

Exercise 10

2D Color Doppler

TTK 4165 MEDICAL SIGNAL PROCESSING

NORWEGIAN UNIVERSITY OF SCIENCE AND TECHNOLOGY

EVEN FLØRENÆS

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Theory exercises

EvenFlorenas

a)

$$\Delta \alpha = 75^\circ$$

$$\text{beam area} = \frac{1 \text{ beam}}{0.5^\circ} = \underline{2 \text{ beam/degree}}$$

$$r = \text{depth} = 15 \text{ cm}$$

$$c = 1540 \text{ m/s}$$

$$t_{\dots} = \frac{2r}{c} = \frac{2 \cdot 0.15 \text{ m}}{1540 \text{ m/s}} = \underline{0.195 \text{ ms}}$$

Maximum pulse firing rate:

$$\begin{aligned} \text{PRF}_{\max} &= \frac{1}{t_{\min}} = \frac{1}{0.195 \text{ ms}} = 5133 \text{ Hz} \\ &= \underline{\underline{5.1 \text{ kHz}}} \end{aligned}$$

Maximum framerate:

$$\begin{aligned} \text{FR}_{\max} &= \frac{1}{t_{\min} \cdot \Delta \alpha \cdot \text{beam area}} \\ &= \frac{1}{t_{\min} \cdot 75^\circ \cdot 2 \frac{\text{beam}}{^\circ}} = \frac{1}{t_{\min} \cdot 150 \text{ beam}} \\ &= \frac{1}{0.195 \frac{\text{ms}}{\text{beam}} \cdot 150 \text{ beam}} = \underline{\underline{34.2 \text{ Hz}}} \end{aligned}$$

b) $PRF = 5 \text{ kHz}$, $f_0 = 2 \text{ MHz}$

Sector = 32° , $r = 13.5 \text{ cm}$

packet size = 8, beam density = $1 \frac{\text{beam}}{2 \text{ degrees}} = 0.5 \frac{\text{beam}}{\text{degree}}$

$$FR = \frac{PRF}{\text{packet size} \cdot \text{sector} \cdot \text{beam density}}$$

$$= \frac{5000 \text{ Hz}}{8 \cdot 32 \cdot 0.5 + 75 \cdot 2} = \frac{5000 \text{ Hz}}{128 + 150}$$

$$= \underline{\underline{18 \text{ Hz}}}$$

c)

Using 2 beamformers gives $PRF_{\text{new}} = 2 \cdot PRF$ in reception, which leads to

$$\Rightarrow FR_{\text{new}} = FR \cdot 2$$

$$= \underline{\underline{36 \text{ Hz}}}$$

d) $v = 1.7 \text{ m/s}$, $f_0 = 2 \text{ MHz}$

$$FR > 2 f_d \rightarrow V_{\text{Nyquist}} = \frac{c \cdot \text{PRF}}{4 f_0}$$

$$V_{\text{Nyquist}} = \frac{1540 \text{ m/s} \cdot 5000 \frac{1}{\cancel{s}}}{4 \cdot 2 \cdot 10^6 \frac{1}{\cancel{s}}}$$

$$= \underline{0.96 \text{ m/s}}$$

For a PRF of 5 kHz

we can only measure velocities up to 0.96 m/s using this setup without aliasing.

We can not measure the serious valve leakage with this setup.

e)

$$\alpha = \frac{0.5 \text{ dB}}{\text{cm} \cdot \text{MHz}}$$

$$\text{noise} = -58 \text{ dB}$$

$$\text{noise} = \frac{f_0 \cdot 2r}{\text{cm} \cdot \text{MHz}} \cdot 0.5 \text{ dB}$$

$$r = \frac{\text{noise}}{2\alpha f_0} = 23.2 \text{ cm}$$

$$\text{PRF}_{\text{max}} = \frac{c}{2r} = \frac{c}{\frac{\text{noise}}{2\alpha f_0}} = \frac{c \cdot 2\alpha f_0 \cdot 100}{\text{noise}} = \underline{\underline{3319 \text{ Hz}}}$$

$$\text{FR}_{\text{max}} = \frac{c}{2r} \cdot \frac{1}{150} = \underline{\underline{22.13 \text{ Hz}}}$$

PRF must be reduced to 3319 Hz, which affects the frame rate to be 22.13 Hz instead of 34.2 Hz.

$$f) \quad f_t = 1.7 \text{ MHz}$$

$$f_r = 3.4 \text{ MHz}$$

$$\text{noise} = 38 \text{ dB}$$

8

$$\text{noise} = (f_t + f_r) \alpha \cdot r$$

$$r = \frac{\text{noise}}{\alpha(f_t + f_r)} = \underline{\underline{14.9 \text{ cm}}}$$

$$\text{PRF}_{\text{max}} = \frac{c}{2r} = \frac{c \cdot \alpha (f_t + f_r)}{2 \text{ noise}} = \underline{\underline{5167.1 \text{ Hz}}}$$

9) If we use packet size = 4 and remove the first one, and only use the remaining three for every packet (effective packet size = 3), the attenuation from B-mode imaging will not affect the remaining doppler pulses. The only affect doppler pulses will be those we remove in post-processing. The remaining doppler pulses will only be affected by slow or constant moving reverberation, which we can filter out using a high-pass filter.

Exercise 10 TTK4165 Medical Signal Processing

Even Florenes Spring 2016

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Documentation

Ex10.m

Purpose: Script answering tasks given in exercise 10 in TTK4165

Made by:

Even [Florenes NTNU 2016](#)

Related files:

imagelog.m: Image a [matrix of ultrasound power in log scale](#)

clutterfilterrespons.m

regressionfilter.m: Removes clutter [from iq signal](#)

Last changes:

2016-04-06 EF: First attempt

2016-04-08 EF: Implemented remaining [exercises](#)

Status:

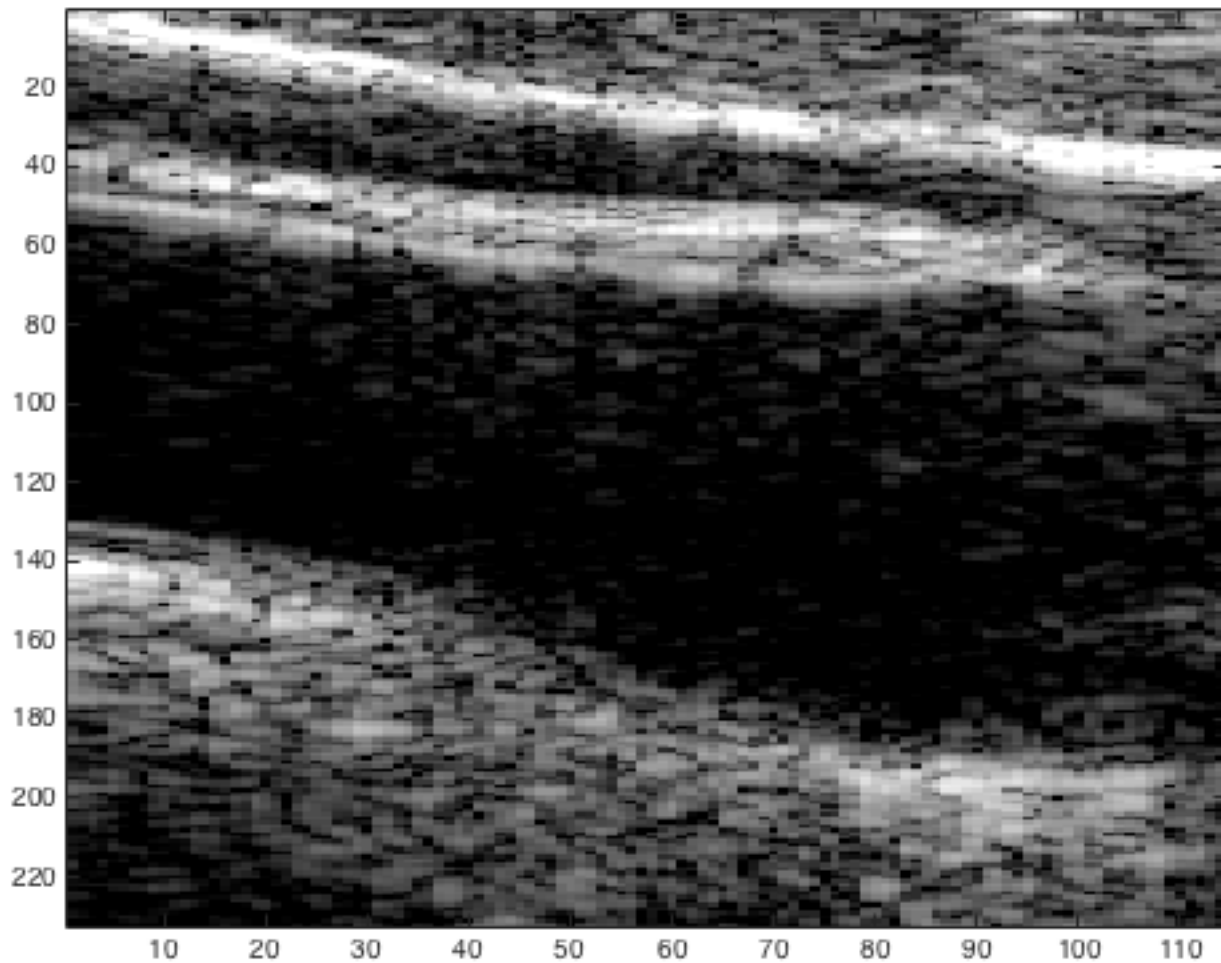
Works

Exercise 1: Visualization

```
load carotid.mat

iq2d = squeeze(iq(6,:,: ,1));

gain = -33;
dyn = 40;
imagelog(abs(iq2d).^2,gain,dyn);
```



Exercise 2: Blood tissue ratio

```
% Set data-points for vessel wall & artery.
r_tissue=48; b_tissue=30;
r_artery=111;b_artery=40;
% Averaging R samples radially and B samples laterally
R=6; B=3;
% Extract data
iq_tissue =iq(:,r_tissue+[0:R],b_tissue+[0:B],1);
iq_artery = iq(:,r_artery+[0:R],b_artery+[0:B],1);
% Calculate intensity.
I_tissue = abs(iq_tissue).^2;
I_artery = abs(iq_artery).^2;
% Average in all three dimensions.
I_tissue = mean(I_tissue(:));
I_artery = mean(I_artery(:));

intensityRatio = 10*log(I_artery/I_tissue);

fprintf('Intensity ratio between artery and tissue: %0.2f dB\n',intensityRatio);
% How much larger is the intensity in the vessel wall compared to the
% vessel?
%
% The intensity, power transferred per unit area, is much larger in the
% vessel wall.
%
%
```

