Biomedical Signal Processing
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Lecture - 54
Tutorial – III (Contd.)

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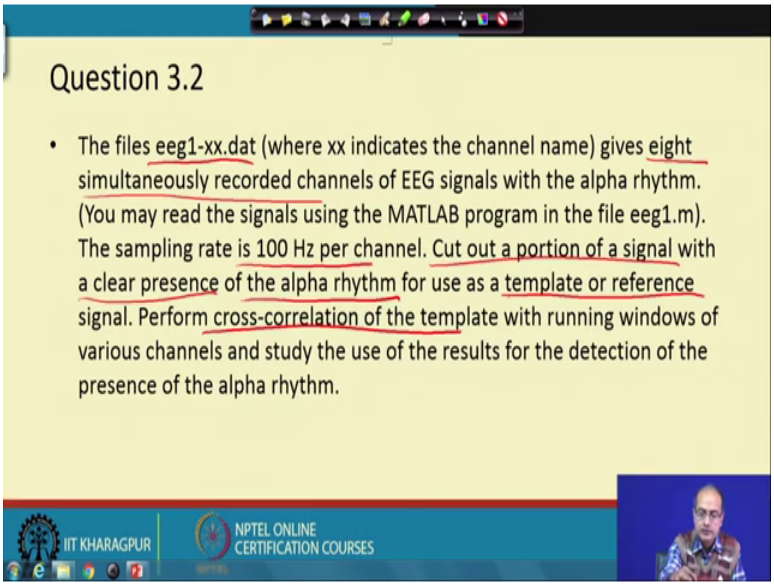

Question 3.2

- The files eeg1-xx.dat (where xx indicates the channel name) gives eight simultaneously recorded channels of EEG signals with the alpha rhythm. (You may read the signals using the MATLAB program in the file eeg1.m). The sampling rate is 100 Hz per channel. Cut out a portion of a signal with a clear presence of the alpha rhythm for use as a template or reference signal. Perform cross-correlation of the template with running windows of various channels and study the use of the results for the detection of the presence of the alpha rhythm.

Our second that tutorial of question 3 is that with EEG signal. With EEG signal here that we would like to know that we have actually 8 simultaneous channels are recorded and they are recorded at 100 hertz, you would like to find out whether the alpha rhythms are present and for that a part of the signal would be taken which has clear actually presence of alpha rhythm with that as a reference or template would like to find out that whether alpha rhythm is present in all this signal and for that we will use the cross correlation of the template.

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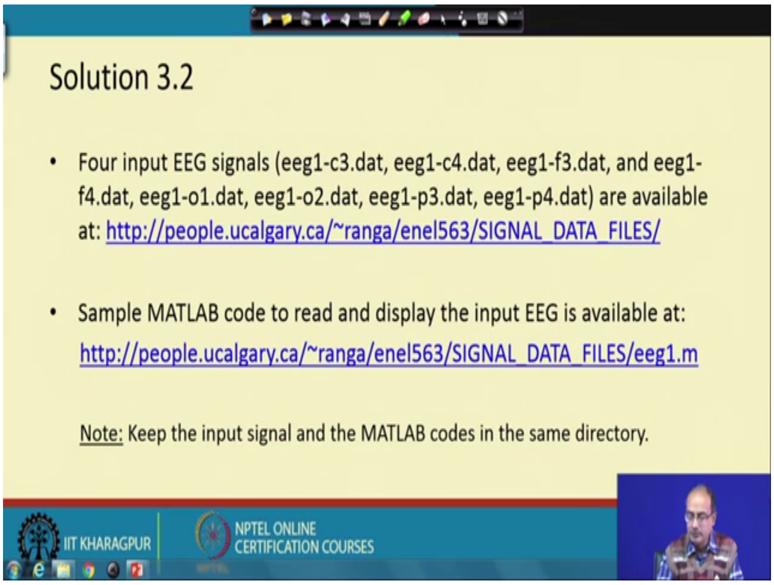

Solution 3.2

- Four input EEG signals (eeg1-c3.dat, eeg1-c4.dat, eeg1-f3.dat, and eeg1-f4.dat, eeg1-o1.dat, eeg1-o2.dat, eeg1-p3.dat, eeg1-p4.dat) are available at: http://people.ucalgary.ca/~ranga/enel563/SIGNAL_DATA_FILES/
- Sample MATLAB code to read and display the input EEG is available at: http://people.ucalgary.ca/~ranga/enel563/SIGNAL_DATA_FILES/eeg1.m

Note: Keep the input signal and the MATLAB codes in the same directory.

So, this is the task. And so, let us proceeds for that. So, first thing is to collect the data file and that the MATLAB file to read the signal, and then we need to keep them both the input signal and the MATLAB code in the working directory of the MATLAB in the same directory.

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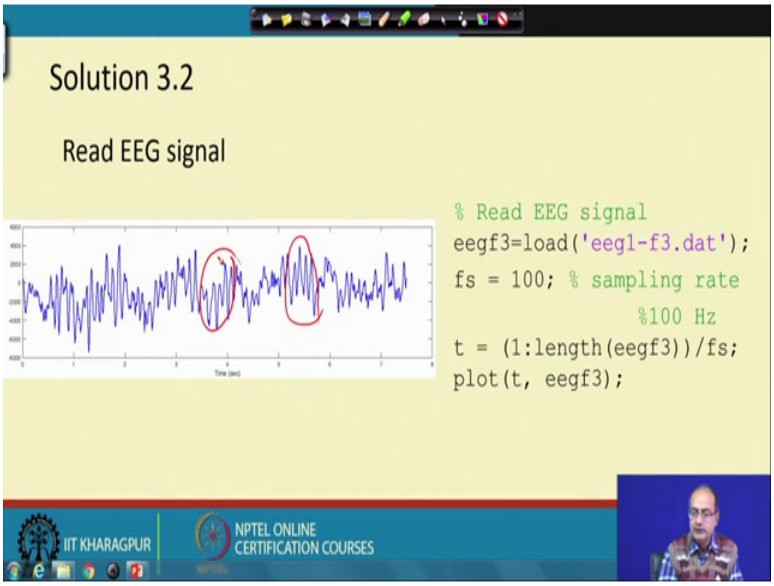

Solution 3.2

Read EEG signal

```
% Read EEG signal
eegf3=load('eeg1-f3.dat');
fs = 100; % sampling rate
               %100 Hz
t = (1:length(eegf3))/fs;
plot(t, eegf3);
```

Next we would like to see that signal. So, first we are using the load command to get ‘eeg 1 dash f 3’ to load this data file and we store that in the variable eeg f 3.

