

```

clc;
close all;
clear;

```

Retrieve sequence information from GenBank database

```

getgenbank('nm_000520','toFile','nm_000520.txt');
% load in Matlab
s = genbankread('nm_000520.txt');
% Load Sequence only
seq = getgenbank('nm_000520','SequenceOnly',true)

```

seq =

```

' TCACATCACAACGACTTGTGGTTTAAATCCTCCGTTTTTCTGCTTCTGAAGTTACTTCAGCCTGGCAAGTCTTTACCTCCCCGTAGGCCTGGCGAGCTG
CATCACAACATTCAAGATTACCCCTAGAGCCATCTGGGAAACTTCTTCTCCAGGTCGCCCTGCGTCTCGCTCCCCACCCCGTTCTTCTCGAGTCGGGTGAGC
TGTCTAGTTCCATCACGGCCGCGACGGCCGACGGGGTGGCCGGTTATTTACTGCTCTACTGGGCCCCGTGAACAGTCTGGCGAGCCGAGCAGTTGCCGACGCCCGG
CACAATCCGCTGCACGTAGCAGGAGCCTCAGGTCCAGGCCGGAAGTGAAAGGGCAGGGTGTGGGTCTCTGGGGTGCAGGCGCAGAGCCGCTCTGGTCACGT
GATTCGCCGATAAGTACGGGGGCGCCGCTCACCTGACCAGGGTCTCAGTGGCCAGCCCCCTCCGAGAGGGGAGACCAGCGGGCCATGACAAGCTCCAGGCTTT
GGTTTTTCGTGCTGCTGGCGGCAGCGTTCGACGAGCGGGCGACGGCCCTCTGGCCCTGGCCTCAGAACTTCCAACCTCCGACCAGCGCTACGTCCTTTACCCGA
ACAACTTTCAATTCCAGTACGATGTCAGCTCGGCCGCGCAGCCCGGCTGCTCAGTCCTCGACGAGGCCCTCCAGCGCTATCGTGACCTGCTTTTCGGTTCCGGGT
CTTGGCCCCGTCCTTACCTCACAGGGAACGGCATACTGGAGAAGAATGTGTGGTTGTCTCTGTAGTCACACCTGGATGTAACCAGCTTCTACTTTGGAGT
CAGTGGAGAATTATACCCTGACCATAAATGATGACCAGTGTTTACTCCTCTCTGAGACTGTCTGGGGAGCTCTCCGAGGTCTGGAGACTTTTAGCCAGCTTGTTT
GGAAATCTGCTGAGGGCACATTCTTTATCAACAAGACTGAGATTGAGGACTTTCCCGCTTTCCTCACCAGGGGCTTGCTGTTGGATACATCTCGCCATTACCTGC
CACTCTCTAGCATCTGGACACTCTGGATGTCATGGCGTACAATAAATTGAACGTGTTCCACTGGCATCTGGTAGATGATCCTTCCCTCCCATATGAGAGCTTCA
CTTTTCCAGAGCTCATGAGAAAGGGTCCCTACAACCTGTCAACCACATCTACACAGCACAGGATGTGAAGGAGGTCATTGAATACGCACGGCTCCGGGGTATCC
GTGTGCTTGCAGAGTTTGACACTCCTGGCCACACTTTTGTCTGGGGACAGGTATCCCTGGATTACTGACTCCTTGCTACTCTGGGTCTGAGCCCTCTGGCACCT
TTGGACCAAGTGAATCCAGTCTCAATAATACCTATGAGTTCATGAGCACATTCTTCTTAGAAGTCAGCTCTGTCTTCCAGATTTTTATCTTCATCTTGGAGGAG
ATGAGGTTGATTTCACCTGCTGGAAGTCCAACCCAGAGATCCAGGACTTTATGAGGAAGAAAGGCTTCGGTGAGGACTTCAAGCAGCTGGAGTCTTCTACATCC
AGACGCTGCTGGACATCGTCTCTTCTTATGGCAAGGGCTATGTGGTGTGGCAGGAGGTGTTGATAATAAAGTAAAGATTAGCCAGACACAATCATAAGGTGT
GGCGAGAGGATATTCCAGTGAATATATGAAGGAGCTGGAACCTGGTCACCAAGGCCGGCTTCCGGGCCCTTCTCTCTGCCCCCTGGTACCTGAACCGTATATCCT
ATGGCCCTGACTGGAAGGATTTCTACATAGTGAACCCCTGGCATTGGAAGGTACCCCTGAGCAGAAGGCTCTGGTGATTGGTGGAGAGGCTTGATGTGGGGAG
AATATGTGGACAACACAACCTGGTCCCCAGGCTCTGGCCCAGAGCAGGGGCTGTTGCCGAAAGGCTGTGGAGCAACAAGTTGACATCTGACCTGACATTTGCCT
ATGAACGTTTTGTACACTTCCGCTGTGAATTGCTGAGGCGAGGTGTCCAGGCCCAACCCCTCAATGTAGGCTTCTGTGAGCAGGAGTTGAACAGACCTGAGCCC
CAGGCACCGAGGAGGGTGCTGGCTGTAGGTGAATGGTAGTGAGGCCAGGCTTCCACTGCATCCTGGCCAGGGGACGGAGCCCTTGCTTTCGTCGCCCTTGCTG
CGTGCCCCCTGTGCTTGGAGAGAAAGGGGCCGGTGCTGGCGCTCGCATCAATAAAGAGTAATGTGGCATTTTTCTATAATAAACATGGATTACCTGTGTTAAAA
AAAAAGTGTGAATGGCGTTAGGGTAAGGGCACAGCCAGGCTGGAGTCAGTGTCTGCCCCCTGAGGTCTTTTAAGTTGAGGGCTGGGAATGAAACCTATAGCCTTT
GTGCTGTTCTGCCTTGCTGTGAGCTATGTCACTCCCTCCCTCCTGACCATATCCAGACACCTGCCCTAATCCTCAGCCTGCTCACTTCACTTCTGCATTA
TATCTCCAAGCGTTGGTATATGGAAAAAGATGTAGGGGCTTGAGGTGTTCTGGACAGTGGGGAGGGCTCCAGACCCAACCTGGTCACAGAAGAGCCTCTCCCC
CATGCATACTCATCCACCTCCCTCCCTAGAGCTATTCTCCTTTGGGTTTCTTGCTGCTTCAATTTTATACAACCATTATTTAAATATTATTAAACACATATTGT
TCTCTAGGAAAAAAAAAAAAAAAAAAAAA '
```