Intensity ratio between artery and tissue: -74.25 dB

Exercise 3: Regression filter for removing clutter

```
% Filter data with current order N.
%y=regressionfilter(squeeze(iq(:,:, :, frameNo),N));
frameNo=1;
packetNo=6;
gain = -20;
for N=-1:4
% Create subplot.
figure(2),subplot(2,3,N+2);
% Filter data with current order N.
y=regressionfilter(iq(:,:, :, frameNo),N);
% Squeeze to remove all other packet-data.
y=squeeze(y(packetNo, :, :));
% Show image.
imagelog(abs(y).^2,gain,dyn);
% Set title.
title(['N=',num2str(N)]);
end
% Comment on the remaining blood and tissue signal for increasing filter
% order:
%
% As we increase N the image becomes darker and darker. For higher N the
% only remaining part in the image is the fluctuation in the artery and
% vein. All of the surrounding vessel wall is removed.
%
%
packetSize=13;
% Set data-points for vessel wall & artery.
r_tissue=48; b_tissue=30;
r_artery=111;b_artery=40;
% Averaging R samples radially and B samples laterally
R=6; B=3;
% Extract data
N = -1:packetSize-2;
iq_tissue =iq(:,r_tissue+[0:R],b_tissue+[0:B],1);
iq_artery = iq(:,r_artery+[0:R],b_artery+[0:B],1);
I_ratio = zeros(1,length(N));
I_tissueMean = zeros(1,length(N));
I_arteryMean = zeros(1,length(N));
for i = 1:length(N)
    y_tissue = regressionfilter(iq_tissue,N(i));
    y_artery = regressionfilter(iq_artery,N(i));
    I_tissue = abs(y_tissue).^2;
    I_artery = abs(y_artery).^2;
    % Average in all three dimensions.
    I_tissueMean(i) = mean(I_tissue(:));
    I_arteryMean(i) = mean(I_artery(:));
    I_ratio(i) = 10*log(I_arteryMean(i)/I_tissueMean(i));
end
figure(3),plot(N,10*log(I_tissueMean)),title('Intensity of vessel wall');
xlabel('N');ylabel('dB');
intensityClutterComponent = abs(10*log(I_arteryMean(2))-10*log(I_arteryMean(1)));
fprintf('The intensity of the clutter component compared to the \n')
fprintf('echo strength from the red blood cells is: %0.2f dB\n',intensityClutterComponent);

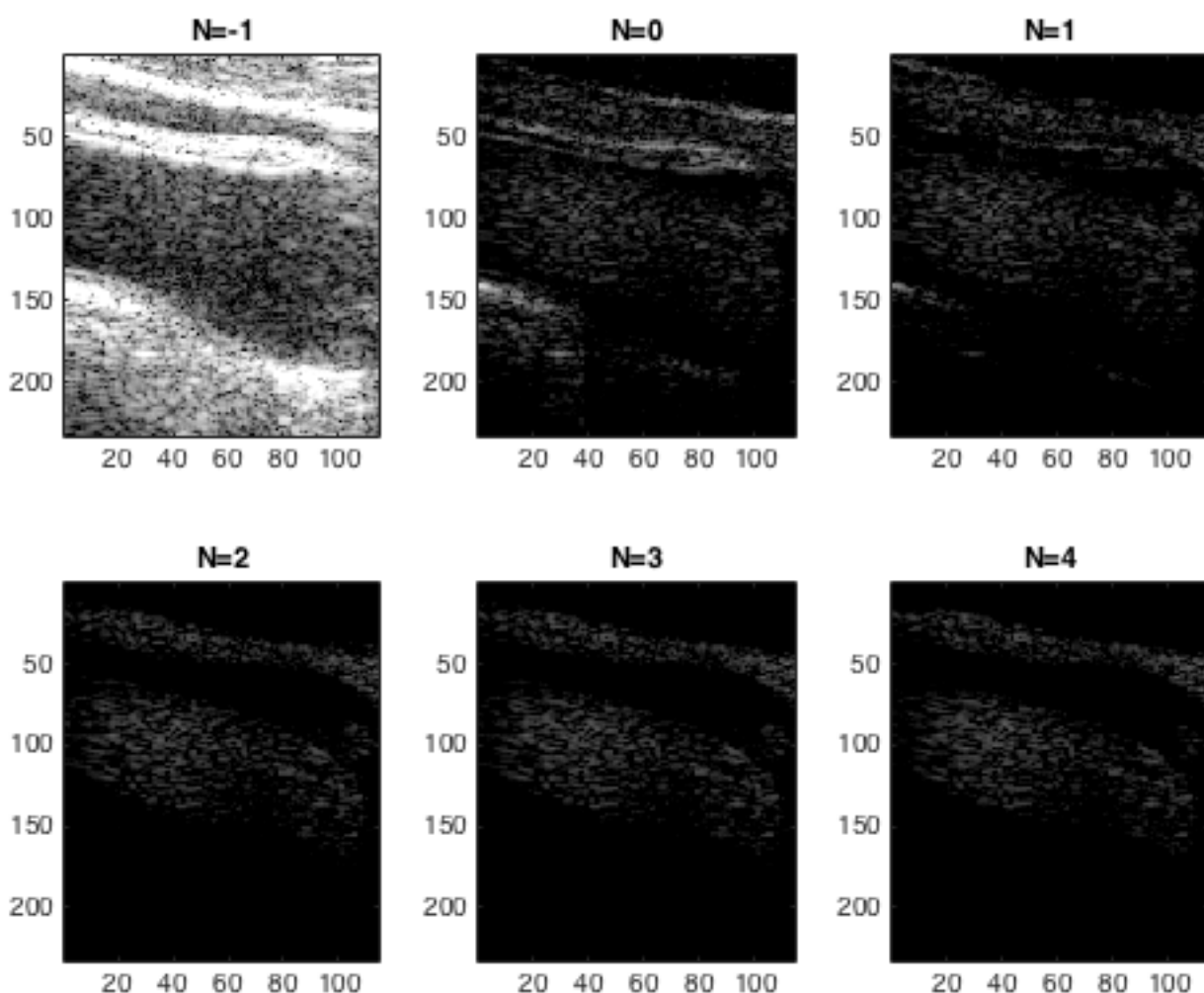
figure(4),plot(N,I_ratio),title('Intensity ratio of artery on tissue');
xlabel('N');ylabel('dB');
% At what filter order is B/V the largest
% B/V is largest at highest filter orden,N,11. After N exceeds 2 B/V
```

