

## Contents

---

- Lab 3.1.1 =====
- Lab 3.1.2 =====
- (2)
- (3)
- (4)
- (6)
- (8)
- Lab 3.2.1 =====
- (1)
- (2)
- (3)
- 3.2.3 =====
- 3.3.1 =====

```
%{  
Yonatan Carver  
ECES 352 - Lab 3  
  
%}  
clear; clc; close all
```

### Lab 3.1.1 =====

---

```
%{  
1) 31 results for "hbb"  
3) 280 results for "hbb AND human[orgn]"  
  
%}
```

### Lab 3.1.2 =====

---

(1)

```
w = 10; % 10Hz  
Fs = 100; % 100Hz  
tt = 0 : 1/Fs : 1; % time axis  
  
x = cos(w * tt);  
  
% plot(tt, x);  
% grid on  
% xlabel('time (s)')  
% title('One second of cos(10Hz * tt) sampled at F_s = 100Hz')
```

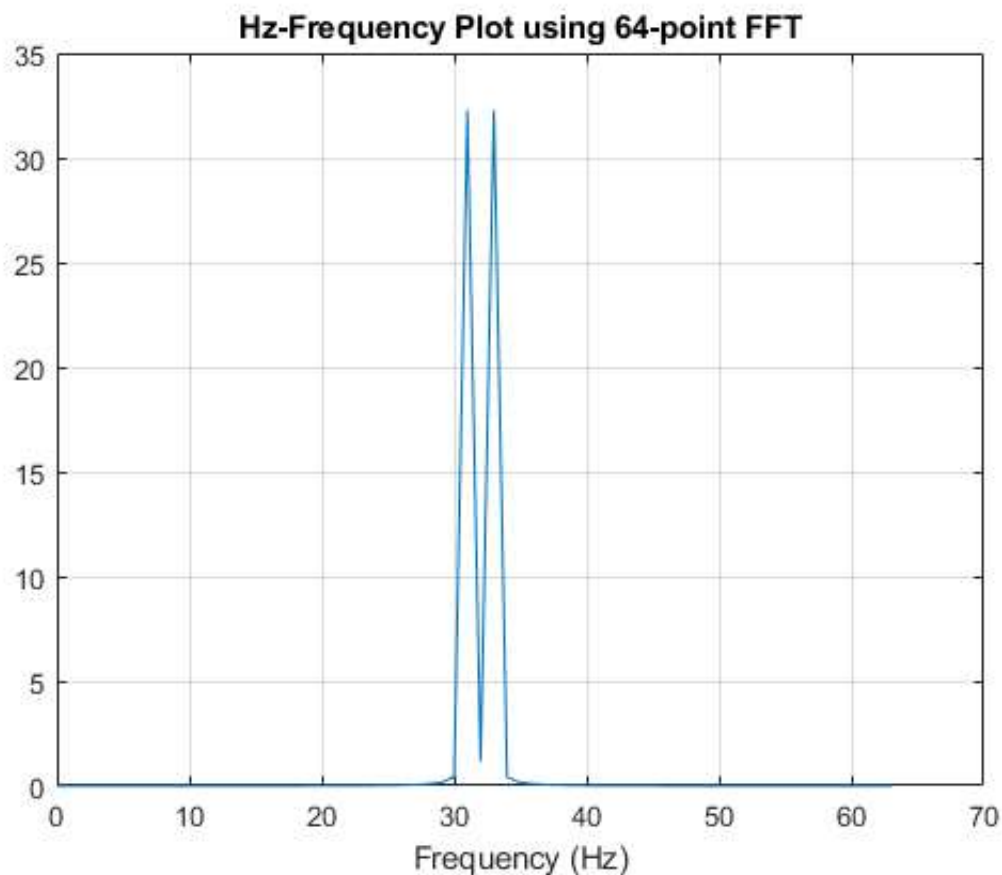
(2)

```
N = 64;  
fft_x = abs(fftshift(fft(x, N)));      % N-point FFT
```