Format long sequence output for easy viewing

```

seqdisp(s.Sequence)
% Count nucleotides in sequence
[seq_counts] = basecount(s.Sequence)% Plot density of nucleotides along sequence
figure(1)
seq_density = ntdensity(s.Sequence)
% Count dimers in nucleotide sequence
figure(2)
[Dimers, Percent] = dimercount(s.Sequence, 'chart', 'pie')
% Count 3-mer in nucleotide sequence
trimer = nmercount(s.Sequence,3)

```

ans =

46×71 char array

```

' 1 TCACATCACA ACGACTTGTG GTTTTAATCC TCCGTTTTTC TGCTTCTGAA GTTACTTCAG'
' 61 CCTGGCAAGT CCTTTACCTC CCCGTAGGCC TGGCGAGCTG CATCACAACA TTCAAGATTTC'
```

```
' 121 ACCCTAGAGC CATCTGGGAA ACTTCTTCT CCAGGTCGCC CTGCGTCCTC GCCTCCCCAC'
' 181 CCCGTTCTTC TCGAGTCGGG TGAGCTGTCT AGTTCCATCA CGGCCGGCAC GGCCGCAGGG'
' 241 GTGGCCGGTT ATTTACTGCT CTACTGGGCC CGTGAACAGT CTGGCGAGCC GAGCAGTTGC'
' 301 CGACGCCCCG CACAATCCGC TGCACGTAGC AGGAGCCTCA GGTCCAGGCC GGAAGTGAAA'
' 361 GGGCAGGGTG TGGGTCTCCT TGGGGTCGCA GGCGCAGAGC CGCCTCTGGT CACGTGATTC'
' 421 GCCGATAAGT CACGGGGGCG CCGCTCACCT GACCAGGGTC TCACGTGGCC AGCCCCCTCC'
' 481 GAGAGGGGAG ACCAGCGGGC CATGACAAGC TCCAGGCTTT GGTTTTCGCT GCTGCTGGCG'
' 541 GCAGCGTTTC CAGGACGGGC GACGGCCCTC TGGCCCTGGC CTCAGAACTT CCAAACCTCC'
' 601 GACCAGCGCT ACGTCCCTTA CCCGAACAAC TTTCAATTCC AGTACGATGT CAGCTCGGCC'
' 661 GCGCAGCCCG GCTGCTCAGT CCTCGACGAG GCCTTCCAGC GCTATCGTGA CCTGCTTTTC'
' 721 GGTTCCGGGT CTTGGCCCCG TCCTTACCTC ACAGGGAAAC GGCATACACT GGAGAAGAAT'
' 781 GTGTGGTTG TCTCTGTAGT CACACCTGGA TGTAACCAGC TTCCTACTTT GGAGTCAGTG'
' 841 GAGAATTATA CCCTGACCAT AAATGATGAC CAGTGTTTAC TCCTCTCTGA GACTGTCTGG'
' 901 GGAGCTCTCC GAGGCTCTGA GACTTTTAGC CAGCTGTGTT GGAAATCTGC TGAGGGCACA'
' 961 TTCTTTATCA ACAAGACTGA GATTGAGGAC TTTCCCGGCT TTCCTCACC GGGCTTGCTG'
'1021 TTGGATACAT CTCGCCATTA CCTGCCACTC TCTAGCATCC TGGACACTCT GGATGTCATG'
'1081 GCGTACAATA AATTGAACGT GTTCCACTGG CATCTGGTAG ATGATCCTTC CTTCCCATAT'
'1141 GAGAGCTTCA CTTTTCCAGA GCTCATGAGA AAGGGGTCTT ACAACCCTGT CACCCACATC'
'1201 TACACAGCAC AGGATGTGAA GGAGGTCATT GAATACGCAC GGCTCCGGGG TATCCGTGTG'
'1261 CTTGCAGAGT TTGACACTCC TGGCCACACT TTGTCTGGG GACCAGGTAT CCCTGGATTA'
'1321 CTGACTCCTT GCTACTCTGG GTCTGAGCCC TCTGGCACCT TTGGACCACT GAATCCAGT'
