Exercises Chapter 14

Problem 14.1

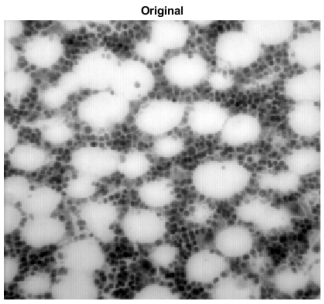
Load bonemarr.tif. Determine thresholds using graytresh and manually. Plot the original and both thresholds.

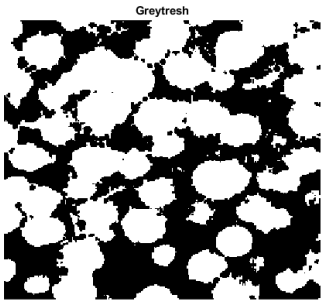
Solution

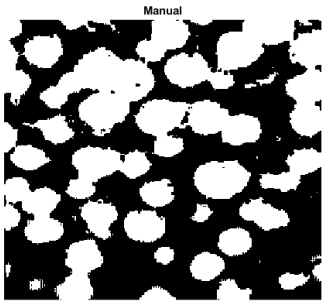
```
[I, map] = imread('C:\dev\biomedeng\Associated Files\Chapter 14\bonemarr.tif')

I_d = im2double(I)

t1 = graythresh(I_d)
bw1 = im2bw(I, t1)

I_t = I_d > 0.7

subplot(1, 3, 1)
imshow(I)
title('Original')

subplot(1, 3, 2)
imshow(bw1)
title('Greytresh')

subplot(1,3, 3)
imshow(I_t)
title('Manual')
```

Result

The graytresh method results in poor thresholding with noise, the function returned 0.6 for the bone marrow image. The manual thresholding at 0.7 creates an image with less noise, increasing it higher than 0.7 means fewer cells are detected.







Problem 14.2

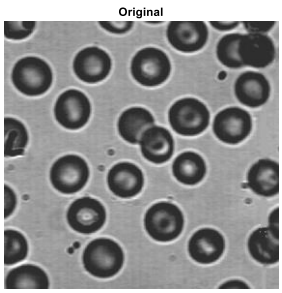
Load blood1.tif and filter it using a double lowpass filter with a 20x20 Gaussian kernel with cutoffs at 0.5 and 4. Threshold the filtered images using graytresh. Display all the images along with histograms to compare.

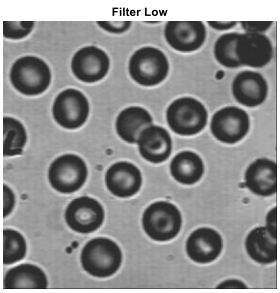
Solution

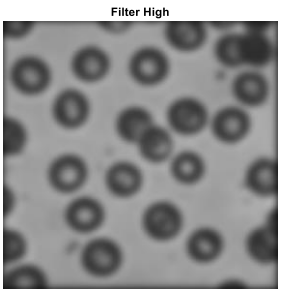
```
[I, map] = imread('C:\dev\biomedeng\Associated Files\Chapter 14\blood1.tif')
I = im2double(I)

b1 = fspecial('gaussian', [20 20], 0.4)
b2 = fspecial('gaussian', [20 20], 4)

I_f1 = imfilter(I, b1)
I_f2 = imfilter(I, b2)

t1 = graythresh(I_f1)
t2 = graythresh(I_f2)
I_t1 = im2bw(I_f1, t1)
I_t2 = im2bw(I_f2, t2)

subplot(2, 3, 1)
imshow(I)
title('Original')
subplot(2, 3, 2)
imshow(I_f1)
title('Filter Low')
subplot(2, 3, 3)
imshow(I_f2)
title('Filter High')
subplot(2, 3, 4)
imhist(I)
title('Original')
subplot(2, 3, 5)
imhist(I_f1)
title('Filter Low')
subplot(2, 3, 6)
imhist(I_f2)
title('Filter High')
figure;

subplot(1, 2, 1)
imshow(I_t1)
title('Treshold Low')
subplot(1, 2, 2)
imshow(I_t2)
title('Treshold High')
```

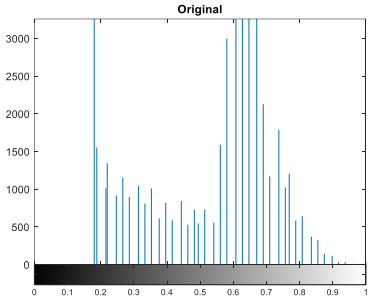
Results

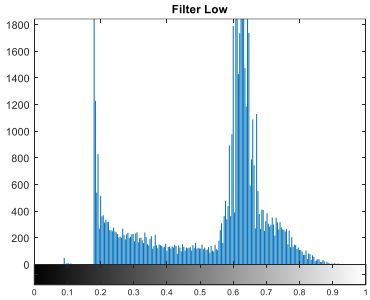
The fspecial('gaussian') produced the lowpass filters. The filter with the higher alpha (4) removes a higher amount of the low-intesnity pixels than the low alpha filter.