(3)

```
range = 0:1:63;
```

```
range = linspace(0, 63, N);  
figure  
plot(range, fft_x)  
grid on  
xlabel('Frequency (Hz)')  
title(['Hz-Frequency Plot using ', num2str(N), '-point FFT'])  
  
% [yy, xx] = findpeaks(fft_x);  
% frequency spikes @ f = 26 & 38
```



(4)

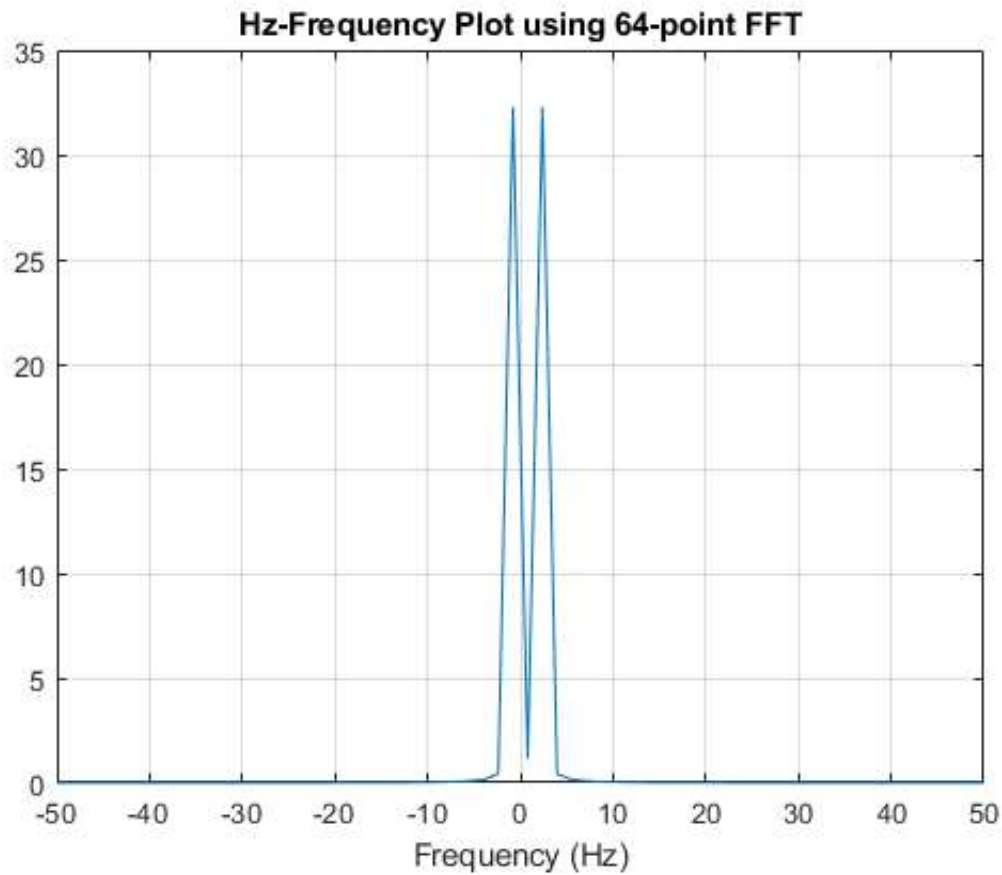
```
range = linspace(-50, 50, N);      % plot from -50 to 50 (100Hz sampling rate)  
  
figure  
plot(range, fft_x)  
grid on
```

```

xlabel('Frequency (Hz)')
title(['Hz-Frequency Plot using ', num2str(N), '-point FFT'])

% frequency spikes @ -8.7302 & 10.3175

