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ECES T580 Lab 2 - Tyler Bradley

```
clc;close all;clear;
```

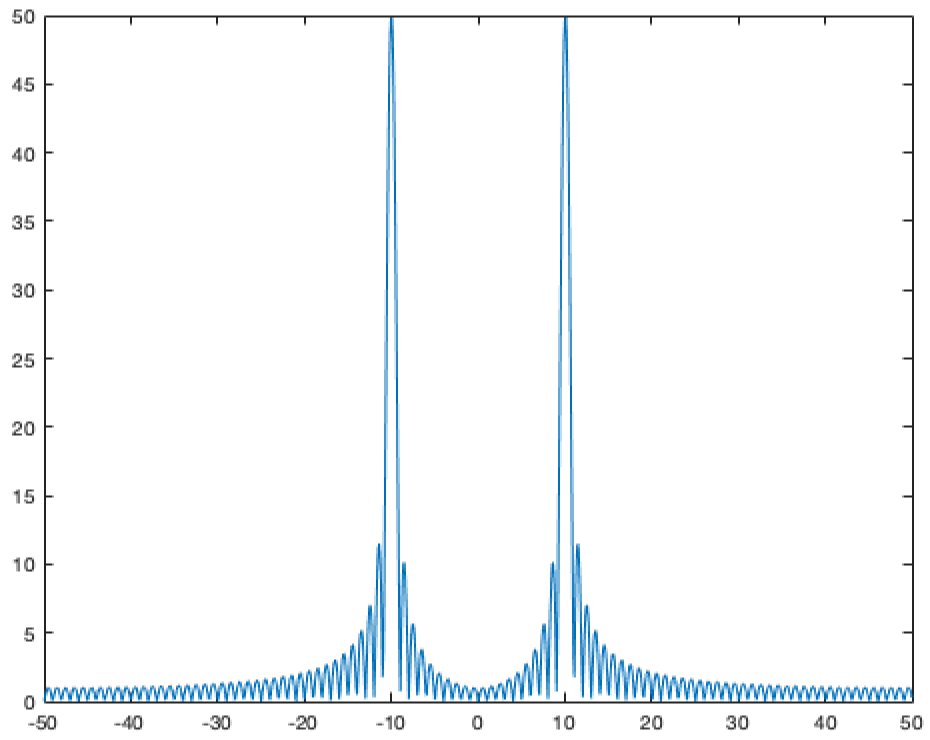
Lab 2.1.1

```
% 1. Enter hbb into the search - how many hits did you get?
% Performing this search resulted in thousands of results across
 multiple
% databases. There were 9,004 nucleotide, 1,561 genes, 11 genomes, and
% 8,678 proteins

% 2. Click on the nucleotide link. To the right (in the Top Organisms
 box),
% they suggest the human,mouse, chimpanzee, etc. HBB genes
% 3. Type hbb AND human[orgn] into the search. Now how many hits do
 you get?
% Note: the AND has to be capitalized. The human[orgn] means that you?
re
% narrowing your search just to humans.
% There are 280 nucleotide results when typing in hbb AND human [ORGN]

% 4. Click on the HBB (Homo sapiens): hemoglobin, beta in the Gene
 search
% (you can also use the link: http://www.ncbi.nlm.nih.gov/gene/3043).
% Explore this record.
% 5. Search for hbb AND human[orgn] AND RefSeqGene in the Nucleotide
 search.
% (this should lead you to http://www.ncbi.nlm.nih.gov/
nuccore/28380636)
% 6. We will actually be obtaining the whole region and doing analysis
 on
% the 81,706 bp linear DNA.
```

Lab 2.1.2: FFT review: linspace, Fs, fftshift, NFFT:

1. Generate one second of a cosine of ?s = 10Hz sampled at Fs = 100Hz and assign it to x. Define a tt as your time axis.

```
Fs = 100;
T = 1/Fs;
t = (0:Fs-1)*T;

x = cos(2*pi*10*t);

plot(t, x)
xlim([0, 1])
xlabel('time (sec)')


% 2. Take 64 points FFT.
fft_64 = fft(x, 64);
abs_Y = abs(fft_64);

% 3. As you remember, the DFT (which the FFT implements) computes N
 samples
% of ?k = 2?(k/N)
% where k = 0, 1, 2, 3, ..., N ? 1. Plot the magnitude of this 64-
points FFT at range 0 to 63, what do
% you think of this graph?
plot(0:63, abs_Y)
% The peaks of the graph appear to be where the wavelength of the
 cosine
% located

% 4. To get the x-axis into a Hz-frequency form, plot this 64-points
 FFT between ?50 to 50 (the 100Hz
% sampling rate) and have N-points between them.
x_lims = linspace(-50, 50, 64);
plot(x_lims, fftshift(abs_Y));

% 5. According to your figure, what frequency is this cosine wave at?
% Answer: The frequency of the cosine is 10Hz

% 6. Remember that the FFT is evaluating from 0 to 2?. We are used to
 viewing graphs from ?? to ?.
% Therefore, you need to shift your graph.
% This is done above in the graph from -50 to 50

% 7. Now according to your shifted graph. what frequency is this at?
% Answer: The frequency is 10 Hz

% 8. Note that the spikes have long drop-offs? Try a 1024-point DFT.
 Note that the peak is closer to
% 10 and the drop-off is quicker. Although, now sidelobes are an
 issue.
fft_1024 = fft(x, 1024);
abs_fft_1024 = abs(fft_1024);

x_lims = linspace(-50, 50, 1024);
plot(x_lims, fftshift(abs_fft_1024));
```



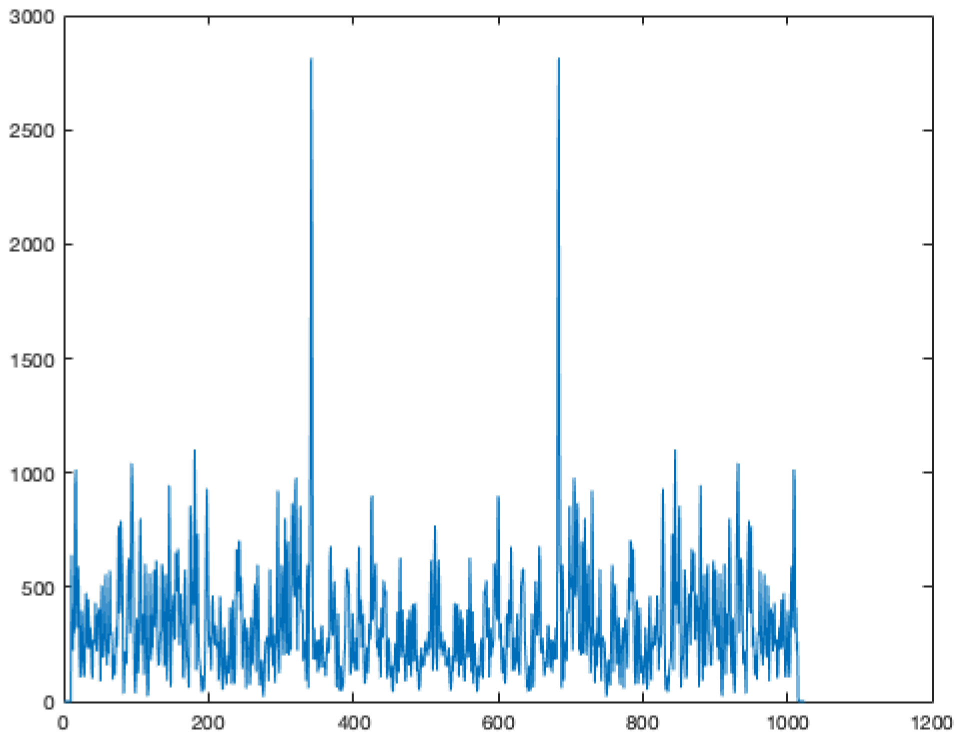
Lab 2.2.1

```
hbb = getgenbank("NG_000007.3");

% 1. How many CDS regions are there in this sequence? (A CDS sequence
 is a coding sequence that
% results in a protein product).
CDS = hbb.CDS;

% There are 5 CDS regions in this sequence

% 2. Look at hbb.CDS(1), what is the length of this region? How would
 you identify the coding and
% non-coding sequences for this hbb.CDS(1) region on Chromosome 11?
CDS(1);

% length of the region
CDS(1).indices(6) - CDS(1).indices(1)

% The coding regions are determined by looking at the sequence between
 the
% odd and even indices, while the non-coding regions is the portion
 between
% the odd indices + 1 and the even indices - 1
% CDS(1) first coding region:
```

```
hbb.Sequence(CDS(1).indices(1):CDS(1).indices(2));

% CDS(1) first non-coding region:
hbb.Sequence((CDS(1).indices(2)+1):(CDS(1).indices(3)-1));


% 3. Write a function that will take a sequence and CDS indices as
 input and outputs the corresponding
% coding and non-coding DNA sequences
% The code for get_coding function is at the bottom of this script
cds1_regions = get_coding(hbb.Sequence, CDS(1).indices);

Warning: The record NG_000007.3 has been replaced by NG_000007.
Returning record 28380636.

ans =

        1421
```