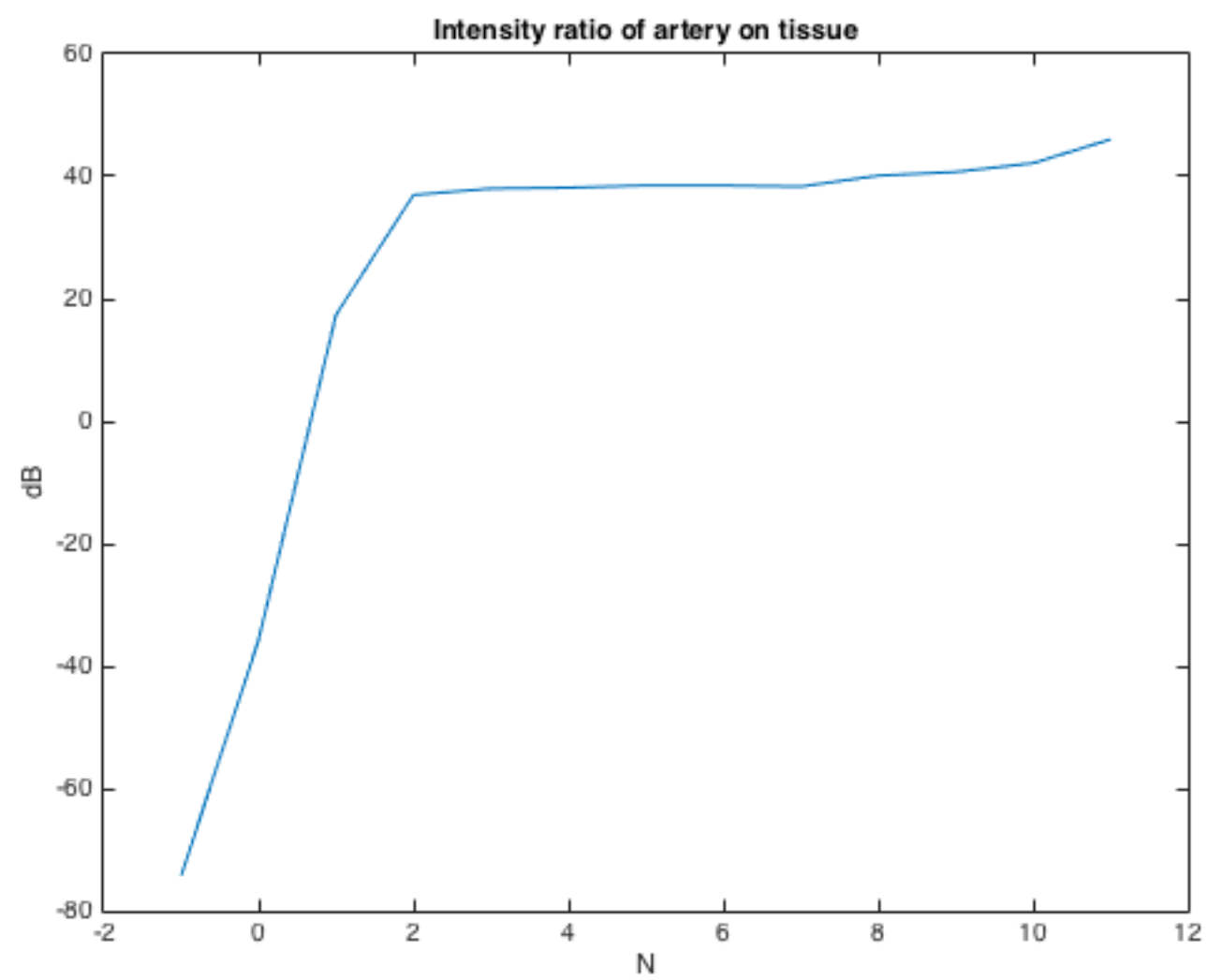
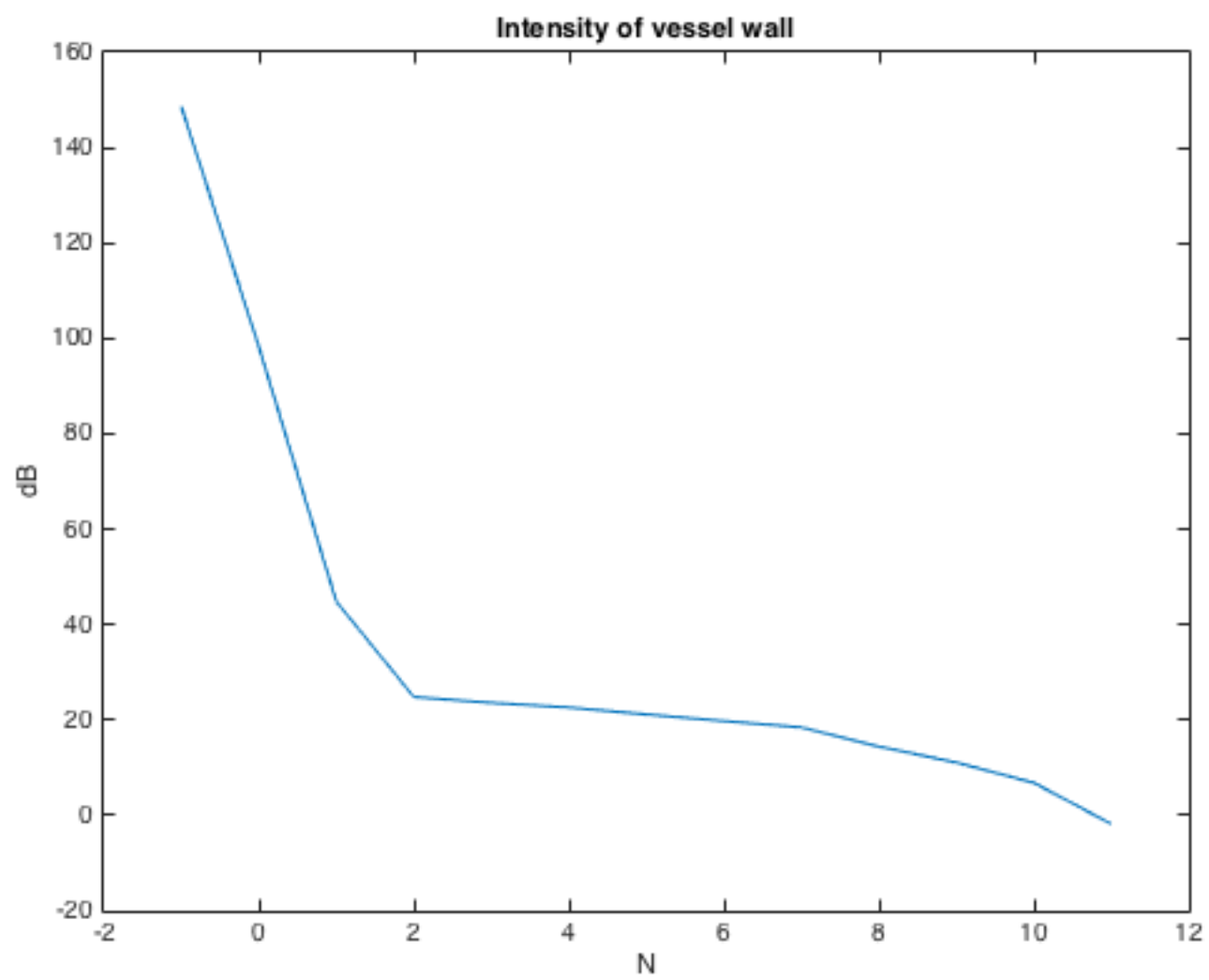
```

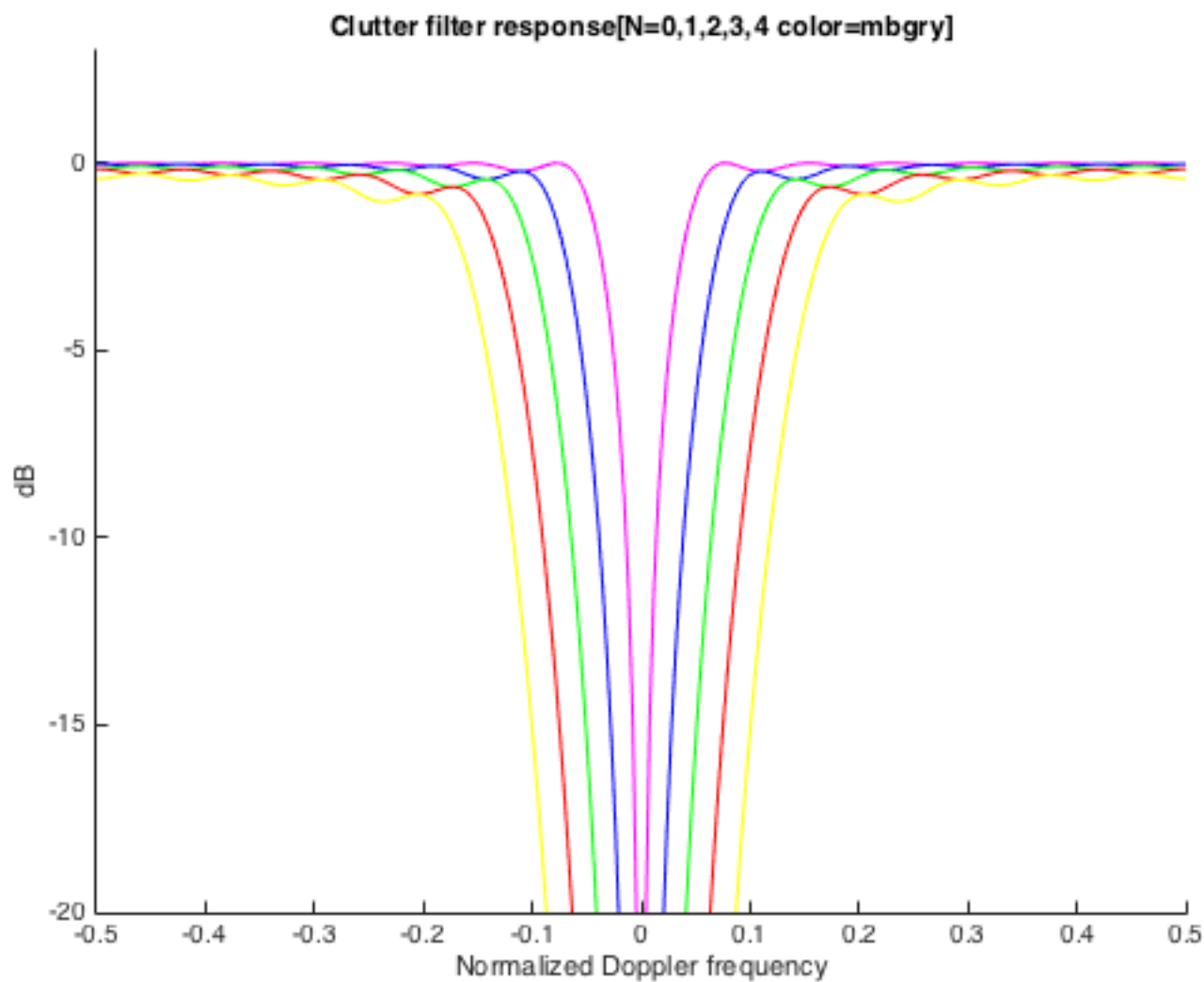
% flattens out, but still increases a little until packSize-2 = 11.
%
figure(5);hold on;
colors = ['mbgry'];
for N=0:4
    [y,c,Fm]=regressionfilter(iq(:,:,frameNo),N);
    [f,H]=clutterfilterrespons(Fm);
    color = colors(N+1);
    plot(f,10*log10(H),[color '-']);
end;
title('Clutter filter response[N=0,1,2,3,4 color=mbgry]'); xlabel('Normalized Doppler frequency'); ylabel('dB');
ylim([-20 3]); xlim([-0.5 0.5]);
hold off
% Comment.
% As we increase the filter orden,N, of the regressionfilter, the filtering
% of the clutter removes more and more of the lower frequencies in the image.
% Using this high pass filter removes stationary parts (low frequency) of
% the image, and leaves moving parts in the image (high frequency). The
% moving parts in the image is the blood flow in the artery and vein,
% and depending on the filter orden some movement in the vessel wall
% is also let trough.
%