```



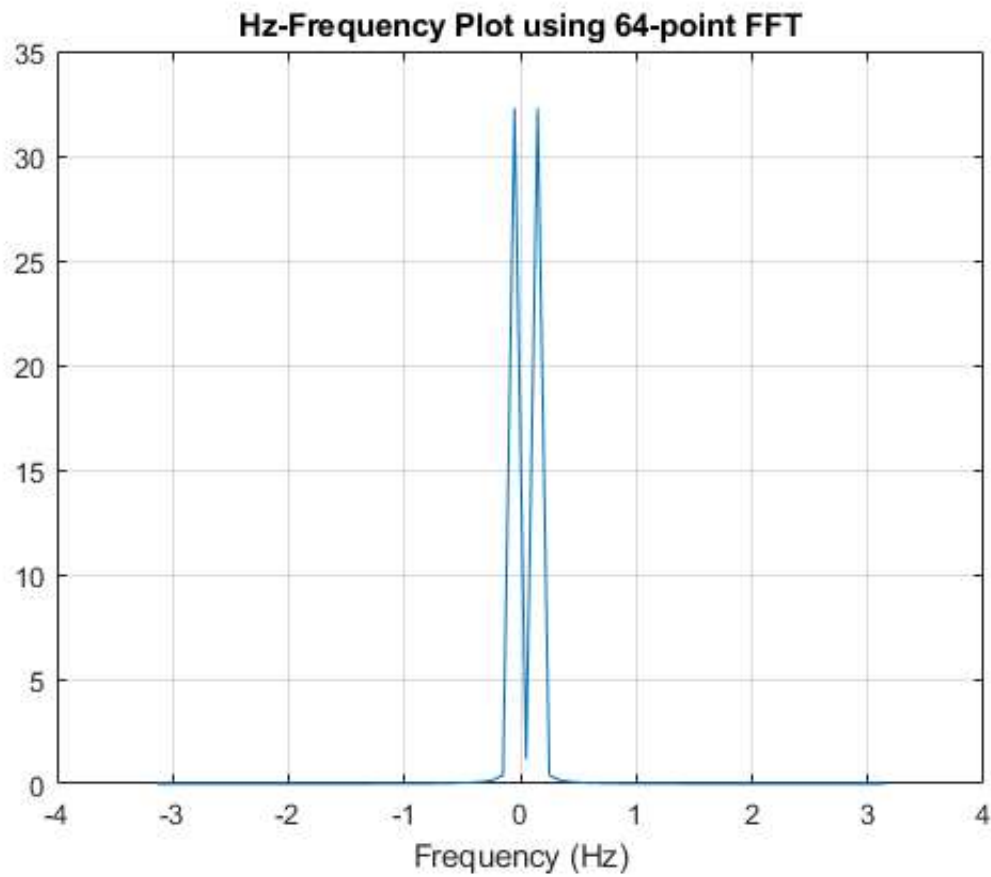
(6)

```

range = linspace(-pi, pi, N);
figure
plot(range, fft_x)
grid on
xlabel('Frequency (Hz)')
title(['Hz-Frequency Plot using ', num2str(N), '-point FFT'])

% frequency spikes @ -0.5484 & 0.6483

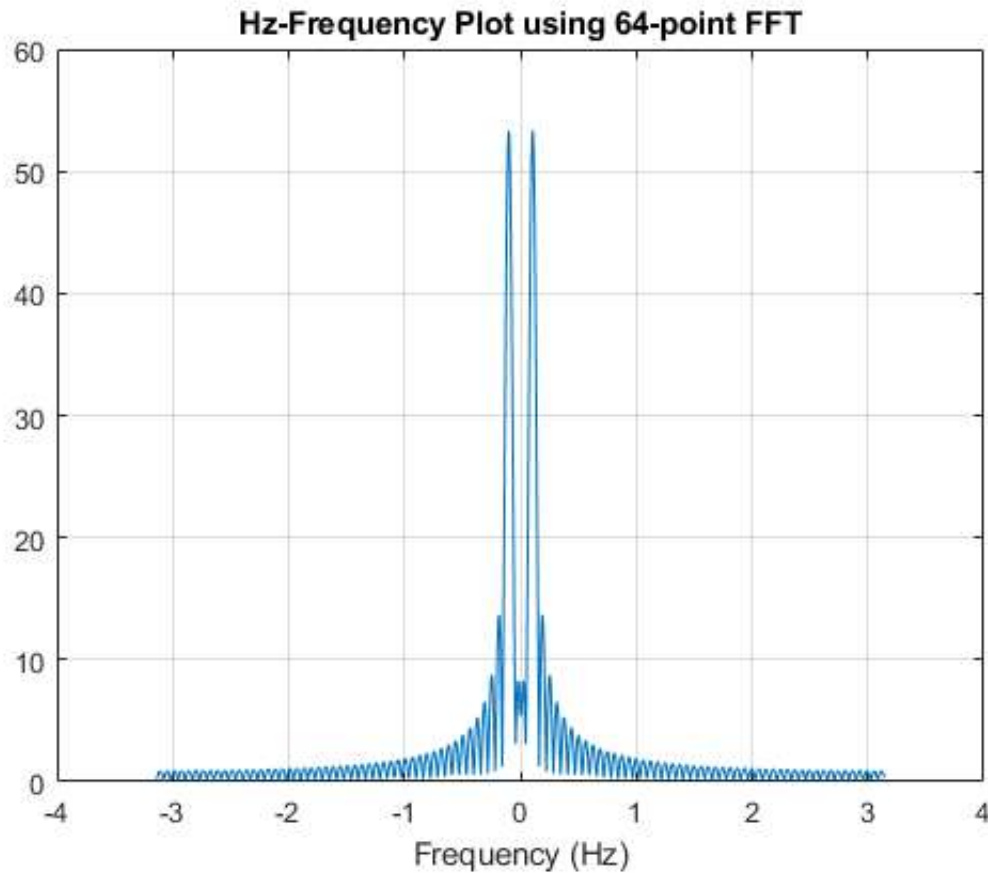
```