'1381 CTCAATAATA CCTATGAGTT CATGAGCACA TTCTTCTTAG AAGTCAGCTC TGTCTTCCCA'
'1441 GATTTTATC TTCATCTTGG AGGAGATGAG GTTGATTTCA CCTGCTGGAA GTCCAACCCA'
'1501 GAGATCCAGG ACTTTATGAG GAAGAAAGGC TTCGGTGAGG ACTTCAAGCA GCTGGAGTCC'
'1561 TTCTACATCC AGACGCTGCT GGACATCGTC TCTTCTTATG GCAAGGGCTA TGTGGTGTGG'
'1621 CAGGAGGTGT TTGATAATAA AGTAAAGATT CAGCCAGACA CAATCATACA GGTGTGGCGA'
'1681 GAGGATATTC CAGTGAAC TAATGAAGGAG CTGGAAGTGG TCACCAAGGC CGGCTTCCGG'
'1741 GCCCTTCTCT CTGCCCCCTG GTACCTGAAC CGTATATCCT ATGGCCCTGA CTGGAAGGAT'
'1801 TTCTACATAG TGGAACCCCT GGCATTTGAA GGTACCCCTG AGCAGAAGGC TCTGGTGATT'
'1861 GGTGGAGAGG CTTGTATGTG GGGAGAATAT GTGGACAACA CAAACCTGGT CCCCAGGCTC'
'1921 TGGCCAGAG CAGGGGCTGT TGCCGAAAGG CTGTGGAGCA ACAAGTTGAC ATCTGACCTG'
'1981 ACATTTGCCT ATGAACGTTT GTCACACTTC CGCTGTGAAT TGCTGAGGCG AGGTGTCCAG'
'2041 GCCCAACCCC TCAATGTAGG CTTCTGTGAG CAGGAGTTTG AACAGACCTG AGCCCCAGGC'
'2101 ACCGAGGAGG GTGCTGGCTG TAGGTGAATG GTAGTGGAGC CAGGCTTCCA CTGCATCCTG'
'2161 GCCAGGGGAC GGAGCCCCTT GCCTTCGTGC CCCTTGCCTG CGTGCCCTG TGCTTGGAGA'
'2221 GAAAGGGGCC GGTGCTGGCG CTCGCATTCA ATAAAGAGTA ATGTGGCATT TTTCTATAAT'
'2281 AAACATGGAT TACCTGTGTT TAAAAAAGG AGTGTGAATG GCGTTAGGGT AAGGGCACAG'
'2341 CCAGGCTGGA GTCAGTGTCT GCCCCGAGG TCTTTTAAGT TGAGGGCTGG GAATGAAACC'
'2401 TATAGCCTTT GTGCTGTTCT GCCTTGCCCTG TGAGCTATGT CACTCCCCTC CCACTCCTGA'
'2461 CCAATATTCCA GACACCTGCC CTAATCCTCA GCCTGCTCAC TTCACTTCTG CATTATATCT'
'2521 CCAAGGCGTT GGTATATGGA AAAAGATGTA GGGGCTTGG GGTGTCTGG ACAGTGGGGA'
'2581 GGGCTCCAGA CCAACCTGG TCACAGAAGA GCCTCTCCCC CATGCATACT CATCCACCTC'
'2641 CCTCCCTAG AGCTATTCTC CTTTGGGTTT CTTGCTGCTT CAATTTTATA CAACCATTAT'
'2701 TTAAATATTA TTAAACACAT ATTGTCTCTT AGGAAAAAAA AAAAAAAAAA A'
```

```
seq_counts =
```

```
struct with fields:
```

```
A: 593
C: 750
G: 716
T: 692
```

```
seq_density =
```

```
struct with fields:
```

```
A: [1×2751 double]
C: [1×2751 double]
G: [1×2751 double]
T: [1×2751 double]
```

```
Dimers =
```

```
struct with fields:
```

AA: 137
AC: 145
AG: 185
AT: 125
CA: 184
CC: 235
CG: 90
CT: 241
GA: 171
GC: 178
GG: 220
GT: 147
TA: 101
TC: 192
TG: 221
TT: 178