```

The intensity of the clutter component compared to the echo strength from the red blood cells is: 11.83 dB







Exercise 4: Complex plots

```

frameNo = 1;
r = 48;
b = 30;
iq1 = iq(:,:,frameNo);
% Plot the complex data. Circle the datapoints.
figure(6);

subplot(3,2,1);
plot(squeeze(iq1(:,r,b)), 'k-o');
% Make the axes scale equally in each direction.
axis('equal');
% Label the axes.
xlabel('Re'); ylabel('Im');
% Save the current axes for later.
axlimits=axis;
% Turn grid on.
grid on;
% Use the relation between phase shift and movement
% to explain how the signal looks.
% In the cessel wall there is small low frequent movements around a fixed
% phase. Subplot (1,1) in figure 6 shows that the phase shift of the area
% is relatively fixed at real axis, but some movements leads to a small
% phase shift in the wall
for N=0:4,
    subplot(3,2,N+2);
    % Filter...
    [y,c]=regressionfilter(iq1,N);
    plot(squeeze(c(:,r,b)), 'kx'); % Set axis.
    axis(axlimits)
    grid on;
    % Set title.

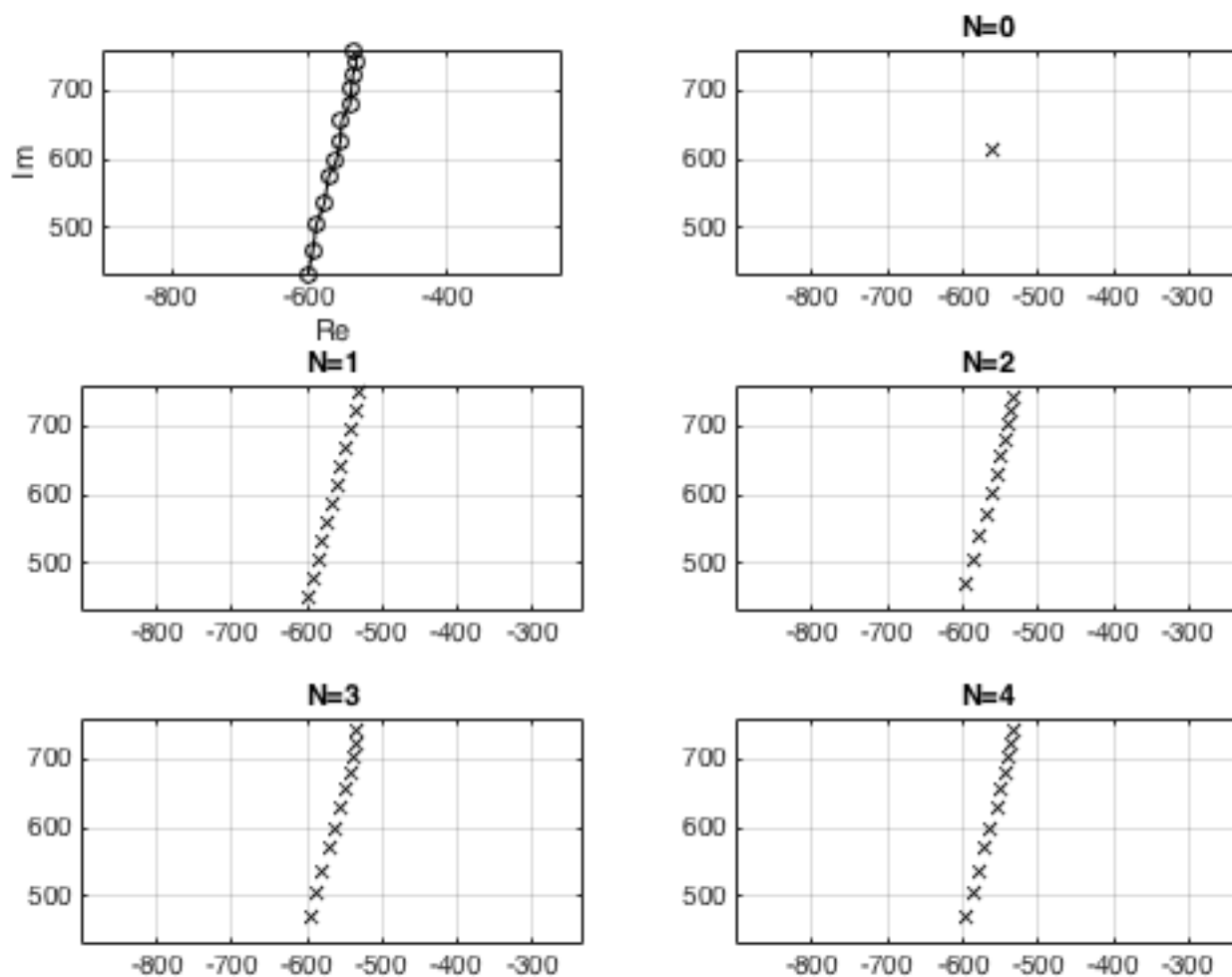
```