Lab 2.2.2

```
coding = strjoin(cds1_regions.coding, "");

% This does not work
% coding_A = (upper(coding)=='A');

% so I wrote a function is_base to do this
% The code for this function can be found at the bottom of this file
coding_A = is_base(coding.char, "a");
coding_T = is_base(coding.char, "t");
coding_C = is_base(coding.char, "c");
coding_G = is_base(coding.char, "g");

% calculating the fft for the sequence
coding_FT = abs(fft(coding_A, 1024)).^2 + abs(fft(coding_T, 1024)).^2
 + abs(fft(coding_C, 1024)).^2 + abs(fft(coding_G, 1024)).^2;

% Set the first ten and last ten elements to zero so they do not weigh
% down the plot
coding_FT(1:10) = repelem(0, 10);
coding_FT(1015:1024) = repelem(0,10);
figure(1)
plot(coding_FT)

nfft_coding_3 = coding_FT(round(1024/3));
```

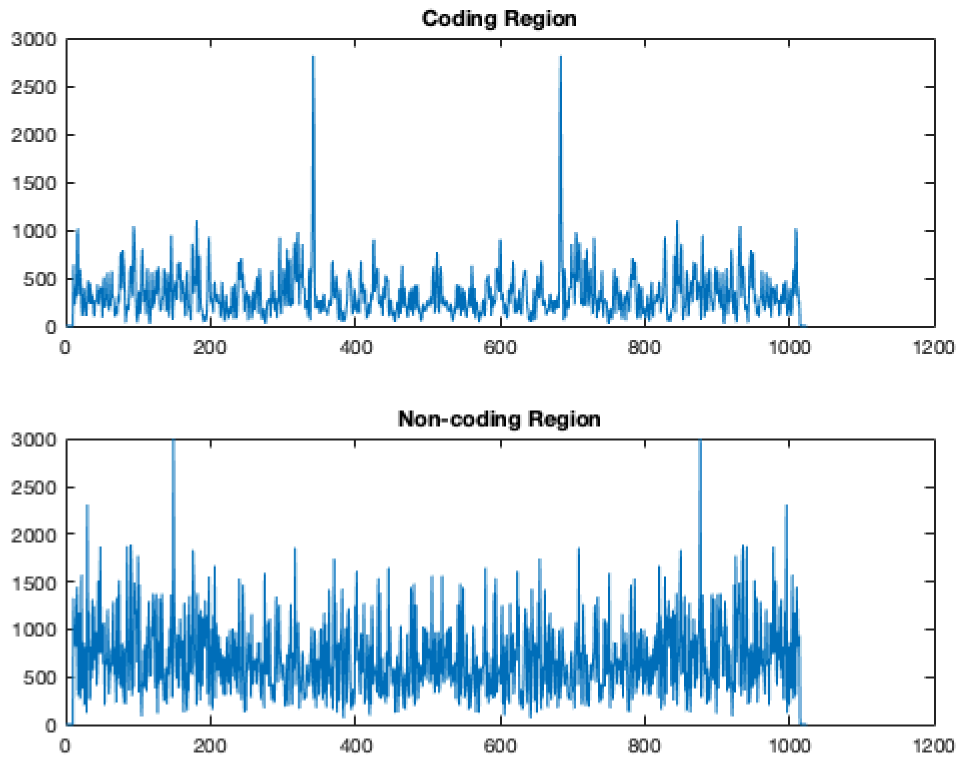


Lab 2.2.3

Now, compute the magnitude spectrum of the noncoding sequence (use the same NFFT value as above)? what does it look like? What is the magnitude of the NFFT/3 point compared to the coding sequence? Show your two plots, explain the peaks to your instructor, and the difference between coding and noncoding regions.

```
non_coding = strjoin(cds1_regions.non_coding, "");

non_coding_a = is_base(non_coding.char, "a");
non_coding_t = is_base(non_coding.char, "t");
non_coding_g = is_base(non_coding.char, "g");
non_coding_c = is_base(non_coding.char, "c");

non_coding_FT = abs(fft(non_coding_a, 1024)).^2 +
 abs(fft(non_coding_t, 1024)).^2 + ...
abs(fft(non_coding_c, 1024)).^2 + abs(fft(non_coding_g, 1024)).^2;

nfft_3 = non_coding_FT(round(1024/3));

% Set the first ten and last ten elements to zero so they do not weigh
% down the plot
non_coding_FT(1:10) = repelem(0, 10);
non_coding_FT(1015:1024) = repelem(0,10);

subplot(2, 1, 1)
```

```
plot(coding_FT)
title("Coding Region")

subplot(2, 1, 2)
plot(non_coding_FT)
title("Non-coding Region")

% The non coding regions seems to have very minor peaks every 200
 bases but
% no clear spikes at NFFT/3. Conversly, the coding region has clear
 peaks
% at the NFFT/3 and 2*NFFT/3 positions.
```



Functions for the Lab

This function corresponds to Lab 2.2.1 #3 and returns the coding and non-coding regions of the input sequence in a struct object with coding and non_coding character arrays