So, next we need to see the plot and for that first we initialize the variable f s that the sampling frequency 100 hertz and t is the time, it is 1 to that the length of the signal is giving the ramp divided by f s or we can say multiplication with 1 by f s is giving us that time instant of each sample. So, that have the sampling interval if we multiply we get the in second we will get the value in the variable t. So, we plot the eeg signal with respect to the time. So, here is a signal here, something we can see that it looks like eeg is present this parts so, clear that alpha rhythms are there.

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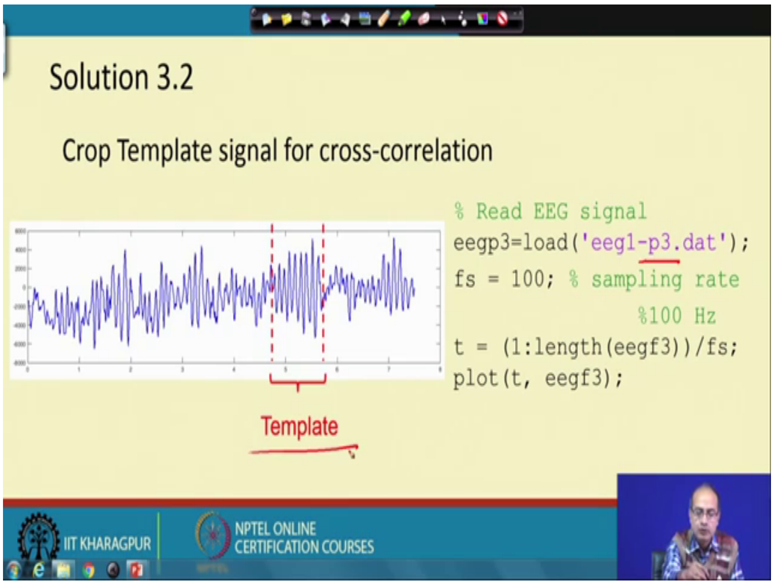

Solution 3.2

Crop Template signal for cross-correlation

```
% Read EEG signal
eegp3=load('eeg1-p3.dat');
fs = 100; % sampling rate
              %100 Hz
t = (1:length(eegf3))/fs;
plot(t, eegf3);
```

So, next we have to find out a template and for that for that we are taking that the p 3 channel. So, we again follow the same procedure as the previous one as we have taken for the previous channel and we plot that signal here we get that channel and with the help of an x part we select this part.

Please keep in mind the selection of play template is very crucial operation and someone who knows that way form should select that. So, the success of the technique completely depends on that template. So, once this selection is done that manually this part it is seen between starting from say 4 to 5 seconds and ending in between 5 to 6 second this segment is selected.

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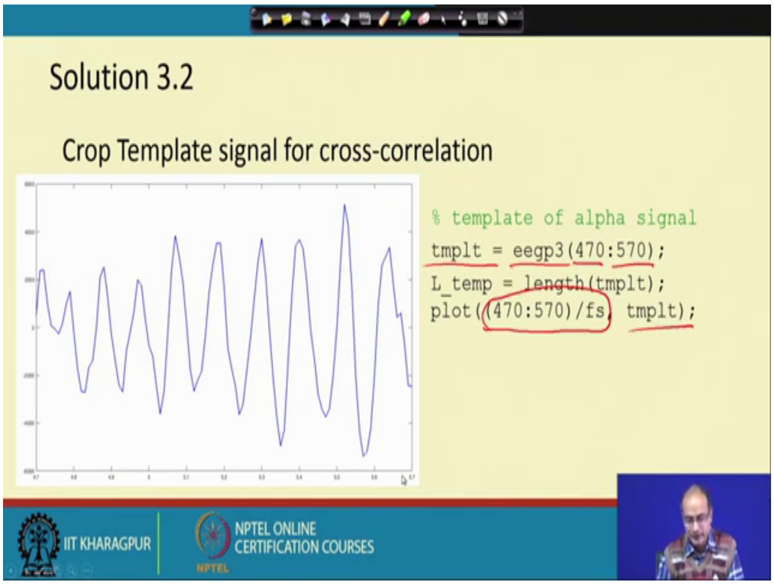

Solution 3.2

Crop Template signal for cross-correlation

```
% template of alpha signal
tmplt = eegp3(470:570);
L_temp = length(tmplt);
plot((470:570)/fs, tmplt);
```

So, would like to see that we say can find that this signal is template is actually in between 470 to 570 100 and 1 samples are there in the eeg p 3 signal. So, that we are taking as template. So, variable length of the template is taken. So, here instead of assigning any variable we are taking the time instant corresponding to that starting from 470 to 570 samples with respect to that this is plotted. Here is the template we get the template here starting 4.7 to 5.7 second this is our starting point for the template matching.

Next is we have to take the correlation. So, for that here we start that operation we have taken eeg f 3 is the signal.