Percent =

0.0498	0.0527	0.0673	0.0455
0.0669	0.0855	0.0327	0.0876
0.0622	0.0647	0.0800	0.0535
0.0367	0.0698	0.0804	0.0647

trimer =

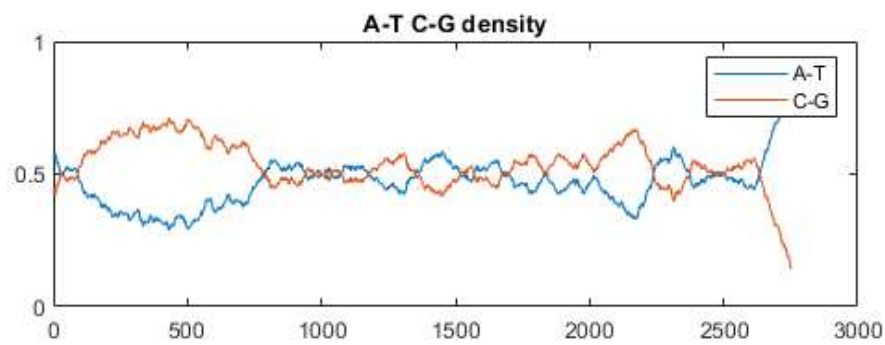
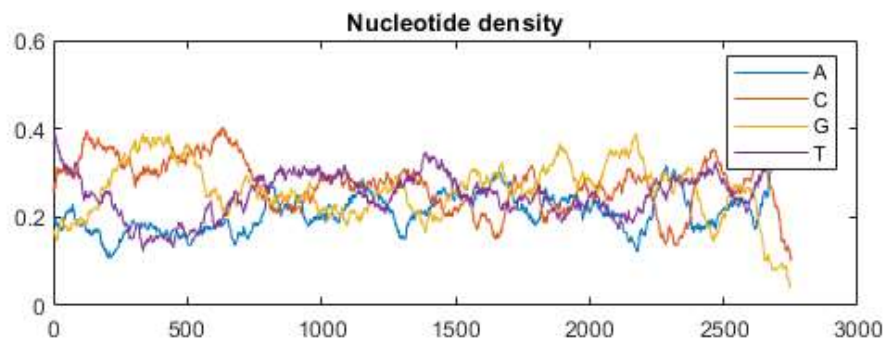
64×2 cell array

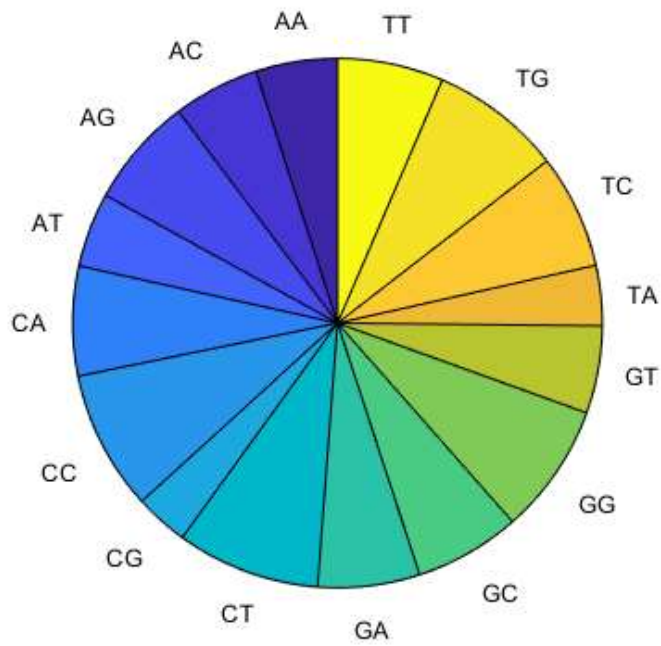
{ 'ctg' }	{ [95] }
{ 'cct' }	{ [81] }
{ 'tgg' }	{ [77] }
{ 'gag' }	{ [68] }
{ 'ggc' }	{ [68] }
{ 'ccc' }	{ [66] }
{ 'tcc' }	{ [66] }
{ 'agg' }	{ [65] }
{ 'cag' }	{ [65] }
{ 'tct' }	{ [63] }
{ 'gct' }	{ [62] }
{ 'ctc' }	{ [61] }
{ 'ctt' }	{ [61] }
{ 'gcc' }	{ [59] }
{ 'ttc' }	{ [58] }
{ 'gga' }	{ [55] }
{ 'tga' }	{ [55] }
{ 'cca' }	{ [54] }
{ 'ggg' }	{ [53] }
{ 'gtg' }	{ [51] }
{ 'ttt' }	{ [51] }
{ 'cac' }	{ [50] }
{ 'tgt' }	{ [48] }
{ 'aaa' }	{ [46] }
{ 'aca' }	{ [46] }
{ 'tca' }	{ [46] }
{ 'agc' }	{ [45] }
{ 'acc' }	{ [44] }
{ 'ggt' }	{ [44] }
{ 'gtc' }	{ [43] }
{ 'aga' }	{ [42] }
{ 'gaa' }	{ [42] }
{ 'ttg' }	{ [42] }
{ 'tgc' }	{ [41] }
{ 'cat' }	{ [39] }
{ 'gca' }	{ [38] }
{ 'gac' }	{ [37] }
{ 'act' }	{ [35] }
{ 'tat' }	{ [35] }
{ 'aag' }	{ [34] }

```

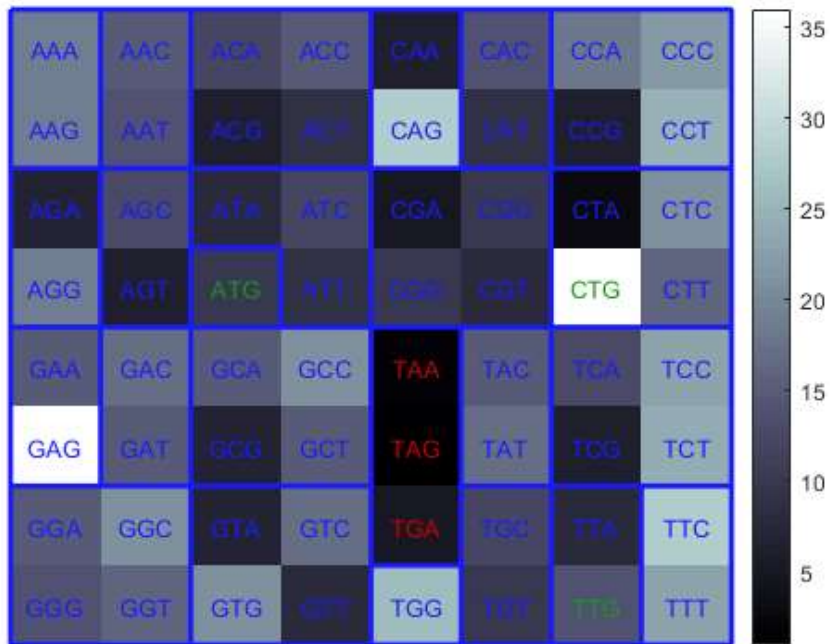
{'att'}    {[34]}
{'ccg'}    {[34]}
{'agt'}    {[33]}
{'atg'}    {[33]}
{'gtt'}    {[32]}
{'caa'}    {[30]}
{'aac'}    {[29]}
{'ata'}    {[29]}
{'atc'}    {[29]}
{'tac'}    {[29]}
{'aat'}    {[27]}
{'tta'}    {[27]}
{'cgg'}    {[25]}
{'cgc'}    {[24]}
{'cta'}    {[24]}
{'gat'}    {[24]}
{'cgt'}    {[22]}
{'gta'}    {[21]}
{'acg'}    {[20]}
{'cga'}    {[19]}
{'gcg'}    {[19]}
{'taa'}    {[19]}
{'tag'}    {[18]}
{'tcg'}    {[17]}