```
function output = get_coding(seq, indices)
num_indices = length(indices);
coding = repelem("a", num_indices/2);
non_coding = repelem("a", (num_indices/2)-1);
n_code = 1;
n_non_code = 1;
for i = 1:num_indices-1
    if mod(i,2) == 1
```

```
        coding(n_code) = seq(indices(i):indices(i+1));
        n_code = n_code + 1;
    else
        non_coding(n_non_code) = seq(indices(i)+1:indices(i+1)-1);
        n_non_code = n_non_code+1;
    end
end

output.coding = coding;
output.non_coding = non_coding;
end

% This function is for Lab 2.2.2 and 2.2.3
% It takes the character string and looks at each of the bases and
% determines if it matches the specified base
function output = is_base(seq, base)
seq_length = length(seq);
out_binary = repelem(0, seq_length);

for i = 1:seq_length
    if seq(i) == base
        out_binary(i) = 1;
    else
        out_binary(i) = 0;
    end
end
output = out_binary;
end

% 1. Assume that the windows have full overlap meaning that each
 window of WINDOW_LENGTH
% overlaps by WINDOW_LENGTH ? 1 data points:
% 2. DNA_SEQUENCE is the DNA sequence of letters (before the binary
 indicator operation).
% 3. NFFT is the number of points to take in the Fourier transform.
% 4. The output will give you the magnitude of the N/3
% point for each position (or consecutive window) in the sequence.
function output = threebasefreq_stft(seq, window_length, nfft)
% calculate the sequence length
seq_length = length(seq);

% create a vector that is preallocated to the length of the expected
 output
fft_vec = repelem(0, seq_length-window_length);
for i = 1:seq_length-window_length
    % create a sub sequence
    sub_seq = seq(i:i+window_length);

    % calculate the u[base] for each of the bases
    sub_a = is_base(sub_seq, "a");
    sub_t = is_base(sub_seq, "t");
    sub_c = is_base(sub_seq, "c");
    sub_g = is_base(sub_seq, "g");
    % calculate the fft
    sub_ft = abs(fft(sub_a, nfft)).^2 + abs(fft(sub_t, nfft)).^2 + ...
abs(fft(sub_c, nfft)).^2 + abs(fft(sub_g, nfft)).^2;

    % find the nfft/3
    nfft_3 = sub_ft(round(nfft/3));
    % square the result to make the effect more clear and put it into
 the
    % output vector
    fft_vec(i) = nfft_3^2;
end
% assign the output vector
output = fft_vec;
end
```