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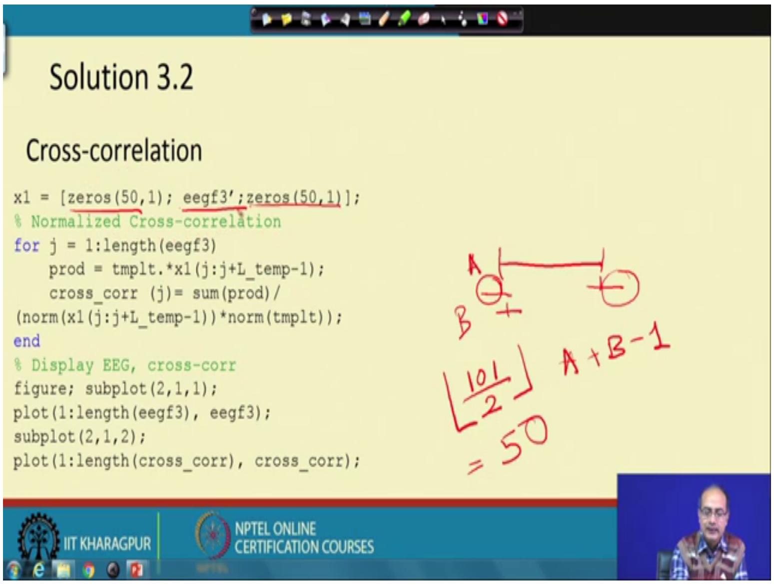

Solution 3.2

Cross-correlation

```
x1 = [zeros(50,1); eegf3';zeros(50,1)];
% Normalized Cross-correlation
for j = 1:length(eegf3)
    prod = tmplt.*x1(j:j+L_temp-1);
    cross_corr (j)= sum(prod)/
(norm(x1(j:j+L_temp-1))*norm(tmplt));
end
% Display EEG, cross-corr
figure; subplot(2,1,1);
plot(1:length(eegf3), eegf3);
subplot(2,1,2);
plot(1:length(cross_corr), cross_corr);
```

Now when we take the correlation we are taking between eeg f 3 say here is the signal and here is another small signal that is template. Now, the overall length would be actually that we need to add if this length is A, this length is B, over length would be A plus B minus 1, but we do not want to see it in that way rather we would like to have same number of points as A. So, how do you do we take the midpoint of the template assign it here and then slide it till this end and in that way what happens we have some samples here outside here some samples outside.

So, to take care of them so, that it does not become computationally infeasible and give error. We have to pad actually our signal both the side and padding would be that we have 100 and 1 samples that is the length of the template. So, if we divide by 2 and take the floor we get 50 ok. So, we take 50 zeros at the beginning 50 zeros at the end and that is the way that we have added and here f 3 was a rho vector so, to make it a column vector. So, we have taken that 0 comma 1.

So, please look at that that it has become a column vector and for that that we have used that the transpose operation. So, that is a minor thing, but these things are very important to write the code properly. Next we go through the main part of it we take the product of the template and the part of the that signal that I would say that padded eeg signal that is kept at x 1 and we are taking that sample by sample product or dot product for that the symbol is dot star. So, we are taking that product and then we taking the sum of that ok.

So, we can say this is this is doing the multiplier accumulator operation mac operation in short and we are not the satisfying satisfied to take autocorrelation or cross correlation we have to take cross correlation coefficient. In other word we need to normalize it with the strength of the template as well as strength of the signal otherwise any variation in one of them we will change that value of that correlation function. So, what we do we divided by that the norm of x 1 and norm of the template.

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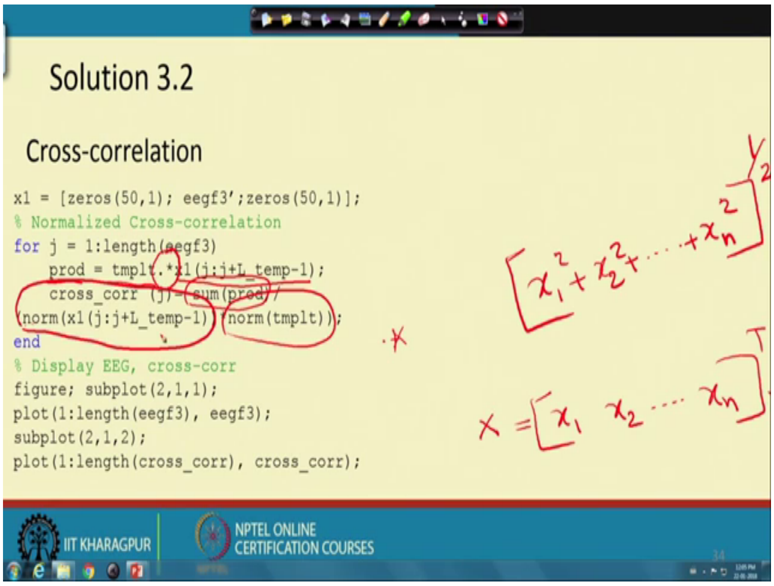

Solution 3.2

Cross-correlation

```
x1 = [zeros(50,1); eegf3';zeros(50,1)];
% Normalized Cross-correlation
for j = 1:length(eegf3)
    prod = tmplt.*x1(j:j+L_temp-1);
    cross_corr (j)= sum(prod)/
(norm(x1(j:j+L_temp-1))*norm(tmplt));
end
% Display EEG, cross-corr
figure; subplot(2,1,1);
plot(1:length(eegf3), eegf3);
subplot(2,1,2);
plot(1:length(cross_corr), cross_corr);
```

$.*$

$\left[x_1^2+x_2^2+\dots+x_n^2\right]^{1/2}$

$x=\left[x_1\ x_2\ \dots\ x_n\right]^T$

Now, what it does say if we have a vector x with all this values x 1, x 2, x n say this is a vector, now it is a column vector now when we take norm it will calculate x 1 square plus x 2 square. So, in that way x n square all of them it will add and it will take square root that is the output of the norm function.

So, we divided by the norm of the 2 constituents one is the template another is the that that part of the corresponding part of the signal and here please look carefully that what we are trying to do that we are sliding the window if this is my is padded signal I am starting from here or let us draw it in this way that up to this if this is a centre.