```

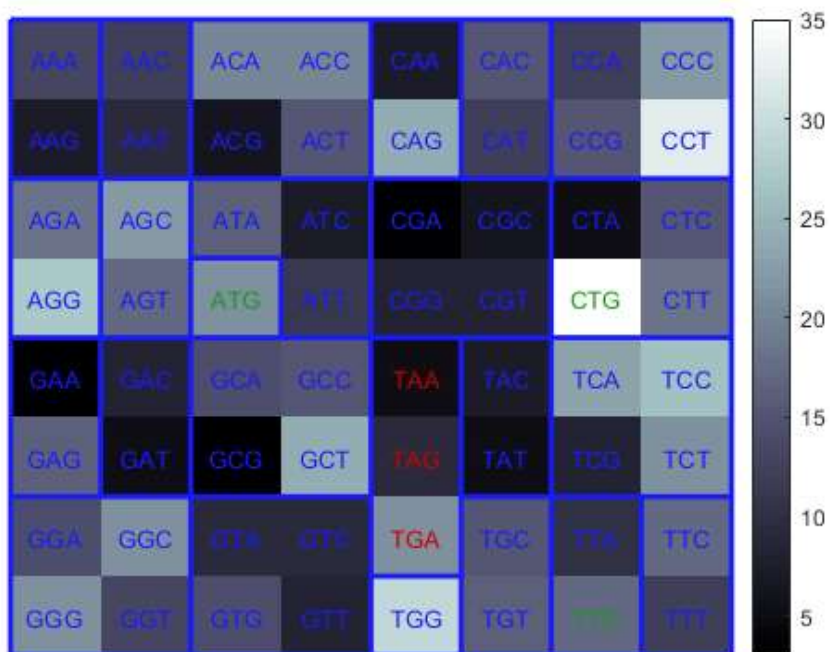




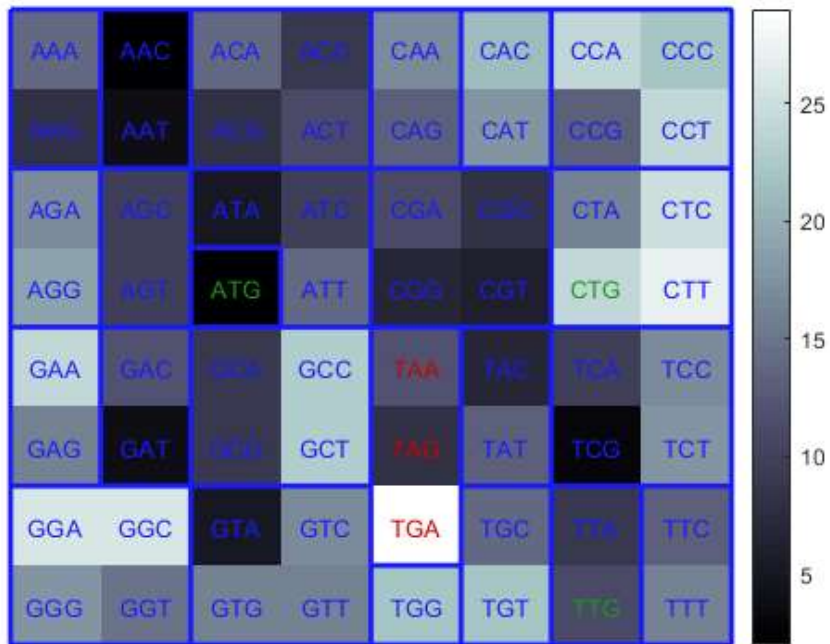
```
%lab1.3.1
% returns codon counts for the first reading frame
% and plot the results in a heat map
%First 3 frames
figure(3)
r1codons = codoncount(s.Sequence,'frame',1,'figure',true);
figure(4)
r2codons = codoncount(s.Sequence,'frame',2,'figure',true);
figure(5)
r3codons = codoncount(s.Sequence,'frame',3,'figure',true);
figure(6)
%Reversing the sequence to get last 3 frames
r4codons = codoncount(s.Sequence,'Reverse','true','frame',1,'figure',true);
figure(7)
r5codons = codoncount(s.Sequence,'Reverse','true','frame',2,'figure',true);
figure(8)
r6codons = codoncount(s.Sequence,'Reverse','true','frame',3,'figure',true);
```



