Reference Manual

Contents

Language Functions

Make Sequence - seq(string)

seq(string)

Takes as a parameter a string containing the value of the sequence to be denoted.

Example: *myseq = seq('GATGGAACTTGACTACGTAAATT')*

myseq2 = seq('GAUGGAACUUGACUACGUAAAUU')

Denotes a sequence named *myseq* containing the DNA sequence GATGGAACTTGACTACGTAAATT and a sequence named *myseq2* containing the RNA sequence *GAUGGAACUUGACUACGUAAAUU*

***NOTE** - The names of myseq and myseq2 are not fixed, meaning that they are open to the user's discretion*

Print File - print(string)

print(string)

Takes as a parameter a string value corresponding to the path of the desired FASTA file and prints the contents of such file to the console.

Example: *print('IOFiles/file.txt')*

Prints the file named *file.txt* contained in the *IOFiles* directory

Complement - comp(id)

comp(id)

Takes as a parameter an id corresponding to a DNA sequence previously initialized and returns the complement of such sequence.

Example: a = *comp(myseq)*

Assigns *a* the value of the complement of the sequence *myseq*

Reverse Complement - rcomp(id)

rcomp(id)

Takes as a parameter an id corresponding to a DNA sequence previously initialized and returns the reverse complement of such sequence.

Example: a = *rcomp(myseq)*

Assigns a the value of the reverse complement of the sequence *myseq*

DNA Transcription - transc(id)

transc(id)

Takes as a parameter an id corresponding to a DNA sequence previously initialized and returns the transcription of such sequence.

Example: *a = transc(myseq)*

Assigns a the value of the transcription of the sequence *myseq* from DNA to RNA

RNA Transcription - rtransc(id)

rtransc(id)

Takes as a parameter an id corresponding to a RNA sequence previously initialized and returns the transcription of such sequence.

Example: *a = rtransc(myseq2)*

Assigns *a* the value of the transcription of the sequence *myseq2* from RNA to DNA

Print Codon Table - ctable(int)

ctable(int)

Takes as a parameter an integer (1 or 2) corresponding to the desired codon table and prints it in the console

Example: *ctable(1)*

ctable(2)

Prints a DNA and an RNA codon table respectively

***NOTE** - The integers 1 and 2 are fixed, meaning that providing any other value would result in a system error*

Translate DNA/RNA - transl(id, type)

transl(id, type)

Takes as a parameter an id corresponding to a DNA or RNA sequence previously initialized and a the type (dna or rna) and returns the translation of such sequence

Example*: a = transl(myseq, dna)*

b = transl(myseq2, dna)

Assigns *a* and *b* the value of the translation of the DNA and RNA sequences *myseq* and *myseq2*, respectively.

Read from File - read(string, string)

read(string, string)

Takes as parameters 2 strings representing the name of the sequence to be read and the FASTA file it is read from and returns the sequence with the name provided

Example: *a = read('Seq 1', 'IOFiles/file.txt')*

Assigns a the value of the sequence named *Seq 1* contained in the FASTA file named *file.txt* contained in the *IOFiles* directory

Write to File - write(id, string)

write(id, string)

Takes as parameter an id and a string corresponding to the value to be written and the file in which it will be written.

Example: *write(myseq, 'IOFiles/myfile'*

Outputs a file named *myfile.txt* containing the value of the sequence *myseq*

GC Content - gccon(string)

gccon(string)

Takes as a parameter a string corresponding to the path of a FASTA file

Example: *gccon('IOFiles/file.txt')*

Prints the value of the GC Content of the sequence contained in the file *file.txt*

RNA Inferring - rnainf(id)

rnainf(id)

Takes as a parameter an id corresponding to a previously initialized RNA sequence and returns the RNA Inference of such sequence

Example: *a = rnainf(myseq2)*

Assigns *a* the value of the RNA inference of the sequence *myseq2*

RNA Inferring File - rnainf2(string)

rnainf2(string)

Takes as a parameter a string corresponding to the path of a file containing an RNA sequence in FASTA format and returns the RNA Inference of such sequence

Example: *rnainf2('IOFiles/file.txt')*

Prints the value of the RNA inference of the sequence contained in the file *file.txt* in the *IOFiles* directory

Open Read Frame - orf(string)

orf(string)