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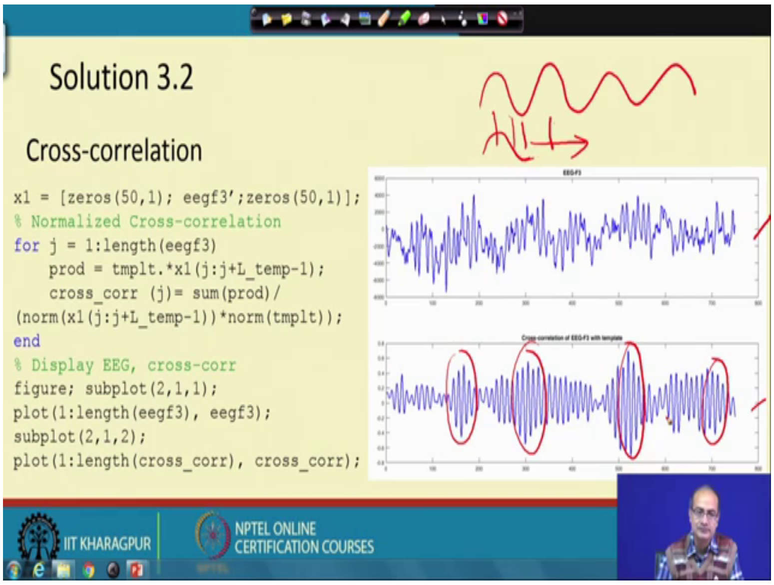

Solution 3.2

Cross-correlation

```
x1 = [zeros(50,1); eegf3';zeros(50,1)];
% Normalized Cross-correlation
for j = 1:length(eegf3)
    prod = tmplt.*x1(j:j+L_temp-1);
    cross_corr (j)= sum(prod)/
(norm(x1(j:j+L_temp-1))*norm(tmplt));
end
% Display EEG, cross-corr
figure; subplot(2,1,1);
plot(1:length(eegf3), eegf3);
subplot(2,1,2);
plot(1:length(cross_corr), cross_corr);
```

This part is the padding zeros are there same way at the end some paddings are there. So, we will actually slide it from here to here ok. So, that is the way it is going we are starting that j to j plus length of the template minus 1. So, from here to here so, that is the way we have taken this part and once the correlation is computed then we have to plot that thing. So, we should the comment figure then divide the length into 2 parts the upper part is subplot 2, 1, 1 then there we are plotting the signal.

With and here instead of the time we are giving the sample number and we know our correlation function that cross corr correlation coefficient it also has same number of samples. So, we are using that index here to plot that thing ok. So, these 2 things are plotted one after another. So, here at the top we see the eeg signal f 3 and below is the cross correlation coefficient and what we see that at some parts that high oscillations are there; that means, some peaks are there with high value that signifies that there is a match.

Otherwise it would be very flat kind of structure if it does not match. So, this oscillation itself talks about that there is a match and immediate question would be that why there is an oscillation there is a match the reason is say let us take 2 sinusoids to understand that say let us take 1 sinusoid is there and we have taken a small template of the same sinusoid a small part, a small part of it we have taken as template.

And here if we slide it if we take the template in this direction when it is aligned it will give high value when it is placed here it will give negative value, but high value in between it will give no match 0. So, that is the reason for oscillation again here it will give a high value. So, that creates this oscillation ok. So, that creative nature of the signal gives raise to this oscillatory kind of output in the cross correlation coefficient.

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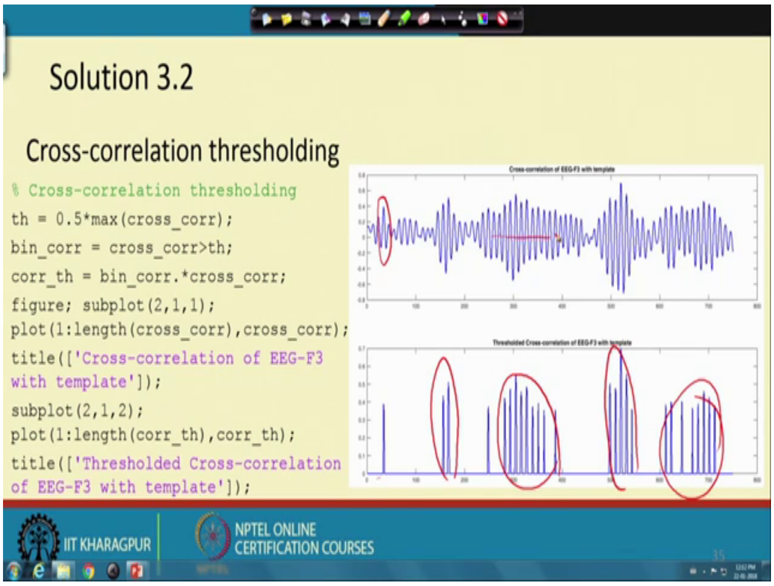

Solution 3.2

Cross-correlation thresholding

```
% Cross-correlation thresholding
th = 0.5*max(cross_corr);
bin_corr = cross_corr>th;
corr_th = bin_corr.*cross_corr;
figure; subplot(2,1,1);
plot(1:length(cross_corr),cross_corr);
title(['Cross-correlation of EEG-F3
with template']);
subplot(2,1,2);
plot(1:length(corr_th),corr_th);
title(['Thresholded Cross-correlation
of EEG-F3 with template']);
```

Next to get a objective value whether this is high enough we need to do the thresholding. So, for that what we have taken we have taken the, that maximum value of the cross correlation coefficient half of that so, very effective you can directly go for that 0.5. So, after taking the threshold we collect the bin information when the cross correlation coefficient is above the threshold.

So, this operation will give us the, that in this is where the value crosses the threshold now if you multiply that been location having value 1 if we take the dot product with the cross correlation we retain only those high values and rest of them becomes 0. So, let us proceed now we would like to see that how it looks like we again use that subplot command the top portion we have taken 2, 1, 1 and plotting the cross correlation first.