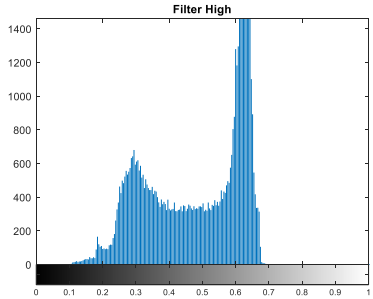


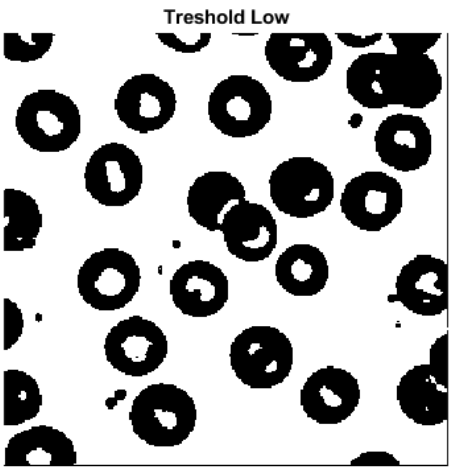


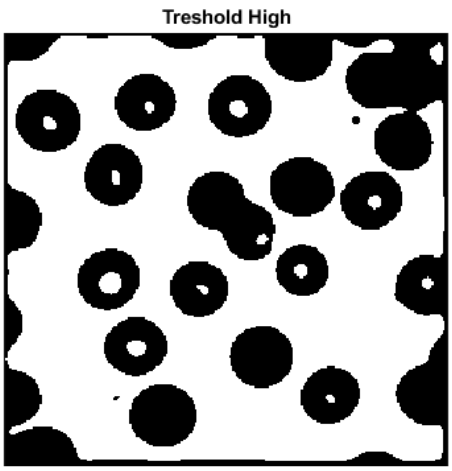












Problem 14.4

Load the spine.tif image. Apply a Laplace filter and threshold the image. Locate edges where the Laplace filter is near zero.

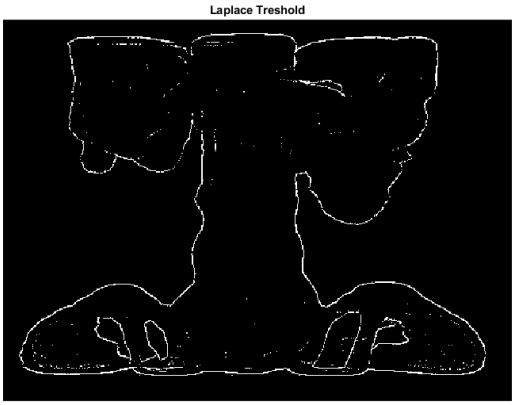
Solution

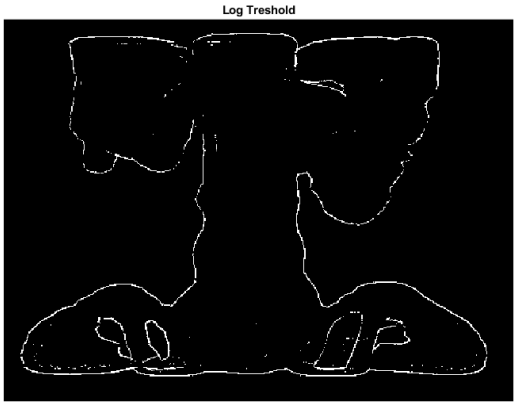
```
[I, map] = imread('C:\dev\biomedeng\Associated Files\Chapter 14\spine.tif')
I = im2double(I)


b1 = fspecial('laplacian')
```

```
b2 = fspecial('log')


I_f1 = imfilter(I, b1)
I_f2 = imfilter(I, b2)


I_t1 = im2bw(I_f1, 0.014)
I_t2 = im2bw(I_f2, 0.03)


subplot(1,3, 1)
imshow(I)
title('Original')
subplot(1,3, 2)
imshow(I_f)
title('Laplpacian')
subplot(1,3, 3)
imshow(I_f2)
title('Logarithmic')
figure;


subplot(1,2, 1)
imshow(I_t1)
title('Laplace Treshold')
subplot(1,2, 2)
imshow(I_t2)
title('Log Treshold')
```

Result

The Laplacian and logarithmic thresholded images are shown below. We see both the Laplace and log filter can effectively detect edges. The log filter uses 0.03 while the Laplace uses 0.014. The Laplacian shows more noise.





Problem 14.10

Load bacteria.tif. Apply edge detection and add to the original image. Use imfill to fill the interior of cells white. Apply a high threshold to get a bacteria-mask. Use erosion and dilation to capture the unfilled cell.

Solution

The image is loaded. Then Canny edge detection is done. The detected edges are dilated to fill the one cell with a non-continuous edge. Then the edges are added to the original image. Imfill fills the cells white. Then it's threshold and eroded to complete the final mask.

```
[I, map] = imread('C:\dev\biomedeng\Associated Files\Chapter 14\bacteria.tif')
I = im2double(I)
I = im2gray(I)
I_e = edge(I,'canny',0.2)% 1. Apply Canny edge filter with 0.2 tresh

%Dilate
structure = strel("disk", 1);
I_dilated = imdilate(I_e, structure);


bw1 = imbinarize(I)
I_comb = I + I_dilated % 2. Add edges to grayscale


I_fill = imfill(I_comb, 'holes')%3. Apply imfill to this combined image that
will make
%the interior of all but one cell white.


I_t = im2bw(I_fill, 0.99)%High treshhold to capture bactira mask

%Capture the last
structure = strel("disk", 2);
I_eroded = imerode(I_t, structure);

subplot(2,4,1)
imshow(I)
title('Original')
subplot(2,4,2)
imshow(I_e)
title('Edges')
subplot(2,4,3)
imshow(I_dilated)
title('Dilated')
subplot(2,4,4)
imshow(I_comb)
title('Combined')


subplot(2,4,5)
imshow(I_fill)
title('Filled')
```

```
subplot(2,4,6)
imshow(I_t)
title('Treshold')


subplot(2,4,7)
imshow(I_eroded)
title('Eroded')
figure;
```

Result

Without the dialation step one cell would remain un-filled.