Takes as a parameter a string corresponding to the path of a file containing an DNA sequence in FASTA format and returns the Open Read Frame of such sequence

Example: *orf('IOFiles/file.txt')*

Prints the value of the Open Read Frame of the sequence contained in the file *file.txt* in the *IOFiles* directory

Complement File - compf(string)

compf(string)

Takes as a parameter a string corresponding to the path of a file containing a sequence in FASTA format and returns the complement of such sequence

Example: *compf('IOFiles/file.txt')*

Prints the value of the complement of the sequence contained in the file *file.txt* in the *IOFiles* directory

Reverse Complement File - rcompf(string)

rcompf(string)

Takes as a parameter a string corresponding to the path of a file containing a sequence in FASTA format and returns the reverse complement of such sequence

Example: r*compf('IOFiles/file.txt')*

Prints the value of the reverse complement of the sequence contained in the file *file.txt* in the *IOFiles* directory

DNA Transcription File- transcf(string)

transcf(string)

Takes as a parameter a string corresponding to the path of a file containing a DNA sequence in FASTA format and returns the transcription of such sequence

Example: transc*f('IOFiles/file.txt')*

Prints the value of the transcription of the sequence contained in the file *file.txt* in the *IOFiles* directory

RNA Transcription File - rtranscf(string)

r***transcf(string)***

Takes as a parameter a string corresponding to the path of a file containing a RNA sequence in FASTA format and returns the transcription of such sequence

Example: rtransc*f('IOFiles/file.txt')*

Prints the value of the transcription of the sequence contained in the file *file.txt* in the *IOFiles* directory

Protein Weight - protw(id)

protw(id)

Takes as a parameter an id corresponding to a previously initialized protein sequence and returns the weight of such protein according to a monoisotopic mass table

Example: a = *protw(myprot)*

Assigns *a* the weight of the protein *myprot*

Motif Interval - motif(id, string)

motif(id, string)

Takes as a parameter an id corresponding to a previously initialized sequence and a string corresponding to the splice of the sequence to which calculate the motif interval

Example: *a = motif(myseq, 'GAT')*

Assigns *a* the value of the Motif Interval of the splice GAT in the sequence *myseq*.

Write Punnett - punnett(string, string)

punnett(string, string)

Takes as parameters two strings corresponding to the alleles needed to for a table, separated by spaces, and outputs a table to the console along with the probability of each combination

Example: *punnett('Aa Bb', 'Cc Dd')*

Outputs in console the punnett table for the alleles *Aa Bb* and *Cc Dd*

Write Punnett File - wpunnett(string, string, string)

wpunnett(string, string, string)

Takes as parameters two strings corresponding to the alleles needed to for a table and a third string corresponding to the path of a file to be created and written with the Punnett table

Example: *wpunnet('Aa Bb', 'Cc Dd' ,'IOFiles/myfile')*

Writes the punnett table for the alleles *Aa Bb* and *Cc Dd* in the file *myfile.txt* contained in the *IOFiles* directory

Protein Inference - protinfer(string)

protinfer(string)

Takes as a parameter a string corresponding to the value of the weight of the protein to be inferred

Example: a = *protinfer('3524.8542 3710.9335 3841.974 3970.0326 4057.0646')*

Assigns a the inferred protein

Hamming Distance - hamdis(id, id)

hamdis(id, id)

Takes as a parameter two ids corresponding to two previously initialized sequences and returns the Hamming Distance between them

Example: *a = hamdis(myseq, myseq1)*

Assigns a the value of the hamming distance between *myseq* and *myseq1*

Recurrence - recur(int, int)

recur(int, int)

Takes as a parameter two integers and returns the recurrence interval

Example: a = recur(5, 7)

Assigns a the value of the recurrence interval between 5 and 7

Draw Phylogenetic Tree - drawtree(int, string)

drawtree(int, string)

Takes as parameter an int (1 or 2) corresponding to the method to output the tree contained in the second parameter, which indicates a file in xml format

Example: drawtree(1, 'IOFiles/tree.xml')

drawtree(2, 'IOFiles/tree.xml')

Draws the tree contained in the tree.xml file on the console and on the pylab view

***NOTE** - The integers 1 and 2 are fixed, meaning that providing any other value would result in a system error*