Next that we are taking plot 2, 1, 2; that means, the lower half and we plot the thresholded the cross correlation that is given as cross th thresholded cross correlation coefficient. So, in the right hand side we get that and we see here only one peak was prominent, in this part here 2 peaks were prominent here multiple of them when they are here also multiples are there above the threshold and as you have thresholded we are getting that only the high values when it is below we have actually discarded the lower part and there is one more reason will come to that that the lower part also put have been useful to for the purpose of detection if only 1 or less than 1 cycle we there, but in this case we have multiple of them.

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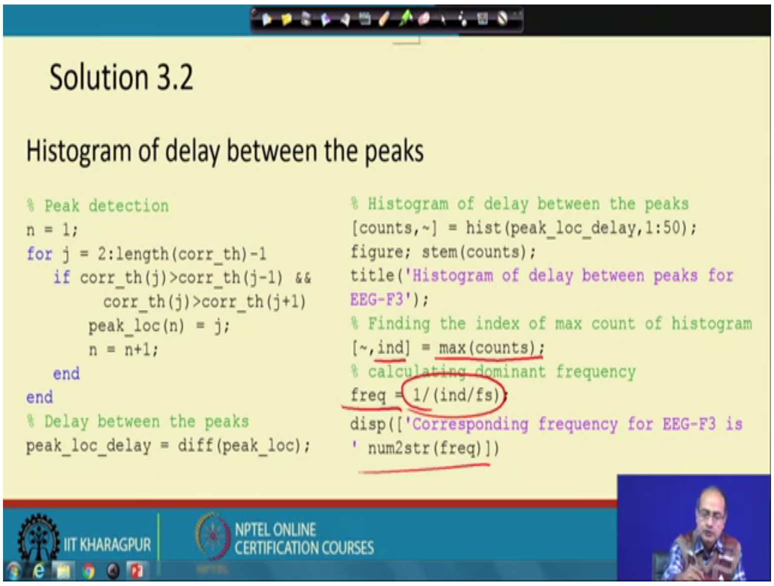

Solution 3.2

Histogram of delay between the peaks

```
% Peak detection
n = 1;
for j = 2:length(corr_th)-1
   if corr_th(j)>corr_th(j-1) &&
         corr_th(j)>corr_th(j+1)
       peak_loc(n) = j;
       n = n+1;
   end
end
% Delay between the peaks
peak_loc_delay = diff(peak_loc);
```

```
% Histogram of delay between the peaks
[counts,~] = hist(peak_loc_delay,1:50);
figure; stem(counts);
title('Histogram of delay between peaks for
EEG-F3');
% Finding the index of max count of histogram
[~,ind] = max(counts);
% calculating dominant frequency
freq = 1/(ind/fs);
disp(['Corresponding frequency for EEG-F3 is
' num2str(freq)])
```

So, it should not have any problem. So, next what we do we create the histogram of delay between the peaks now why we are interested in the delay of it, the delay between the 2 peaks we will give the length of that that oscillation or one cycle of it. So, we would like to find that because that will give the pod city of the signal. So, for that what we do we start with the correlation threshold and we need to identify the correct location of the peak.

So, for that we go through that thresholded correlation and we are measuring that where the at location j if it is higher than the previous sample and it is higher, then the next sample then we can tell that a peak has come and we store that peak location and we increment the, the count and that how many peaks have found. So, we proceed in that way then once we take the difference of this peak location we get the peak location delay.

So, now we have the peak location delay next with the help of that we find out the histogram that we create the histogram of peak location delay and as there would be number of them number of values would be there we are restricting it into the first 50 delays, because high values with very least count they are not of an use. So, we restricted they are.

So, that we get a good picture and we plot that figure and here we are actually it keeping only the counts the second variable we are using till day that is to tell that we do not need to store that variable histogram is giving 2 outputs. The next one is not required for our operations and we use the command stem to plot that; that means, it will give us post kind of structures so, let us see that how it looks.

Before we go for the plot we check for few more things that for our operation after the histogram that we would like to see that where the count is maximum in which being the maximum counts are there that is the we are getting the mode of the delay and we find out the location of that that gives us that this much delay is occurring most of the time and these delay; however, in terms of number of samples.

So, to get the, that the frequency we need to normalize with the sampling frequency so, we need to take care of that and the corresponding frequency of oscillation is given here.

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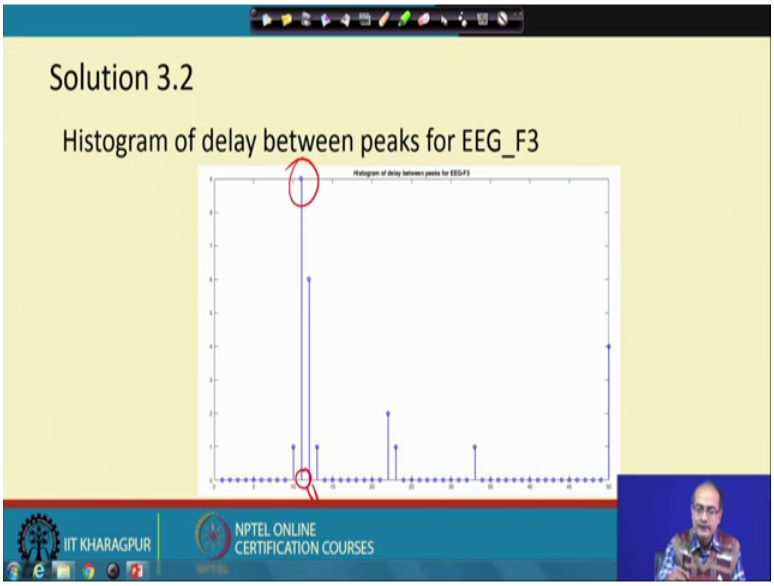

Solution 3.2

Histogram of delay between peaks for EEG_F3

So, let us proceed that here is the plot the stem plot and what we get that this is the highest count. So, we have taken the provision here it would be 11 we have taken that and now that is converted to frequency and appropriately normalized with the sampling frequency.