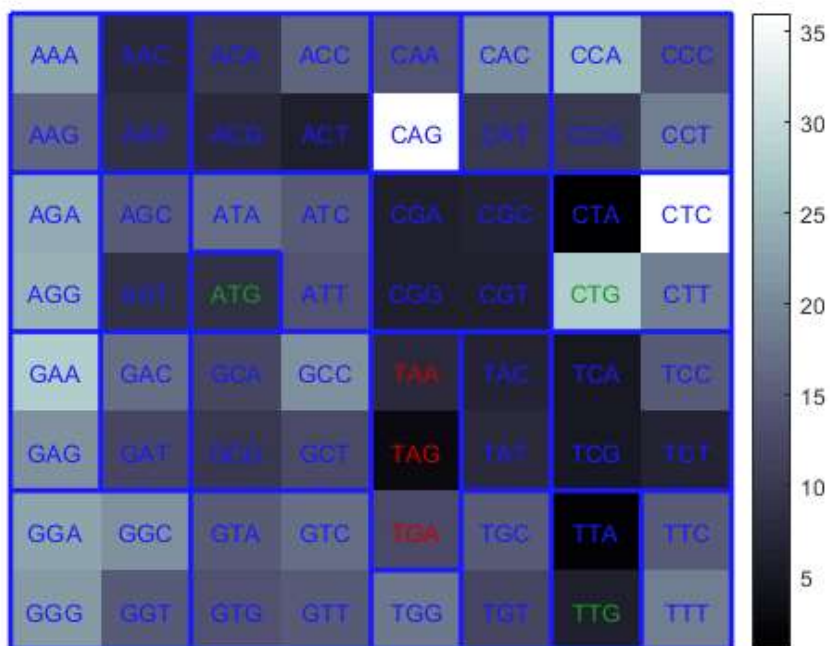
Genetic Code: Standard



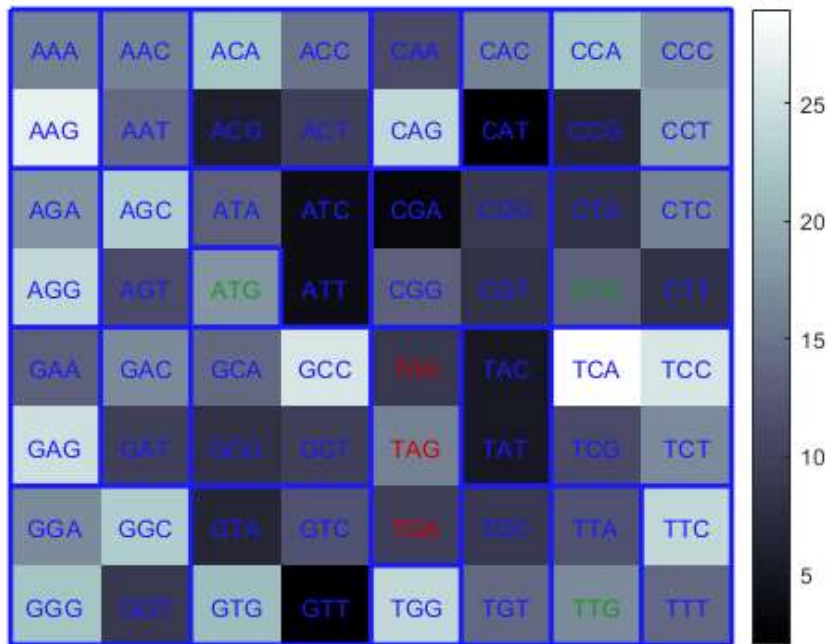
Genetic Code: Standard



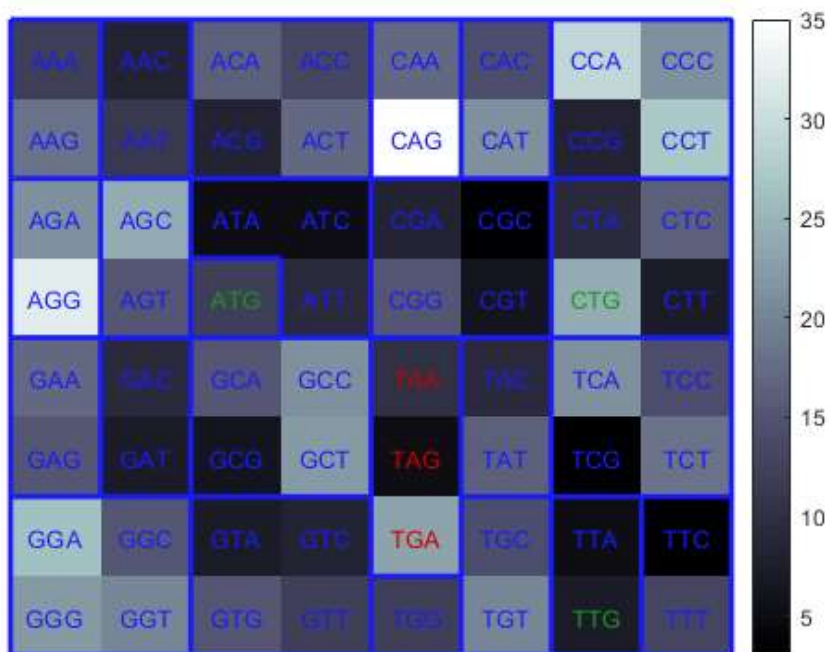
Genetic Code: Standard



Genetic Code: Standard



Genetic Code: Standard



Genetic Code: Standard

```
%Lab1.3.2
%ORFs of minimum length 50 in Frame 1
orfminlength_50=seqshoworfs(s.Sequence,'Frames',1,'MinimumLength',50);
%ORFs of minimum length 500 in Frame 1
orfminlength_500=seqshoworfs(s.Sequence,'Frames',1,'MinimumLength',500);
```



```
Open Reading Frames

Frame 1

000001    tcacatcacaaacgacttgtggttttaatectecgtttttctgcttctgaagttacttcagcctg
000065    gcaagtcctttacctccccgtaggcctggcgagctgcatcacaaacattcaagattcacccetaga
000129    gccatctgggaaactttctctccaggctgcgcctgcgtcctcgccctccccaccccggttcttctc
000193    gagtcgggtgagctgtctagtccatcacggccggcacggccgcaggggtggccgggtattttac
000257    tgctctactgggcccgtgaacagctctggcgagccgagcagttgccgacgcccggcacaaatccgc
000321    tgcacgtagcaggagcctcaggtccaggccggaagtgaaggggcaggggtgtgggtcctcctggg
000385    gtgcagggcgcagagccgcctctggtcacgtgattcgccgataagtcacgggggcgcgcgtcac
000449    ctgaccagggtctcacgtggccagccccctccgagagggggagaccagcggggccatgacaagctc
000513    caggctttgggttttcgctgctgctggcggcagcgttcgcaggacggggcagcggcctctggccc
000577    tggcctcagaacttccaaacctccgaccagcgtacgtcctttacccgaaacactttcaattec
000641    agtacgatgtcagctcggccgcgcagcccggtgctcagtcctcgacgaggccttcacagccta
000705    tcgtgacctgcttttcgggttcgggtcttggccccgctccttacctcacagggaaacggcataca
000769    ctggagaagaatgtgttgggttgtctctgtagtcacacctggatgtaaccagcttccactttgg
000833    agtcagtgaggaaattataacctgaccataaatgatgaccagtggtttactcctctctgagactgt
000897    ctggggagctctccgaggtctgggagacttttagccagcttggttggaaatctgctgagggcaca
000961    ttctttatcaacaagactgagattgaggactttcccgctttcctcacggggccttgctgttgg
001025    atacatctcgccattacctgccactctctagcatcctggacactctggatgtcatggcgtaaaa
