  
as data structures?





# Histogram-Directed Thresholding

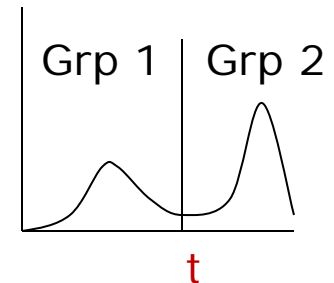
**How can we use a histogram to separate an image into 2 (or several) different regions?**



**Is there a single clear threshold? 2? 3?**

# Automatic Thresholding: Otsu's Method

Assumption: the histogram is bimodal



Method: find the threshold  $t$  that minimizes the **weighted sum of within-group variances** for the two groups that result from separating the gray tones at value  $t$ .

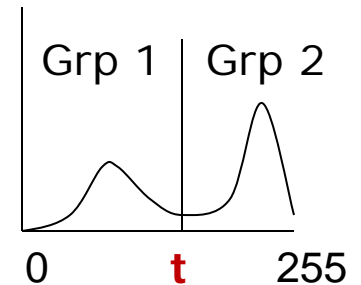
What is variance?

# Computing Within-Group Variance

- For each possible threshold  $t$
- For each group  $i$  (1 and 2)
  - compute the **variance** of its gray tones  $\sigma_i^2(t)$
  - compute its **weight**  $q_i(t) = \sum_{\tau \text{ in Grp } i} P(\tau)$

where  $P(\tau)$  is the normalized histogram value for gray tone  $\tau$ , normalized by sum of all gray tones in the image and called the **probability of  $\tau$** .

- Within-group variance =  $q_1(t) \sigma_1^2(t) + q_2(t) \sigma_2^2(t)$



See text (Section 3.8) for the efficient recurrence relations; in practice, this operator works very well for true bimodal distributions and not too badly for others, but not the CTs.

# Thresholding Example



original gray tone image



binary thresholded image

# Connected Components Labeling

Once you have a binary image, you can identify and then analyze each **connected set of pixels**.

The connected components operation takes in a binary image and produces a **labeled image** in which each pixel has the integer label of either the background (0) or a component.



binary image (after morphology)



connected components  
(shown in pseudo-color)

# Methods for CC Analysis

1. Recursive Tracking (almost never used)
2. Parallel Growing (needs parallel hardware)
3. Row-by-Row (most common)
  - Classical Algorithm (see text)
  - Efficient Run-Length Algorithm (developed for speed in real industrial applications)