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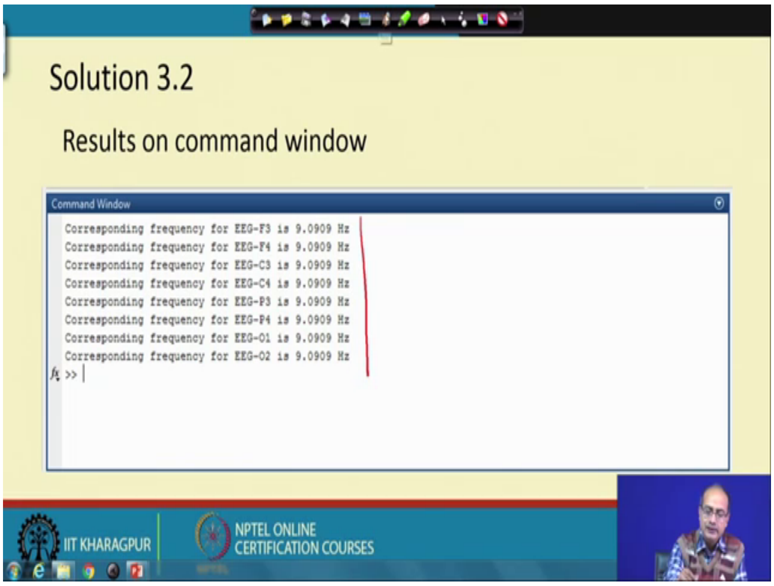

Solution 3.2

Results on command window

```
Corresponding frequency for EEG-F3 is 9.0909 Hz
Corresponding frequency for EEG-F4 is 9.0909 Hz
Corresponding frequency for EEG-C3 is 9.0909 Hz
Corresponding frequency for EEG-C4 is 9.0909 Hz
Corresponding frequency for EEG-P3 is 9.0909 Hz
Corresponding frequency for EEG-P4 is 9.0909 Hz
Corresponding frequency for EEG-O1 is 9.0909 Hz
Corresponding frequency for EEG-O2 is 9.0909 Hz
>>
```

And in that way we expect to get the result. So, for each of the signal that we get we get that each of this case that it is giving us a little more than 9 hertz actually frequency.

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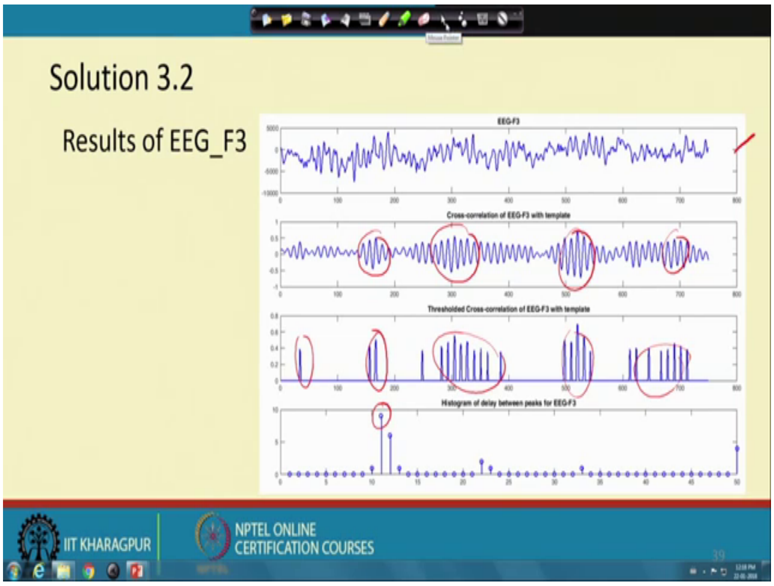

Solution 3.2

Results of EEG_F3

And we know that we have a range for the alpha it is within that range. So, first we go through the output of the F 3 we get here is the signal, signal is not very clean, but time to time alpha are there. So, that is depicted by the correlation that high value of the correlation coefficient is suggesting that and once we threshold it we get that minor occurrences also and when they are having the very close actually occurrences that helps us to get the delays. So, with respect to that we are getting the maximum value here and corresponding to that we have calculated the frequency.

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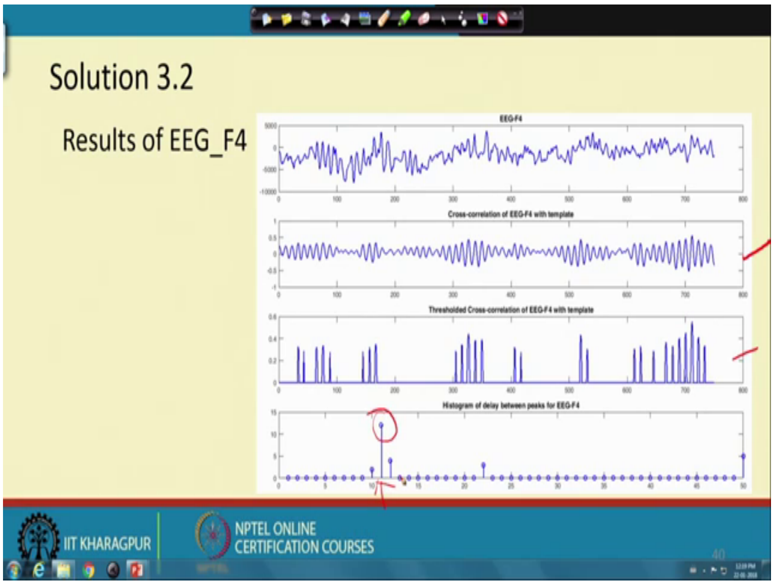

Solution 3.2

Results of EEG_F4

Next we go for the next signal F 4 the same way we have calculated the auto correlation coefficient thresholded it and find out the peak of the histogram and the corresponding location for F 4.