(8)

```
fft_x = abs(fftshift(fft(x, 1024)));    % 1024-point fft
range = linspace(-pi, pi, 1024);
figure
plot(range, fft_x)
grid on
xlabel('Frequency (Hz)')
title(['Hz-Frequency Plot using ', num2str(N), '-point FFT'])
[yy, xx] = findpeaks(fft_x);

% frequency spikes @ -0.6295 & 0.6357
```



### Lab 3.2.1 =====

```
clear; clc; close all

hbb = genbankread('hbb_region_chr11.gb'); % load *.gb file as a struct
cds_indices = hbb.CDS.indices; % get range of indices of CDS
```

(1)

There are 5 CDS regions in the sequence length(hbb.CDS)

(2)

The length of hbb.CDS(1).translation is 147 length(hbb.CDS(1).translation)

(3)

```
% use function "get_sequence_ft"
% function sequence_FT = get_sequence_ft(hbb, sequence_number)

N = 1024;

sequence1_ft = get_sequence_ft(hbb, 1, N);
sequence2_ft = get_sequence_ft(hbb, 2, N);
sequence3_ft = get_sequence_ft(hbb, 3, N);

figure
```

```

plot(sequence1_ft)
title('FFT of Coding Region: Sequence 1, from cds\_index 1 to index 2')
grid on

figure
plot(sequence2_ft)
title('FFT of Coding Region: Sequence 2, from cds\_index 3 to index 4')
grid on

figure
plot(sequence3_ft)
title('FFT of Coding Region: Sequence 3, from cds\_index 5 to index 6')
grid on

[y1, x1] = findpeaks(sequence1_ft);
[y2, x2] = findpeaks(sequence2_ft);
[y3, x3] = findpeaks(sequence3_ft);