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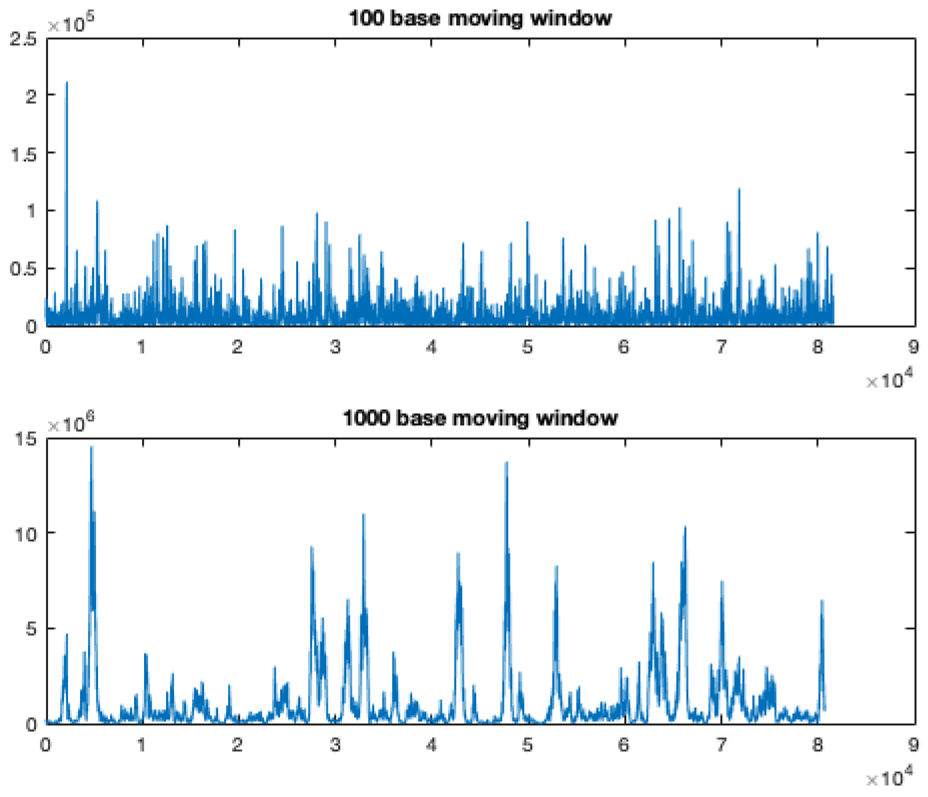
Lab 2.3.1

```
clc;close all;clear;
hbb = getgenbank("NG_000007.3");

% 1. Make a function called threebasefreq_stft.m that can be called
 like this:
% Threebaseperiodicity_vs_position = threebasefreq_stft (DNA_SEQUENCE,
 WINDOW_LENGTH, NFFT)
% see "Functions for the Lab" section

% 2. After you implement your function, test it on the whole 81,706 bp
 sequence of the HBB gene. Show
% two plots of the results (similar to the figure in Hint 5 ) by using
 a) threebasefreq_stft(seq,100,1024)
% and b) threebasefreq_stft(seq,1000,1024).
threebase_100 = threebasefreq_stft(hbb.Sequence, 100, 1024);
threebase_1000 = threebasefreq_stft(hbb.Sequence, 1000, 1024);

subplot(2, 1, 1);
plot(threebase_100);
title("100 base moving window");

subplot(2, 1, 2);
plot(threebase_1000);
title("1000 base moving window");

% 3. Compare and contrast your results. Include all Matlab codes in
 your report.
% Looking at the output from the two moving window periods shows some
% differing results. The results using a 100 base moving window does
 not
% show any clear pattern that centers around the expected exon
 positions
% for this gene. However, the results from the 1000 base moving window
% showed expected trends around the exon positions for the hbb gene.
 There
% were a few positions that showed elevated
```

```
Warning: The record NG_000007.3 has been replaced by NG_000007.
Returning record 28380636.
```