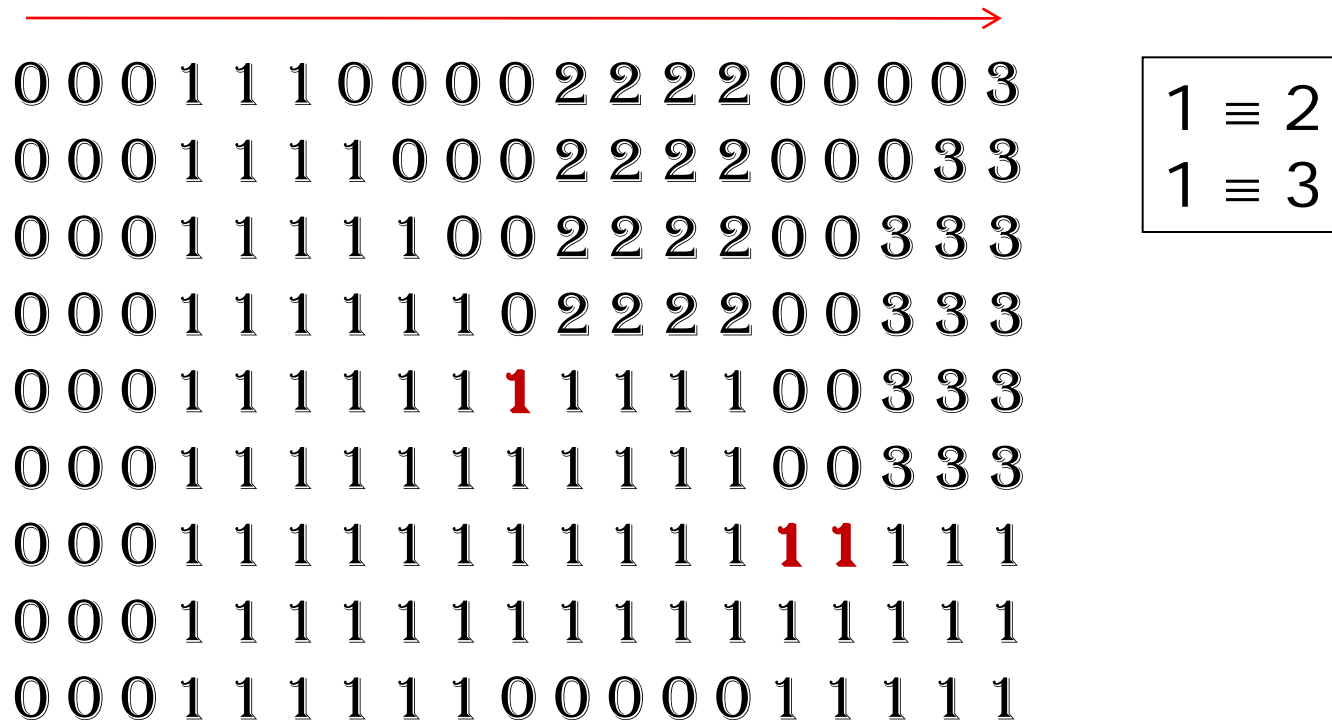
# Equivalent Labels

Original Binary Image

0	0	0	1	1	1	0	0	0	0	1	1	1	1	0	0	0	0	1
0	0	0	1	1	1	1	0	0	0	1	1	1	1	0	0	0	1	1
0	0	0	1	1	1	1	1	0	0	1	1	1	1	0	0	1	1	1
0	0	0	1	1	1	1	1	1	0	1	1	1	1	0	0	1	1	1
0	0	0	1	1	1	1	1	1	<b>1</b>	1	1	1	1	0	0	1	1	1
0	0	0	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1	1
0	0	0	1	1	1	1	1	1	1	1	1	1	1	<b>1</b>	<b>1</b>	1	1	1
0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
0	0	0	1	1	1	1	1	1	0	0	0	0	0	1	1	1	1	1

