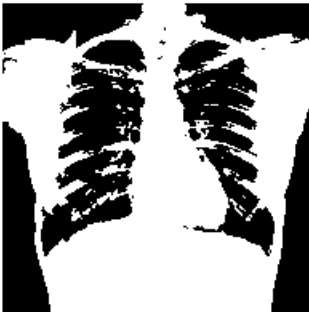


```
% Cargar imagen y darle tamaño adecuado
f = imread('radiograph1.jpg');
f = double(f(:,:,1));
f = f/max(max(f));
f = imresize(f,0.15);
figure
imshow(f,[]);
```

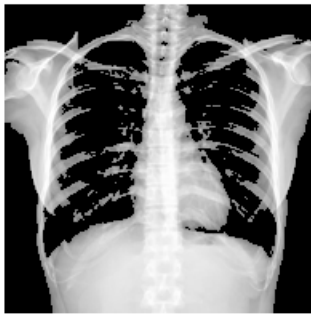


## Thresholding

```
%Creacion de segmentos para tipos de tejido
seg1 = f > 0.5;
imshow(seg1,[]);
```



```
imshow(seg1.*f,[]);
```



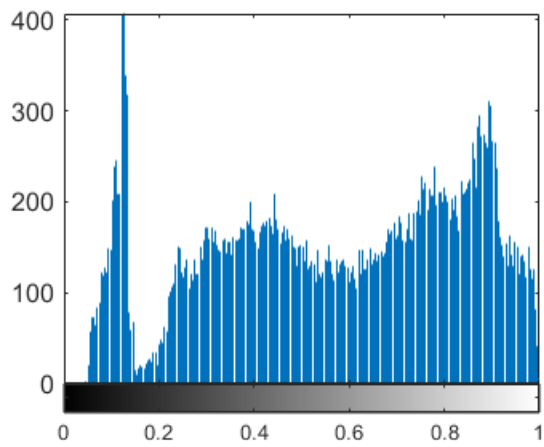
```
seg1 = f < 0.75;  
imshow(seg1,[]);
```



```
imshow(seg1.*f,[]);
```



```
imhist(f)
```



```
%Use a third threshold based on hist  
seg1 = f > 0.25;  
imshow(seg1,[]);
```

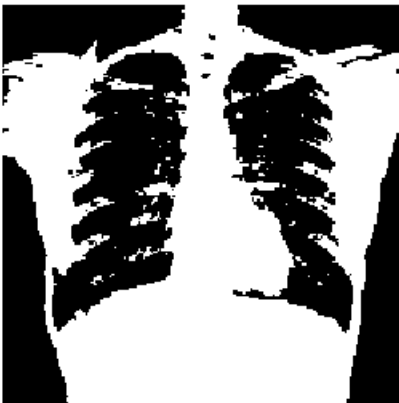


```
imshow(seg1.*f,[]);
```

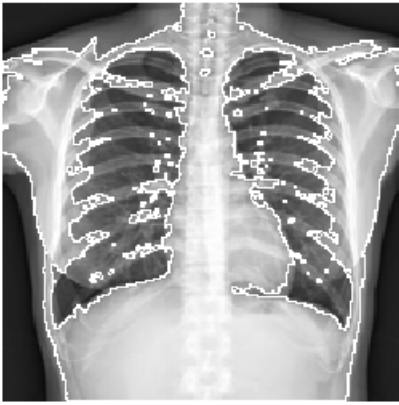


Otsu method

```
thr = graythresh(f);  
seg1 = f > thr;  
imshow(seg1,[]);
```



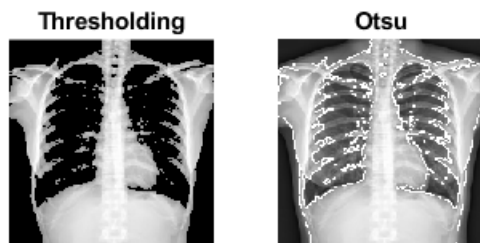
```
dyp = [0,1;-1,0];  
dyp = [1,0;;0,-1];  
edgemap = abs(conv2(seg1,dyp, 'same'))+abs(conv2(seg1,dyp, 'same'));  
imshow(f+edgemap,[0,1]);
```



%Compare otsu provided threshold vs the one you selected in the prev step

```
figure(1)
subplot(1,2,1)
imshow(seg1.*f,[]);
title('Thresholding')

subplot(1,2,2)
imshow(f+edgemap,[0,1]);
title('Otsu')
```



Do u trust the otsu method?