Functions for the Lab

This function corresponds to Lab 2.2.1 #3 and returns the coding and non-coding regions of the input sequence in a struct object with coding and non_coding character arrays

```
function output = get_coding(seq, indices)
num_indices = length(indices);
coding = repelem("a", num_indices/2);
non_coding = repelem("a", (num_indices/2)-1);
n_code = 1;
n_non_code = 1;
for i = 1:num_indices-1
    if mod(i,2) == 1
        coding(n_code) = seq(indices(i):indices(i+1));
        n_code = n_code + 1;
    else
        non_coding(n_non_code) = seq(indices(i)+1:indices(i+1)-1);
        n_non_code = n_non_code+1;
    end
end

output.coding = coding;
output.non_coding = non_coding;
end

% This function is for Lab 2.2.2 and 2.2.3
% It takes the character string and looks at each of the bases and
% determines if it matches the specified base
function output = is_base(seq, base)
seq_length = length(seq);
out_binary = repelem(0, seq_length);

for i = 1:seq_length
    if seq(i) == base
        out_binary(i) = 1;
    else
        out_binary(i) = 0;
    end
end
output = out_binary;
end

% 1. Assume that the windows have full overlap meaning that each
 window of WINDOW_LENGTH
% overlaps by WINDOW_LENGTH ? 1 data points:
% 2. DNA_SEQUENCE is the DNA sequence of letters (before the binary
 indicator operation).
% 3. NFFT is the number of points to take in the Fourier transform.
% 4. The output will give you the magnitude of the N/3
% point for each position (or consecutive window) in the sequence.
function output = threebasefreq_stft(seq, window_length, nfft)
% calculate the sequence length
seq_length = length(seq);

% create a vector that is preallocated to the length of the expected
 output
fft_vec = repelem(0, seq_length-window_length);
for i = 1:seq_length-window_length
    % create a sub sequence
    sub_seq = seq(i:i+window_length);

    % calculate the u[base] for each of the bases
    sub_a = is_base(sub_seq, "a");
    sub_t = is_base(sub_seq, "t");
    sub_c = is_base(sub_seq, "c");
    sub_g = is_base(sub_seq, "g");

    % calculate the fft
    sub_ft = abs(fft(sub_a, nfft)).^2 + abs(fft(sub_t, nfft)).^2 + ...
abs(fft(sub_c, nfft)).^2 + abs(fft(sub_g, nfft)).^2;

    % find the nfft/3
    nfft_3 = sub_ft(round(nfft/3));
    % square the result to make the effect more clear and put it into
 the
    % output vector
    fft_vec(i) = nfft_3^2;
end
% assign the output vector
output = fft_vec;
```

```
end
```

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