%{
signal: sequence1
a = sort(y1);
b = sort(y2);
c = sort(y3);

x1(find(y1 == a([end])))
232.4562
frequency peaks @ 308 & 690
=====
x2(find(y2 == b([end])))
251.8894
frequency peaks @ 292 & 706

x2(find(y2 == b([end-2])))
224.3544
frequency peaks @ 92 & 906

x2(find(y2 == b([end-4])))
209.4380
frequency peaks @ 329 & 669
=====
x3(find(y3 == c([end])))
165.9027
frequency peaks @ 328 & 670

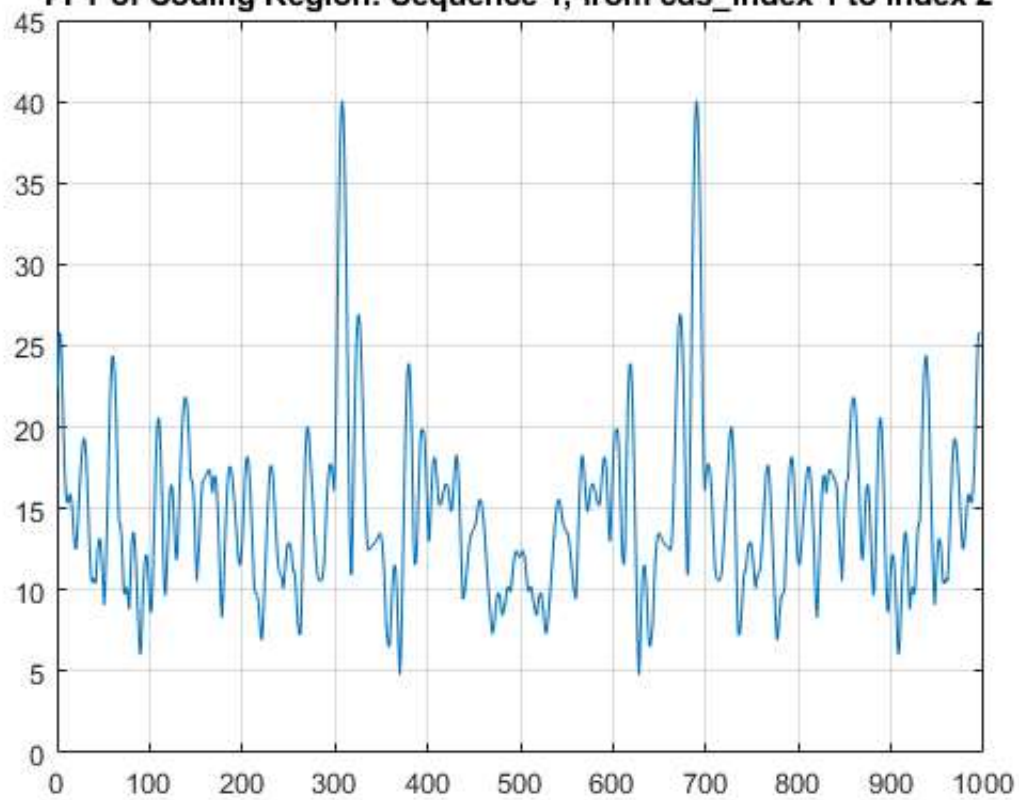
x3(find(y3 == c([end-2])))
142.8912
frequency peaks @ 164 & 834

x3(find(y3 == c([end-4])))
126.3875
frequency peaks @ 230 & 768

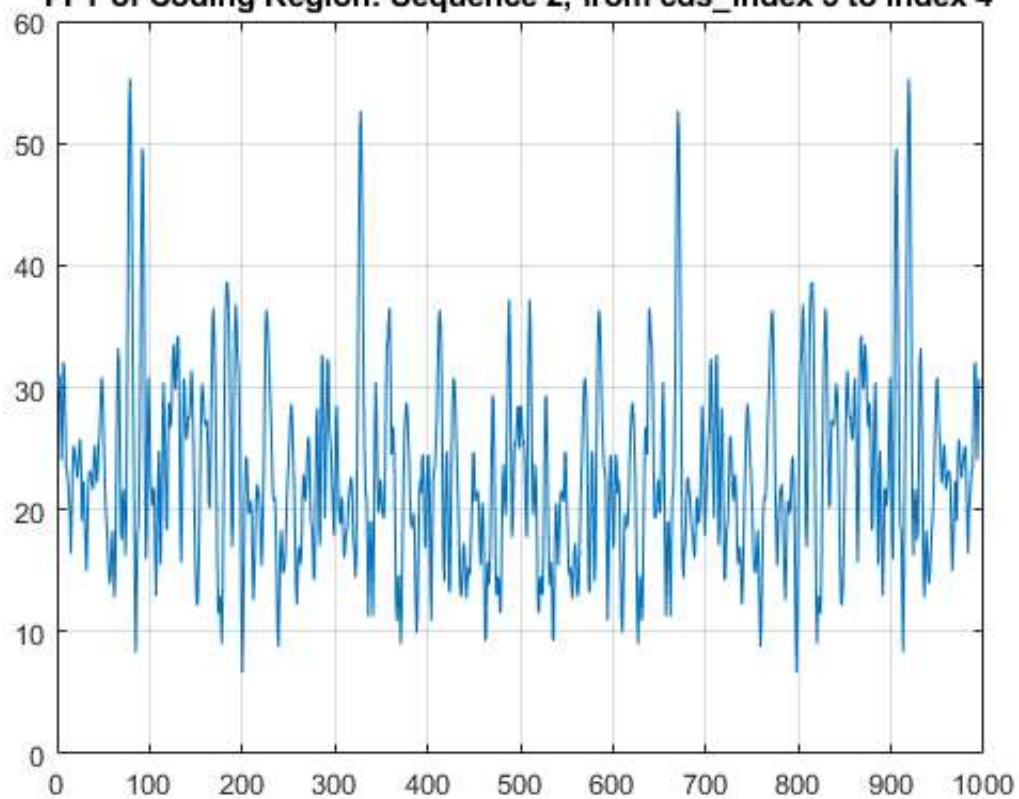
%}

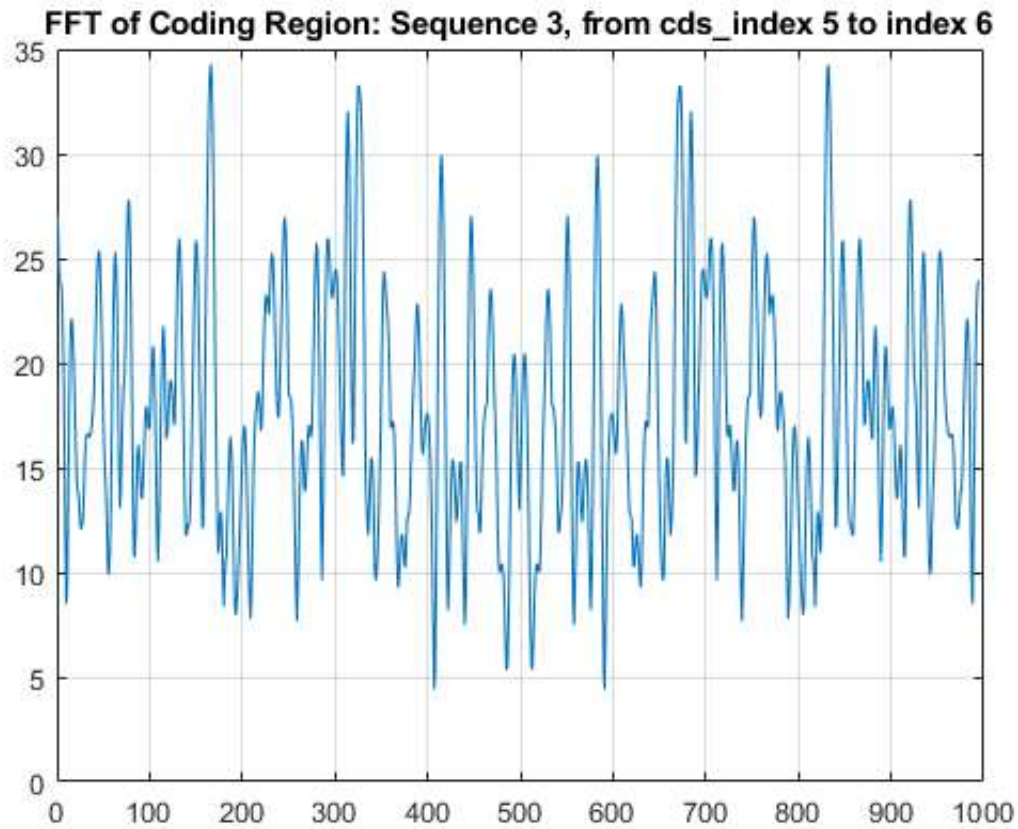
```