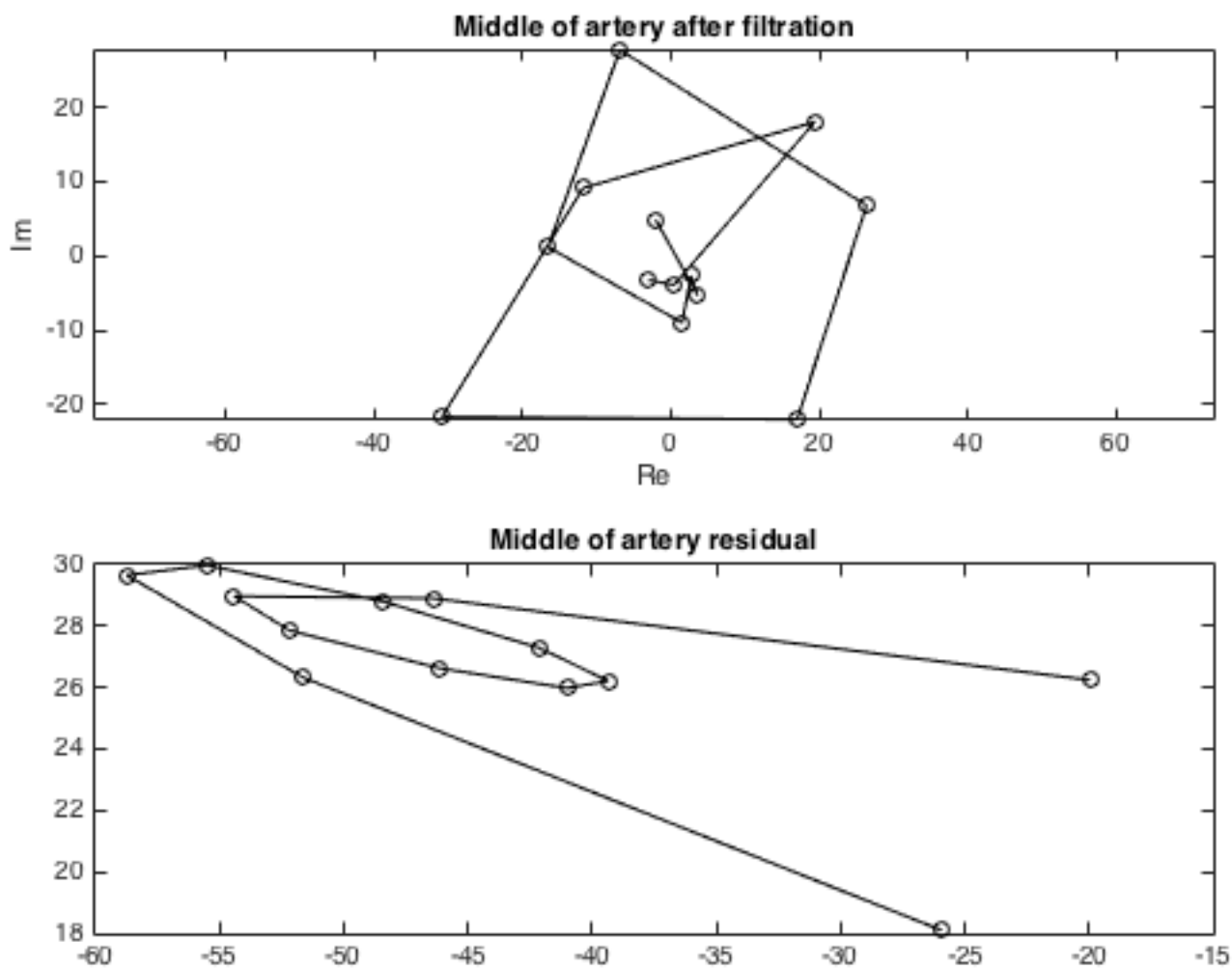
```

title(['N=',num2str(N)]);
end;
%How does the clutter component look?
% The clutter component looks more and more like the complex plot of the iq
% data as we increase the filter orden N. This shows that the
% regressionfilter is able to remove the phase shift due to clutter
% movements.
r = 111;
b= 40;
figure(7)
subplot(2,1,1),plot(squeeze(y(:,r,b)),'k-o');
title('Middle of artery after filtration');
axis('equal'); % Make the axes scale equally in each direction.
xlabel('Re');
ylabel('Im'); % Label the axes.

%Is the adaption between signal and clutter polynomial as good in blood as in tissue?
% After filtration the the blood signal complex plot is centered around 0.
% This shows we have managed to remove most of the clutter component, have
% a complex plot of the movement due to blood flow.
%
subplot(2,1,2),plot(squeeze(c(:,r,b)),'k-o');
title('Middle of artery residual');
%What does the residual signal look like?
% The residual is centered around Im = 28, Re = -45 which shows that there
% is strong clutter component from the movement of the vessel wall.