# Equivalent Labels

The Labeling Process:  
Left to Right, Top to Bottom

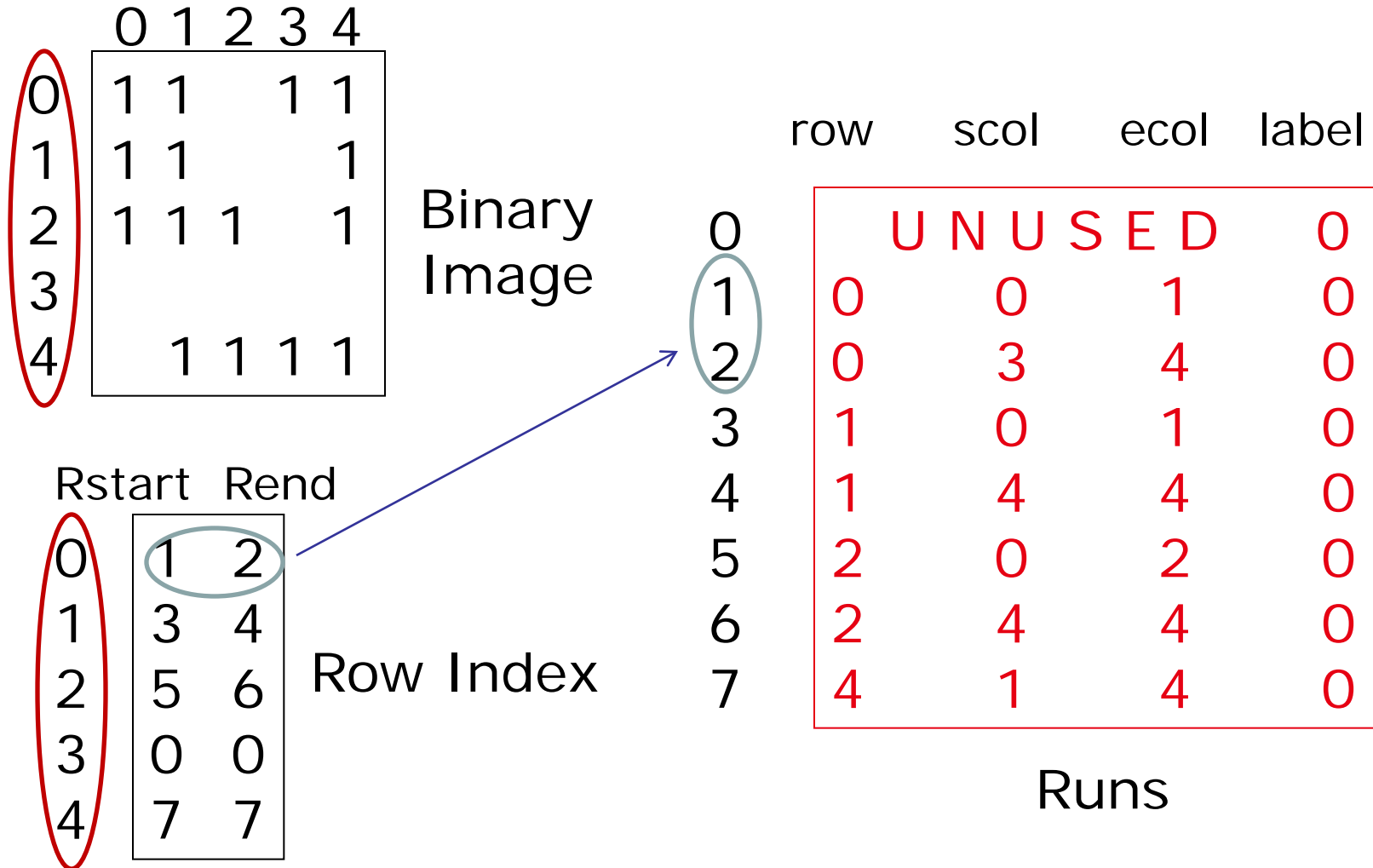


What CSE algorithm does this kind of thing on a different structure?



# Run-Length Data Structure

used for speed of processing and to gain from hardware



# Run-Length Algorithm

```
Procedure run_length_classical
```

```
{
```

```
  initialize Run-Length and Union-Find data structures
```

```
  count <- 0
```

```
/* Pass 1 (by rows) */
```

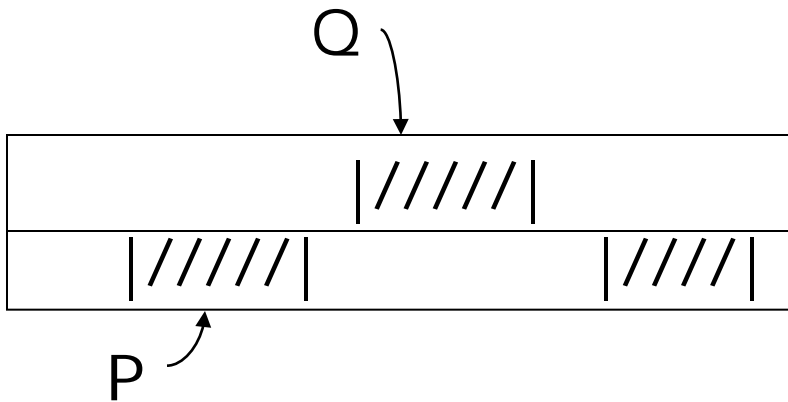
```
  for each current row and its previous row
```

```
  {
```

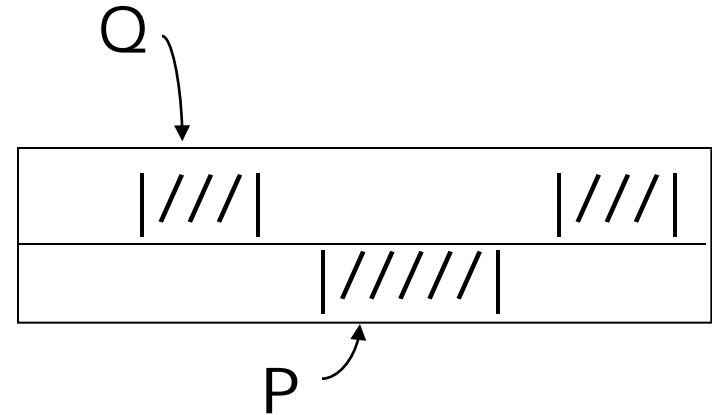
```
    move pointer P along the runs of current row
```

```
    move pointer Q along the runs of previous row
```

