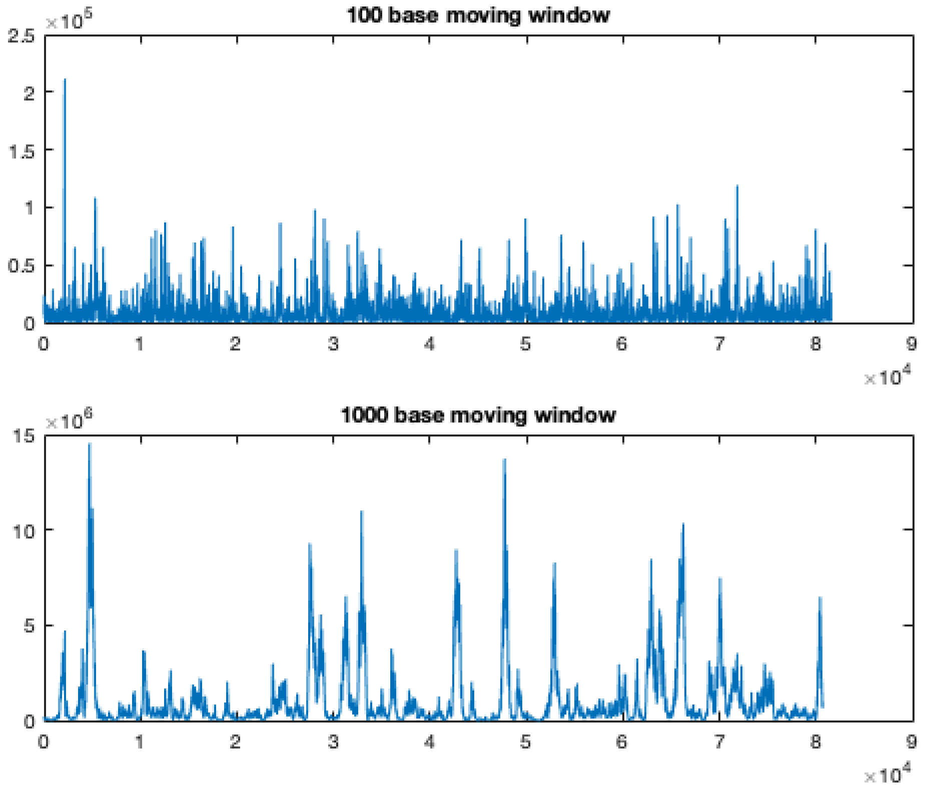
# Lab 2.3.1

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Warning: The record NG_000007.3 has been replaced by NG_000007.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