```





Exercise 5: Velocity estimation using the autocorrelation method

```

framenos = 5;
iq1=squeeze(iq(:,:,:,framenos));
N=3;
y=regressionfilter(iq1,N);
% Get packetsize in data.
packetsize=size(iq,1);

% Make two matrices with lag ? = 1 of the clutter-filtered data.
y1 = y(1:packetsize-1,:,:);
y2 = y(2:packetsize,:,:);

R1=conj(y1).*y2;
R1=squeeze(mean(R1));
R=10; B=3;
b=ones(R,B)/(R*B);
R1=filter2(b,R1);
%Find the phase angle.
phaseangle= angle(R1);

figure(8);colormap('default');
subplot(1,2,1),imagesc(phaseangle);
% Show colorbar.
colorbar; title('Phaseangle before filtration');

P=squeeze(mean(abs(y).^2));
% Spatial averaging.
P=filter2(b,P);
% Normalization.
P=P/max(P(:));
dyn = -14;
beta=10.^(dyn/10);% 16 dB dynamic range

```

```

index=find(P<beta); % Get indexes.
phaseangle(index)=0;

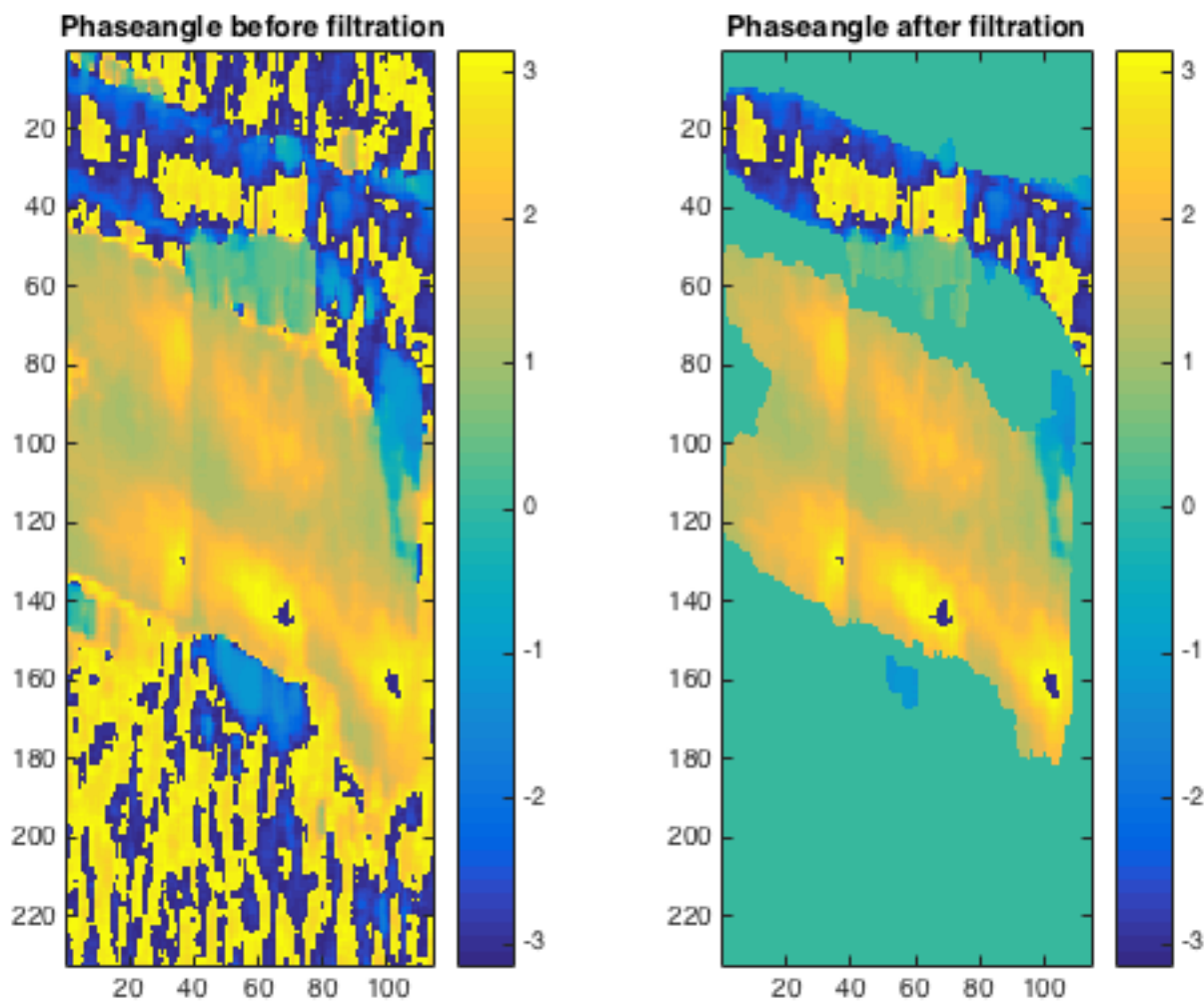
figure(8);colormap('default');
subplot(1,2,2),imagesc(phaseangle);
% Show colorbar.
colorbar; title('Phaseangle after filtration');

% What sign does the phase shift in the artery have?
% The artery have phase shift with positive sign ranging in general between
% 1.5-3 given by the colorbar.

% What is the relation between sign and flow direction?
% Red, orange, yellow (warm colors) is used for positive values and show
% flow direction towards the ultrasound transducer, and blue (cold colors)
% is used for negative sign which indicates flow away from the transducer.

% What sign does the phase shift in the vein have? Comment.
% The vein have phase shift with negative sign, which shown with blue
% color. The artery transports blood from the heart towards the brain in
% the imaged area, which is here towards the transducer.
% The vein transports the blood back from the brain towards which in the
% imaged area is away from the transducer.