001089    taaattgaacgtgttccactggcatctggtagatgatccttccctcccatatgagagcttccact
001153    ttccagagctcatgagaaaggggtcctacaacctgtcaccacatctacacagcacaggatg
001217    tgaaggaggtcattgaatacgcacgggtccgggggtatccgtgtgcttgacaggtttgacactcc
001281    tggccacactttgtcctggggaccagggtatccctggattactgactccttgctactctgggtct
001345    gagccctctggcacctttggaccagtgaaatccagctctcaataataacctatgagttcatgagca
```

```
Open Reading Frames

Frame 1

000001    tcacatcacaaacgacttgtggttttaatectecgtttttctgcttctgaagttacttcagcctg
000065    gcaagtcctttacctccccgtaggcctggcgagctgcatcacaaacattcaagattcacccetaga
000129    gccatctgggaaactttctctccaggctgcgcctgcgtcctcgccctccccaccccggttcttctc
000193    gagtcgggtgagctgtctagtccatcacggccggcacggccgcaggggtggccgggtattttac
000257    tgctctactgggcccgtgaacagctctggcgagccgagcagttgccgacgcccggcacaaatccgc
000321    tgcacgtagcaggagcctcaggtccaggccggaagtgaaggggcaggggtgtgggtcctcctggg
000385    gtgcagggcgcagagccgcctctggtcacgtgattcgccgataagtcacgggggcgcgcgtcac
000449    ctgaccagggtctcacgtggccagccccctccgagagggggagaccagcggggccatgacaagctc
000513    caggctttgggttttcgctgctgctggcggcagcgttcgcaggacggggcagcggcctctggccc
000577    tggcctcagaacttccaaacctccgaccagcgtacgtcctttacccgaaacactttcaattec
000641    agtacgatgtcagctcggccgcgcagcccggtgctcagtcctcgacgaggccttcacagccta
000705    tcgtgacctgcttttcgggttcgggtcttggccccgctccttacctcacagggaaacggcataca
000769    ctggagaagaatgtgttgggttgtctctgtagtcacacctggatgtaaccagcttccactttgg
000833    agtcagtgaggaaattataacctgaccataaatgatgaccagtggtttactcctctctgagactgt
000897    ctggggagctctccgaggtctgggagacttttagccagcttggttggaaatctgctgagggcaca
000961    ttctttatcaacaagactgagattgaggactttcccgctttcctcacggggccttgctgttgg
001025    atacatctcgccattacctgccactctctagcatcctggacactctggatgtcatggcgtaaaa
001089    taaattgaacgtgttccactggcatctggtagatgatccttccctcccatatgagagcttccact
001153    ttccagagctcatgagaaaggggtcctacaacctgtcaccacatctacacagcacaggatg
