

Put this file in the same directory as your python script. Change the name of the file in the next line to test your code.

TEST SEQ CLASS

Make instance of Seq called 's' and test methods

```
In [2]: s=Seq(" gATATAGGACctttaGGACCAC ", "my_gene", "H.sapiens")
s.print_record()
s.make_kmers()
a=s.kmers
```

```
H.sapiens my_gene: GATATAGGACCTTTAGGACCAC
```

```
In [3]: t=Seq(" AGAGAGAGTGTGT", 'gene2', 'D')
```

```
In [4]: t.print_record()
t.make_kmers()
b=t.kmers
out=set(a) & set(b)
```

```
D gene2: AGAGAGAGTGTGT
```

```
In [5]: print(s)
print(s.gene)
print(s.species)
```

```
GATATAGGACCTTTAGGACCAC
my_gene
H.sapiens
```

```
In [6]: s.make_kmers(5)
print(s.kmers)
```

```
['GAT', 'ATA', 'TAT', 'ATA', 'TAG', 'AGG', 'GGA', 'GAC', 'ACC', 'CCT', 'CTT', 'TTT', 'TTA', 'TAG', 'AGG', 'GGA', 'GAC', 'ACC', 'CCA', 'CAC', 'GATAT', 'ATATA', 'TATAG', 'ATAGG', 'TAGGA', 'AGGAC', 'GGACC', 'GACCT', 'ACCTT', 'CCTTT', 'CTTTA', 'TTTAG', 'TTAGG', 'TAGGA', 'AGGAC', 'GGACC', 'GACCA', 'ACCAC']
```

```
In [7]: print(s.fasta())
```

```
>H.sapiens my_gene
GATATAGGACCTTTAGGACCAC
```

TEST DNA CLASS ¶

Make instance of DNA called 'd' and test methods

```
In [51]: d=DNA(" -tcaaaGCGGCGGATCTCCCaatga\n", "my_dna", "D. terebrans", "AX5667")  
d.print_info()
```

AX5667 D.terebrans my_dna: NTCAAAGCGGCGGATCTCCCAAATGA

```
In [52]: print(d)  
print(d.analysis())  
print(d.fasta())
```

NTCAAAGCGGCGGATCTCCCAAATGA
13
>D.terebrans my_dna
NTCAAAGCGGCGGATCTCCCAAATGA

```
In [53]: rc=d.reverse_complement()  
print(rc)
```

TCATTTGGGAGATCCGCCGCTTTGAN

```
In [54]: all_6_frames=d.six_frames()  
print(all_6_frames)
```

('NTCAAAGCGGCGGATCTCCCAAATGA', 'TCAAAGCGGCGGATCTCCCAAATGA', 'CAAAGCGGCGGATCTCCCAAATGA', 'TCATTTGGGAGATCCGCCGCTTTGAN',
'CATTGGGAGATCCGCCGCTTTGAN', 'ATTTGGGAGATCCGCCGCTTTGAN')

TEST RNA CLASS

Make instance of RNA called 'r' and test methods

```
In [38]: r=RNA(" g?ATATAGGACctttaGGACCAC  ","my_rna","G.gallus","R5990999")  
r.print_info()  
print(r)
```

```
R5990999 G.gallus my_rna: GNAUAUAGGACCUUUAGGACCAC  
GNAUAUAGGACCUUUAGGACCAC
```

```
In [39]: r.make_codons()  
print(r.codons)
```

```
['GNA', 'UAU', 'AGG', 'ACC', 'UUU', 'AGG', 'ACC']
```

```
In [40]: print(r.translate())
```

```
XYRTFRT
```

```
In [41]: print(r.fasta())
```

```
>G.gallus my_rna  
GNAUAUAGGACCUUUAGGACCAC
```

TEST Protein CLASS

Make instance of Protein called 'p' and test methods

```
In [42]: p=Protein(" WCVALKKKCCYhhhhh-yyrsQ\t", "my_prot", "D.melanogaster", "56008009")  
print(p)
```

```
WCVALKKKCCYHHHHHXYYYRSQ
```

```
In [43]: print(p.fasta())
```

```
>D.melanogaster my_prot  
WCVALKKKCCYHHHHHXYYYRSQ
```

```
In [44]: print(p.kmers)
```

```
[]
```

```
In [45]: p.kmers=[]  
p.make_kmers(5)  
print(p.kmers)
```

```
['WCVAL', 'CVALK', 'VALKK', 'ALKKK', 'LKKKC', 'KKKCC', 'KKCCY', 'KCCYH', 'CCYHH', 'CYHHH', 'YHHHH', 'HHHHH', 'HHHHX',  
'', 'HHHXY', 'HHXY', 'HXY', 'XY', 'YY', 'YYS', 'YYSQ']
```

```
In [46]: testp=Protein('VIKING', 'test', 'unknown', 999)
```

```
In [47]: print(testp)
```

```
VIKING
```

```
In [48]: testp.make_kmers(2)  
print(testp.kmers)
```

```
['VI', 'IK', 'KI', 'IN', 'NG']
```

```
In [49]: x=testp.total_hydro()  
print(x)
```

```
5.399999999999999
```

```
In [50]: m=testp.mol_weight()  
print(m)
```

```
732.8699999999999
```