

HW6_1

Code

```
clc; clear;
close all
signal = csvread('Data.csv');
signal=signal*1000;
n=length (signal);
% 1. What is the first index of i in the for-loop? Is it 1? If not, then why?
% 2. What is the last index of i in the for-loop? Is it n?
% 3. What is the size of the slope array? Is it the same as that of signal?
% 1)
% % i=2 because we use loop and in loop we need i-1, so start index is 1 for
% acces value
% % 2)
% yes,n is the last index of loop...and first value is 0
% 3)
% no, slope is shorter n-1
t=1;
for i=2:n
    slope(i-1)=(signal(i)-signal(i-1))/2;
end
% Anamoly detection using slopes
for i = 1:n-1
    % we already compute sloop and use it
    % sloop(i)=sloop(i)
    if (slope(i)<=150)
        % disp(slope(i))
        new_signal(i) = signal(i+1);
    end
end
% Determine the length of new_signal using the length() function.
n_clean = length(new_signal);
disp(['length of signal is: ',num2str(n)])
disp(['length of slope: ',num2str(length(slope))])
disp(['length of new clear signal is: ',num2str(n_clean)])

for i=1:n
    if i == 1
        moving_avg(i) = (signal(i)+signal(i+1))/2;
    elseif i == n
        moving_avg(i) = (signal(i-1)+signal(i))/2;
    else
        moving_avg(i) = (signal(i-1)+signal(i)+signal(i+1))/3;
    end
end

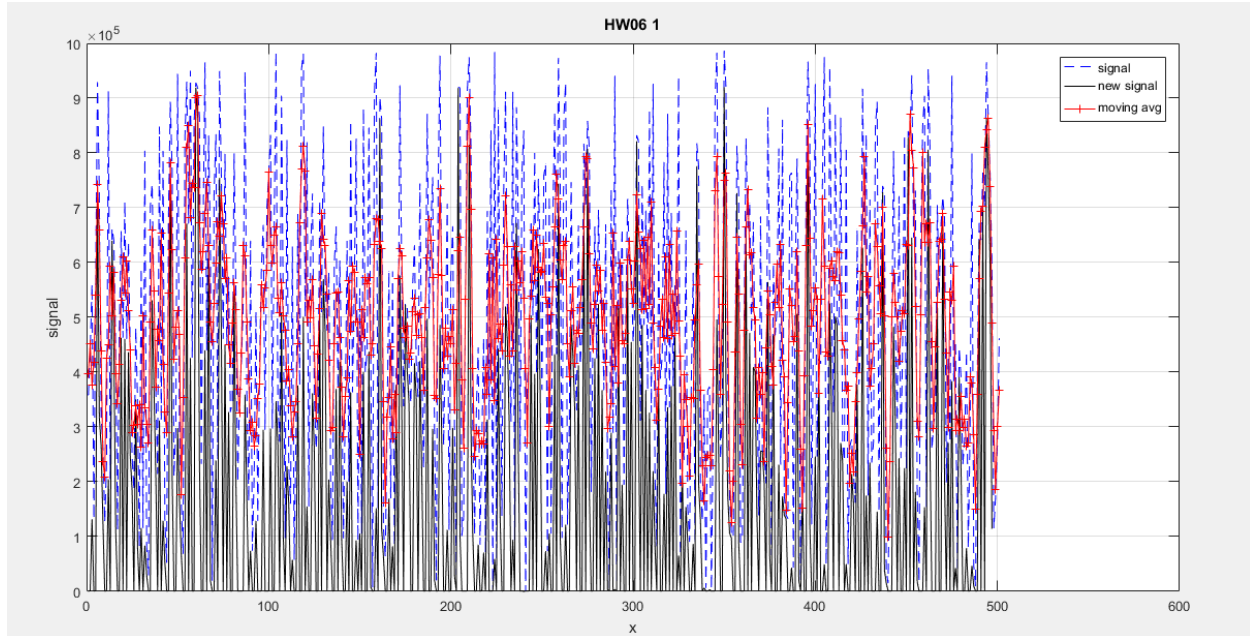
figure()
x =1:n;
plot(x,signal,'b--'); % blue dot
hold on;
plot(x(1:n_clean),new_signal,'k'); % black line
plot(x,moving_avg,'r-+');
legend('signal','new_signal','moving_avg')
xlabel('x')
```

```

grid
ylabel('signal')
title('HW06_1')