Los errores en este metodo son mas dificil de comprender y observar

No tiene sentido biologicamente

```
% Select your own imagen and compute this threshold
a = imread('PatioCentral.jpg');
a = double(a(:,:,1));
```

```

a = a/max(max(a));
a = imresize(a,0.15);
figure
imshow(a,[]);

```



```

thr = graythresh(a);
segA = a > thr;
imshow(segA,[]);

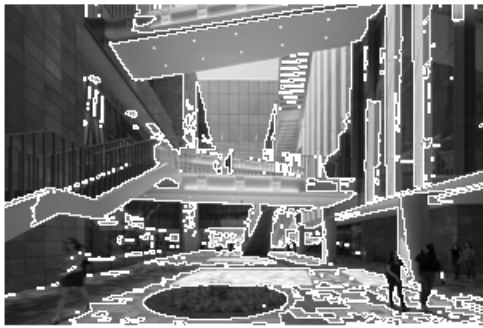
```



```

dyp = [0,1;-1,0];
dyp = [1,0;0,-1];
edgemap = abs(conv2(segA,dyp,'same'))+abs(conv2(segA,dyp,'same'));
imshow(a+edgemap,[0,1]);

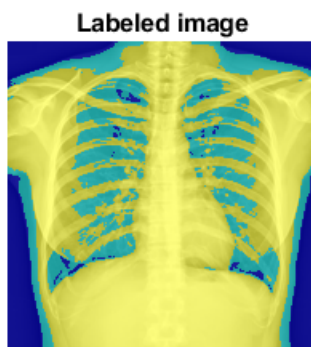
```



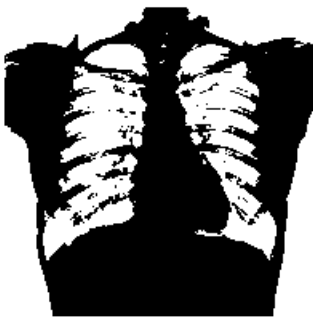
## Kmeans Seg

```
[L,centers] = imsegkmeans(int8(255*f),3);
B = labeloverlay(f,L);
[L1,centers1] = imsegkmeans(int8(255*f),5);
B1 = labeloverlay(f,L1);
```

```
figure
imshow(B)
title('Labeled image')
```



```
figure
imshow(int8(255*f) < centers(1),[])
```



```
imshow(int8(255*f) < centers(2),[])
```



```
imshow(int8(255*f) < centers(3),[])
```



```
edgemap = abs(conv2(L,dxp,'same'))+abs(conv2(L,dyp,'same'));  
imshow(f+edgemap,[0,1]);
```





```
% Do the same procedure but with five centers
```

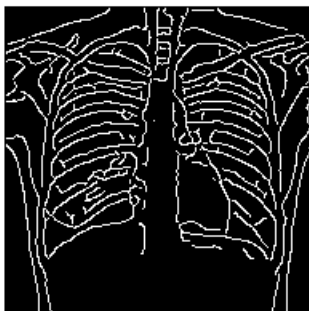
```
figure
subplot(1,2,1)
imshow(B)
title ('Tres centros')
subplot(1,2,2)
imshow(B1)
title ('Cinco centros')
```

```
% Is the segmetation better?
```

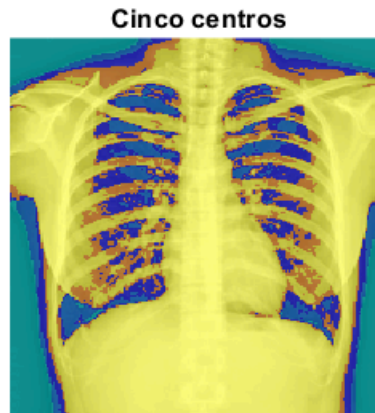
```
% Por parte del analisis biologico el proceso con cinco centros para ser
% mas preciso en la deteccion y display de los tipos de tejido, en este
% caso podemos ver con mayor facilidad el aire en los pulmones
```

## Watershed

```
edgeC = edge(f, 'Canny');
figure
imshow(edgeC, [])
```



```
D = bwdist(edgeC);  
imshow(D,[])
```

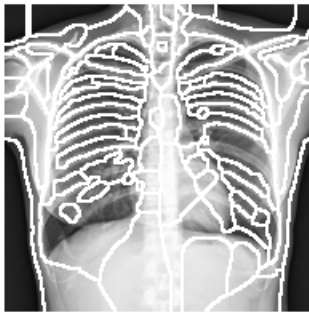


```
title('Distance Transform of Binary Image')
```

**Distance Transform of Binary Image**



```
L = watershed(D);  
edgemap = abs(conv2(L,dxp,'same'))+abs(conv2(L,dyp,'same'));  
imshow(f+edgemap,[0,1]);
```



```
L(edgeC) = 0;
```

Display the resulting label matrix as an RGB image

```
rgb = label2rgb(L, 'jet', [.5 .5 .5]);  
figure  
imshow(rgb)  
title('Watershed Transform')
```