# Case 1: No Overlap



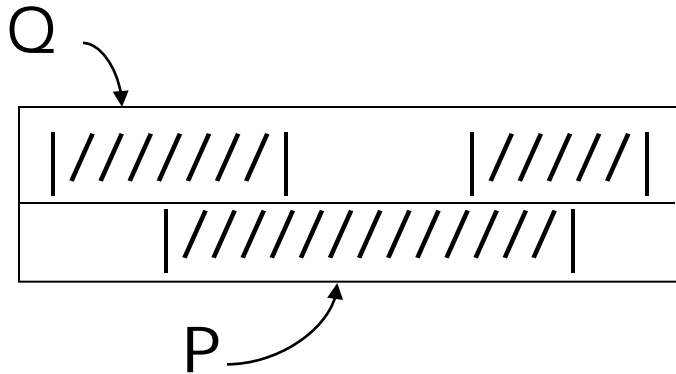
```
/* new label */  
count <- count + 1  
label(P) <- count  
P <- P + 1
```



```
/* check Q's next run */  
Q <- Q + 1
```

# Case 2: Overlap

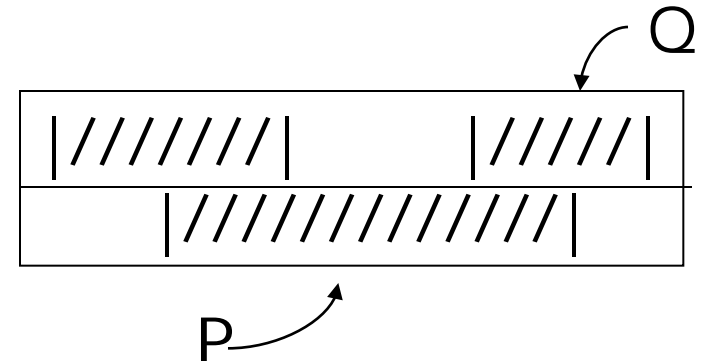
Subcase 1:  
P's run has no label yet



label(P) <- label(Q)  
move pointer(s)

}

Subcase 2:  
P's run has a label that is  
different from Q's run



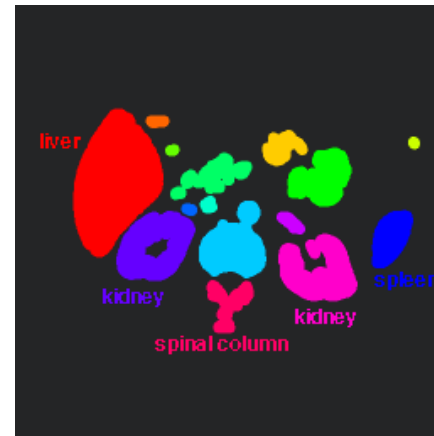
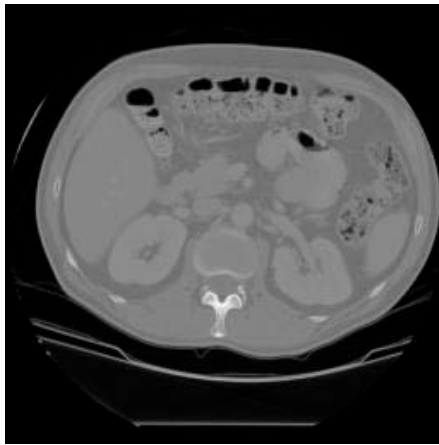
union(label(P),label(Q))  
move pointer(s)

# Pass 2 (by runs)

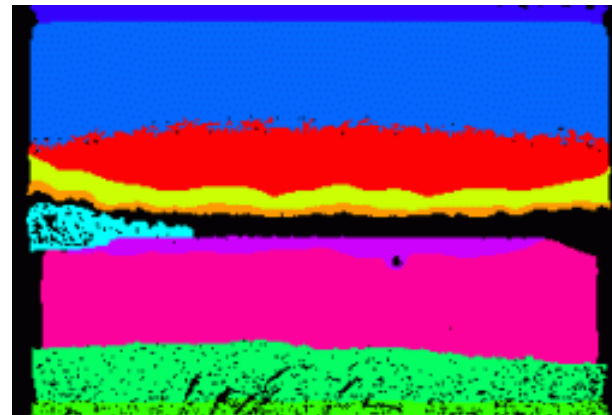
```
/* Relabel each run with the name of the
   equivalence class of its label */
For each run M
{
  label(M) <- find(label(M))
}
}
```

where union and find refer to the operations of the Union-Find data structure, which keeps track of sets of equivalent labels.

# Labeling shown as Pseudo-Color



connected components of 1's from thresholded image



connected components of cluster labels