```

Output



```

length of signal is: 501
length of slope: 500
length of new clear signal is: 497

```

Sloop test

```

clc
clear
signal = csvread('Data.csv');
data=signal(1:5);
t=1;
for i=2:length(data)
    sloop_temp(i-1)=(data(i)-data(i-1) )/(2);
end
data
sloop_temp

```

Output

```
data =
```

```
357.3500  437.7600  560.2600  130.8800  563.0000
```

```
sloop_temp =
```

```
40.2050   61.2500 -214.6900  216.0600
```

By hand

Date: _____

$$\text{data} = 357.35, 437.76, 560.26, 130.88, 563$$

$$\text{sloop} = \frac{\text{data}_1 - \text{data}_0}{2}$$

$$\text{sloop}_1 = \frac{437.76 - 357.35}{2} = 40.2050$$

$$\text{sloop}_2 = \frac{560.26 - 437.76}{2} = 61.25$$

$$\text{sloop}_3 = \frac{130.88 - 560.88}{2} = -214.69$$

$$\text{sloop}_4 = \frac{563 - 130.88}{2} = 216.06$$

$$\text{sloop} = \{40.2050, 61.25, -214.69, 216.06\}$$

Question 02

Code

```
clc
clear
close all
image= csvread('ab_mid.csv');
[M, N] = size(image);
blur = image;
figure(1)
subplot(2,1,1)
imshow(image);
title('original image')
subplot(2,1,2)
imshow(blur)
title('blur without filter ')
r = 3;
I = ones(r);
% If I is a 3x3 array, then what is the size of the array subset to
% perform elementwise multiplication?

% need the same size of array , we select the image size 3*3 and perfrom
% the operation on

% 2. Applying the kernel is similar to taking moving average on each point,
% only this time the average is taken
% in two dimensions. How can you take the average of all the points in
% a 2D array?

% % for the 2D average we need to two loop in form of nested and need to
% for applying kernal we need to append the image with zeros

% 3. The mean-product of kernel with the array subset is stored to the
% corresponding location of the blur
% matrix. Would the elements of blur bordering the edges be different or
% the same as the ones in image?

%different , it only same if all the value is contant then filter give the
%same result
```

```

% 4. Why would i for the max value get assigned to Y and j to X?
% getting the location of kidney
% initialize X, Y and max to zero
% Run FOR-loops over the image
row=M;
col=N;
hl=1;
vl=1;
blur=im2double(blur);
y=0*blur;
x_pad=zeros(row+2*vl,col+2*hl); %Padded Matrix (hl increase col)
x_pad(1+vl:row+vl,1+hl:col+hl)=blur(:,:);
for i=1+vl:row+vl %Going through rows
    for j=1+hl:col+hl %Going through values one by one
        y(i-vl,j-hl)=sum(x_pad(i,j-hl:j+hl))+sum(x_pad(i-vl:i+vl,j));
        %Summing Values around current entry according 2 vl and hl
        y(i-vl,j-hl)=y(i-vl,j-hl)-x_pad(i,j); %Current Values gets added
        %twice. Once in row and once in Col
    end
end
end

max_=max(max(y));
[X,Y]=find(y==max_);
y=y/(2*hl+2*vl+1);
y=im2uint8(y);
% Print location of kidney. Will you use %d, %s or %f to print the
% indices?
fprintf('Located stone at (%d,%d) \n',X,Y);
figure(2)
subplot(2,1,1)
imshow(image);
title('original image')
subplot(2,1,2)
imshow(y)
title('image after kernal')

```

Output

original image



blur without filter



original image



image after kernal