001217    tgaaggaggtcattgaatacgcacgggtccgggggtatccgtgtgcttgacaggtttgacactcc
001281    tggccacactttgtcctggggaccagggtatccctggattactgactccttgctactctgggtct
001345    gagccctctggcacctttggaccagtgaaatccagctctcaataataacctatgagttcatgagca
```

```
%Lab 1.3.3
% Estimate P(stop) from the sequence nm_000520 and determine the threshold given ? = 0.05
```

```

% Find the total of stop codons in each frame
frame1_Pstop = r1codons.TAA + r1codons.TAG + r1codons.TGA
frame2_Pstop = r2codons.TAA + r2codons.TAG + r2codons.TGA
frame3_Pstop = r3codons.TAA + r3codons.TAG + r3codons.TGA
frame4_Pstop = r4codons.TAA + r4codons.TAG + r4codons.TGA
frame5_Pstop = r5codons.TAA + r5codons.TAG + r5codons.TGA
frame6_Pstop = r6codons.TAA + r6codons.TAG + r6codons.TGA

%sum of all frames above

Frametotal = frame1_Pstop + frame2_Pstop + frame3_Pstop + frame4_Pstop + frame5_Pstop + frame6_Pstop

%Total number of codons in sequence
% calculate the value in each codon
c1=struct2cell(r1codons);
c2=struct2cell(r2codons);
c3=struct2cell(r3codons);
c4=struct2cell(r4codons);
c5=struct2cell(r5codons);
c6=struct2cell(r6codons);
%total codons in sequence
Total = sum([c1{:}]) + sum([c2{:}]) + sum([c3{:}]) + sum([c4{:}]) + sum([c5{:}]) + sum([c6{:}])
%probability of stop codons
Pstop = (Frametotal./Total)

```

```
frame1_Pstop =
```

```
8
```

```
frame2_Pstop =
```

```
35
```

```
frame3_Pstop =
```

```
49
```

```
frame4_Pstop =
```

```
24
```

```
frame5_Pstop =
```

```
35
```

```
frame6_Pstop =
```

```
38
```

```
Frametotal =
```

```
189
```

```
Total =
```

```
5498
```

```
Pstop =
```

```
0.0344
```

```
%probability of k non stop  
%Given confident level alpha  
alpha= 0.05 ;
```

k is the length of the sequence

```
k = log(0.05) / log(1-(Pstop));  
%optimal length  
knew = k + 1 + 1
```

knew =

87.6391