		sequence file	file
5.	The genetic information encoded in the DNA must remain uncorrupte		
	A. True	B. False	
6.	_____ is a python package for sequence analysis implemen		
	A. .read()	B. .parse()	C. pym
7.	BLAST can be used to infer functional and evolutionary relationships members of gene families.		
	A. True	B. False	
8.	Sequence alignment is the process of arranging two or more sequences (of DN identify the region of similarity between them.		
	A. True	B. False	
9.	Which term refers to the genetic makeup of an organism that contribu		
	A. Phenotype	B. Genotype	C. All
10	Which one of these BioPython code is Not true.		
	A-with open("PML.fasta") as handle: print(sum(len(Y) for Y inSeqIO.parse(handle,"fasta "))) handle.close()	B- with open("PML.fasta") as handle: print(sum(len(Y) for Y in SeqIO.parse(handle,"fasta ")))	C. with open(" handle for Y in SeqIO. "))
11	Which strand of DNA carries the genetic information used in transcri		
	A. Leading strand	B. Lagging strand	C. Cod

Best wishes Dr.Nesma

	.parse() equation.
sed on matplotlib.	
	D. pairtwist2
en sequences as well as help identify	
or protein sequences) in a specific order to	
ts phenotype?	
	D. Genome.
asta") as (sum(len(Y) andle,"fasta	D. d-handle.open("PML.fasta")
nd	D. Non-coding strand