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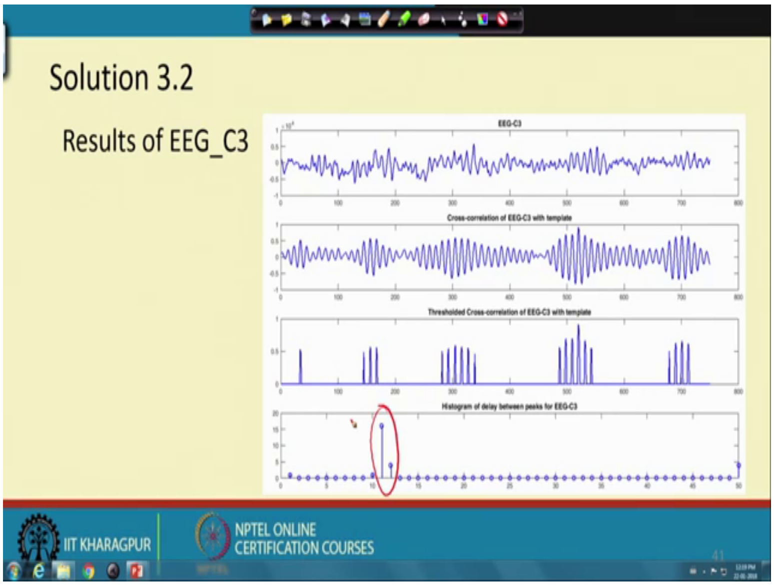

Solution 3.2

Results of EEG_C3

So, next go for F 5 again we find the peak at the, the same location this is EEG C 3.

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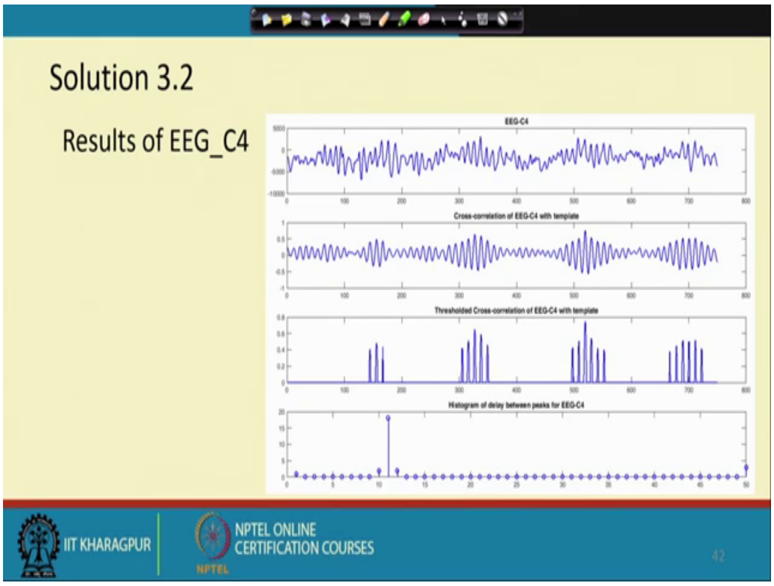

Solution 3.2

Results of EEG_C4

Next we go for C 4 same nature.

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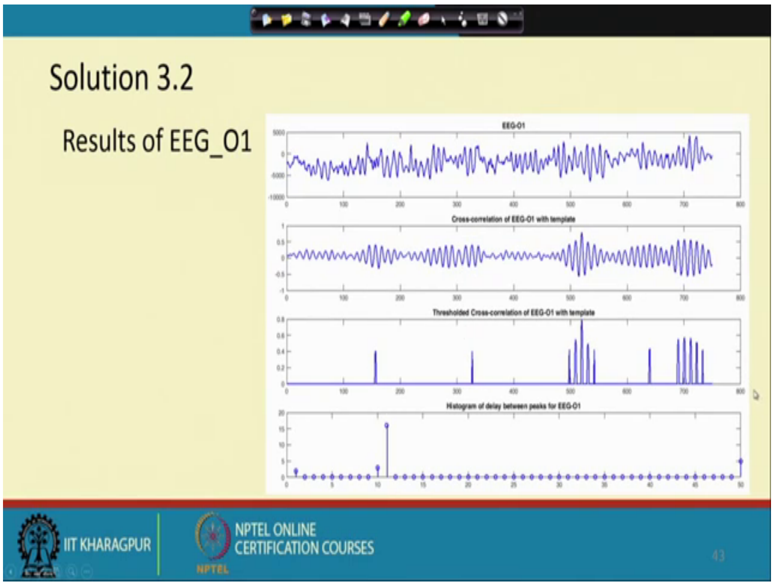

Solution 3.2

Results of EEG_O1

Next O 1 again we have the name nature.

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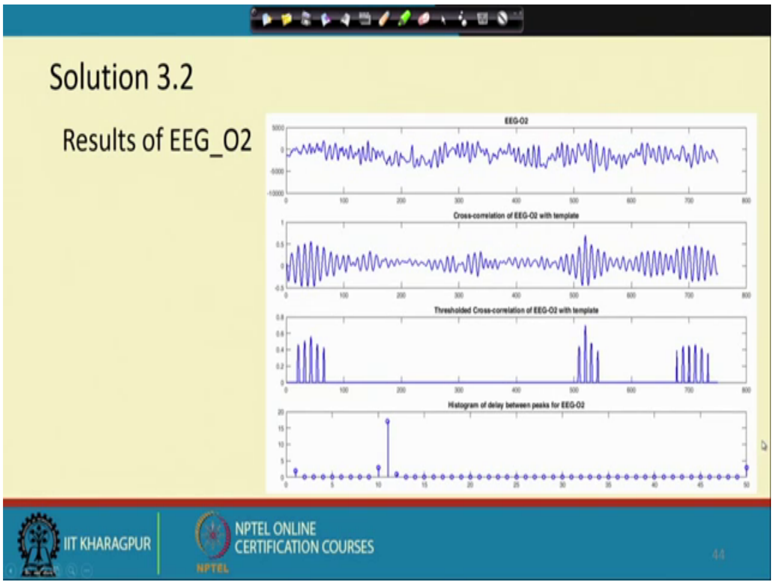

Solution 3.2

Results of EEG_O2

O 2.