**FFT of Coding Region: Sequence 1, from cds\_index 1 to index 2**



**FFT of Coding Region: Sequence 2, from cds\_index 3 to index 4**





### 3.2.3 =====

---

N = 1024;

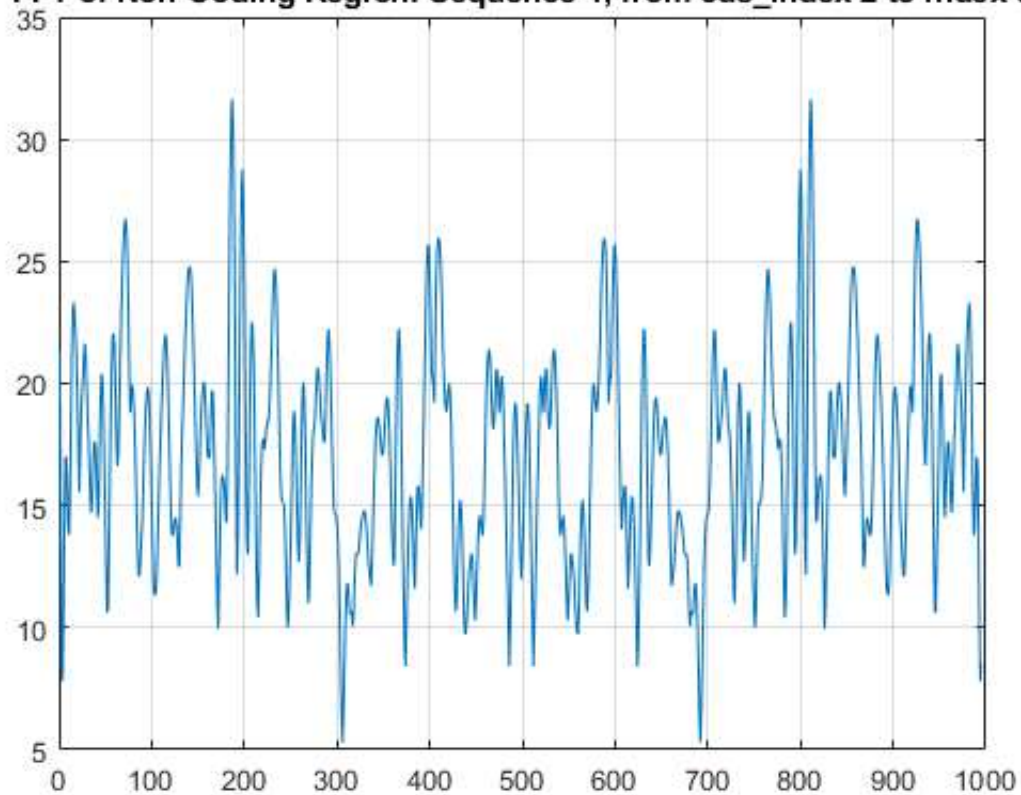
```
sequence1a_ft = get_sequence_ft(hbb, '1a', N);
sequence2a_ft = get_sequence_ft(hbb, '2a', N);

figure
plot(sequence1a_ft)
title('FFT of Non-Coding Region: Sequence 1, from cds\_index 2 to index 3')
grid on

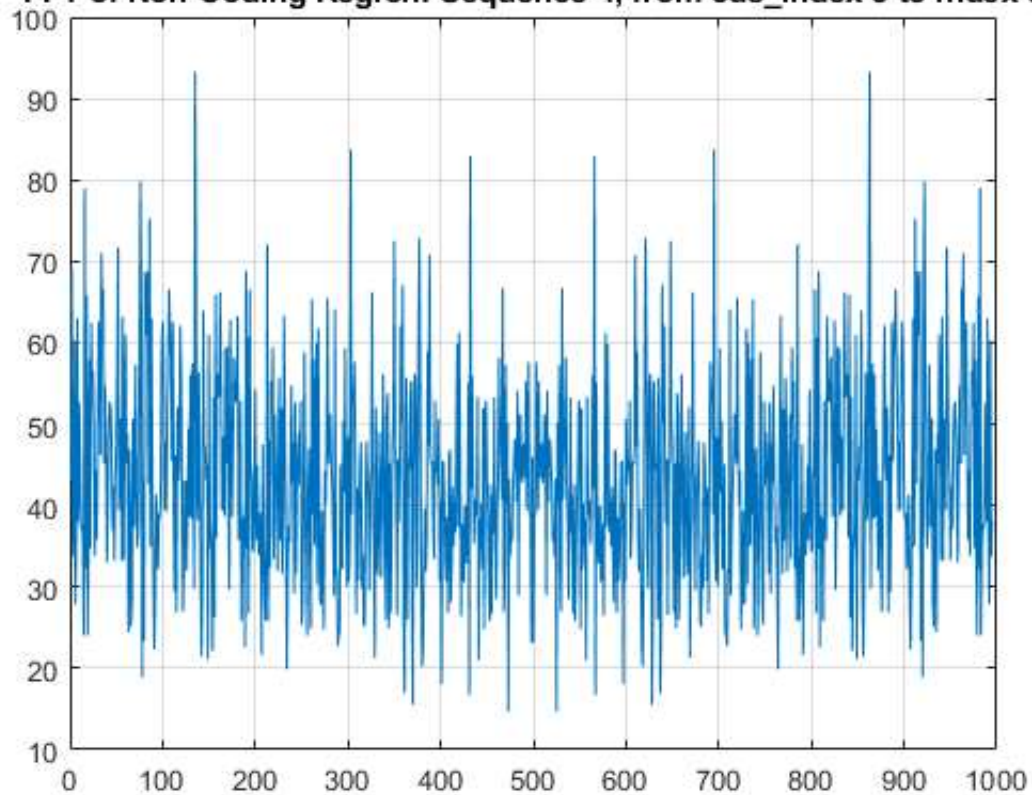
figure
plot(sequence2a_ft)
title('FFT of Non-Coding Region: Sequence 4, from cds\_index 3 to index 5')
grid on
```



**FFT of Non-Coding Region: Sequence 1, from cds\_index 2 to index 3**



**FFT of Non-Coding Region: Sequence 4, from cds\_index 3 to index 5**



```
DNA_SEQUENCE = hbb.Sequence;  
WINDOW_LENGTH = 10;  
NFFT = 1024;  
  
% DNA_SEQUENCE = hbb.Sequence;  
% WINDOW_LENGTH = 1000;  
% NFFT = 1024;  
  
output = threebasefreq_stft(DNA_SEQUENCE, WINDOW_LENGTH, NFFT);  
plot(output)
```