```



Color encoding

Simple code to make a combined color and grayscale tissue image Make a `cf_colormap` with 66 colors: A `cf_colormap` has three columns, one for red (R), one for green (G), and one for blue (B)

```

cf_colormap=zeros(66,3);
% The first 64 colors are for grayscale

```



```

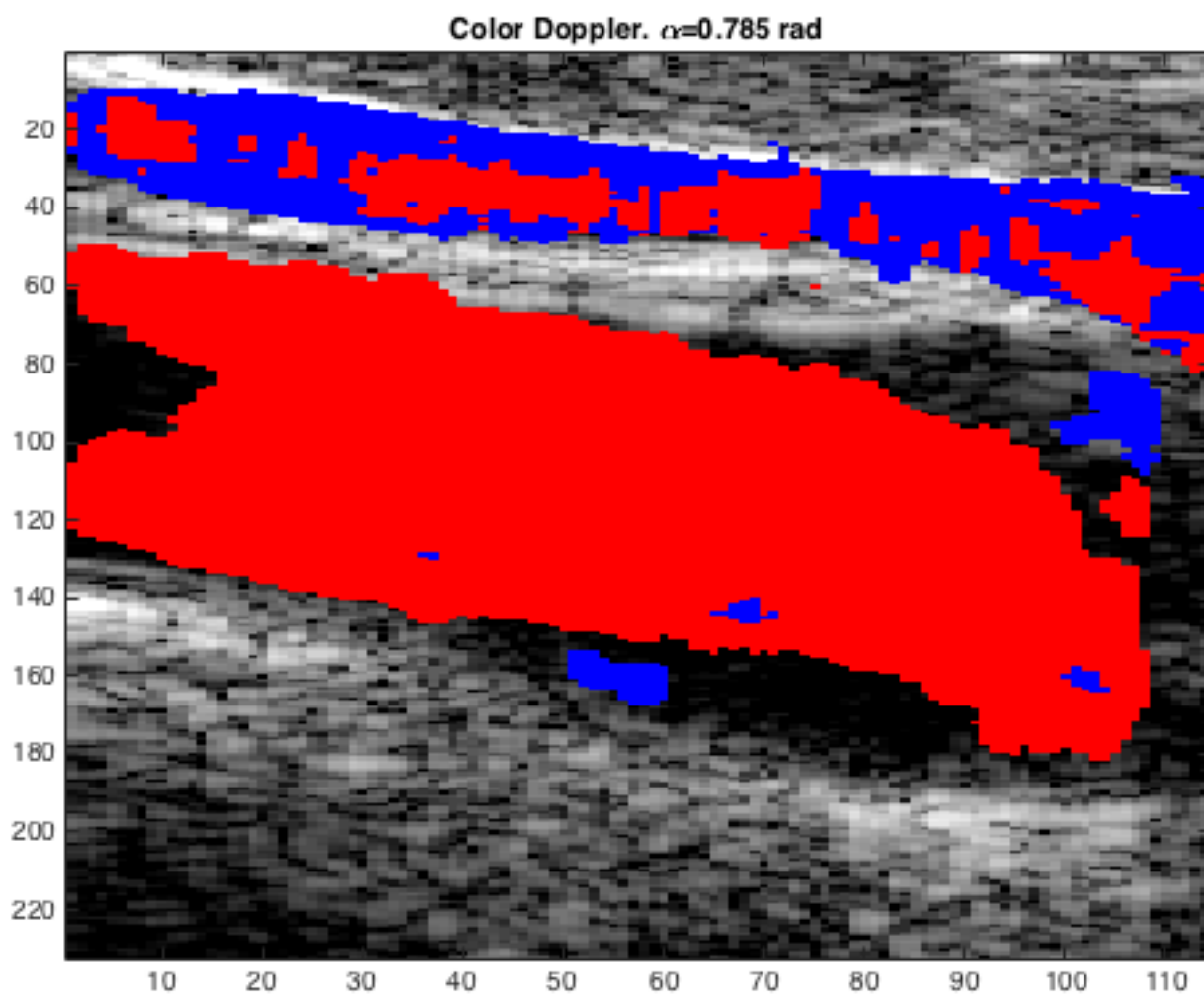
cf_colormap(1:64,:) = gray(64);
% The last to colors are red and blue
redindex=65;
blueindex=66;
cf_colormap(redindex,:)= [1 0 0]; %R=1, G=0, B=0
cf_colormap(blueindex,:)= [0 0 1]; %R=0, G=0, B=1
% Tissueimage: Grayscale with 64 levels, from IMAGELOG
% Phaseangle: Matrix with estimated phaseangle for all points in the % image.
alfa = pi/4;
positiveindex=find(phaseangle>alfa);
negativeindex=find(phaseangle<-alfa);

iq2d = squeeze(iq(6,:,: ,1));

gain = -33;
dyn = 40;
tissue_image = imagelog(abs(iq2d).^2,gain,dyn);

% Set the pixels with positive and negative phase-angle to red and blue
cf_image=tissue_image;
cf_image(positiveindex)=redindex;
cf_image(negativeindex)=blueindex;
%Show colorflow image using our custom colormap:
figure(9),image(cf_image);
colormap(cf_colormap);
title(['Color Doppler. \alpha=',num2str(alfa,3),' rad']);

```



Graded color encoding

```

% Graded red-blue color encoding
redbluemap=zeros(64,3);
redbluemap(1:32,1)=[31:-1:0]'/31;% 1 .. 32: shades of red

```



```

redbluemap(33:64,3)=[0:1:31]'/31;% 33 .. 64: shades of blue
redbluemap = fliplr(redbluemap);
% Stack the grayscale and red-blue scale on top of each-other => a scale with 128 colors:
cf_graded_colormap=zeros(128,3);
cf_graded_colormap(1:64,:)=gray(64); %[1..64]: Grayscale
cf_graded_colormap(65:128,:)=redbluemap;%[65..128]:Color
% Set pixels with low phase shifts to zero,
phaseangle(find(abs(phaseangle)<alfa))=0;
% Find indexes to points where the phase shift is not zero:
index=find(phaseangle~=0);
% Make phase angle in the area [-pi..pi] to indexes [65..128]
phaseangle=phaseangle/pi*31.5; % [-pi .. pi] -> [-31.5 .. 31.5]
phaseangle=round(phaseangle+32.5);% [-31.5 .. 31.5] -> [1 .. 64]
phaseangle=phaseangle+64; % [1 .. 64] -> [65 .. 128]
% Combine images
tissue_image(index)=phaseangle(index);
% Show image
figure(10);
image(tissue_image); colormap(cf_graded_colormap); colorbar;

```