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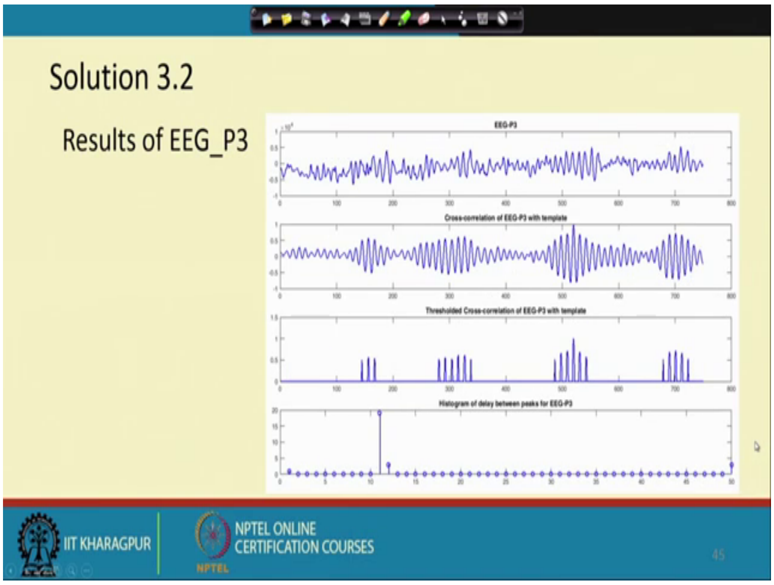

Solution 3.2

Results of EEG_P3

P 3.

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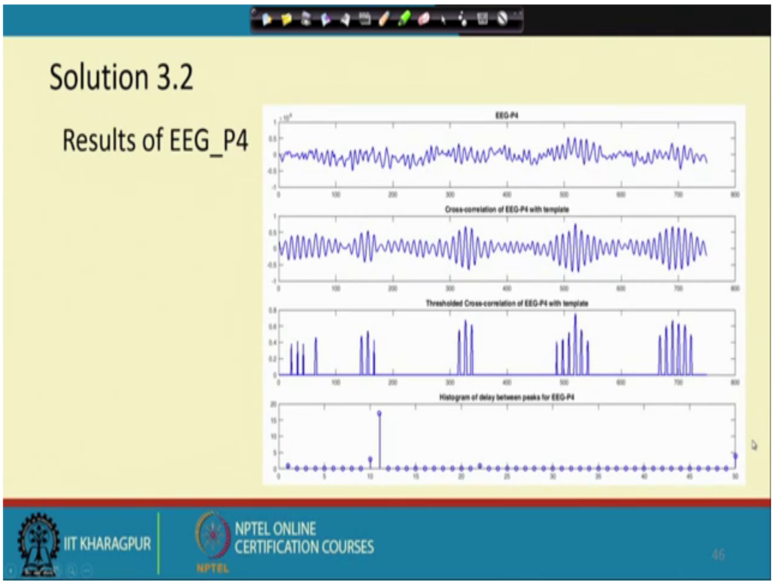

Solution 3.2

Results of EEG_P4

P 4 all the cases we got very similar output.

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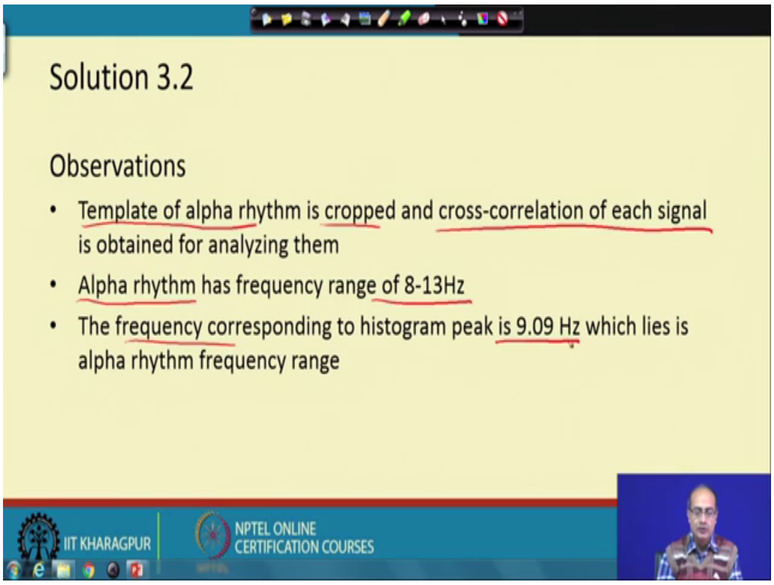

Solution 3.2

Observations

- Template of alpha rhythm is cropped and cross-correlation of each signal is obtained for analyzing them
- Alpha rhythm has frequency range of 8-13Hz
- The frequency corresponding to histogram peak is 9.09 Hz which lies is alpha rhythm frequency range

And hence, we summarize that our finding. Our observations are: we have the template of alpha rhythm that is cropped, and we take the cross relation of each signal for the purpose of the analysis. Here, please keep in mind that selection of the template is very crucial; only an expert can peak that without that a proper selection of the, the template the whole technique will fall apart.

Next what will get that, alpha rhythm we know the range of it is within 8 to 13 hertz and our histogram peak we get at 9 hertz which falls very well within this range. So, we can say for each of these 8 signals we had alpha rhythm present.

We can conclude that. And with that we conclude the second problem of tutorial 3.

Thank you.