Question 1

Evaluate the following terms. If we type them into the shell, what will be the output or echo from IDLE? If any of these causes an error, please write "error" instead. The type of your answer is important, e.g. the integer 5 is different from '5' or 5.0.

Evaluate the Following:	Answer:
<pre>print(sorted('abc'))</pre>	['a', 'b', 'c']
True and sqrt(-1)	Error
6 + 5 * 4 / 2 ** 2 - 1	10.0
not True or False	False
False or not True	False
3*(('b' * 2)+'a')	'bbabbabba'
(2+1>1)+(1)*True	2
('a'+'b')*3 == 'a'*3 + 'b'*3	False
int(-3.2)	-3
'1G o3o\'dh 5joodba'[1::2]	'Good job'

Question 2

Each row of the table is a separate program/file. What is the output of each of them when we run it? If the code produces errors or runs into infinite loops, please state 'error' or 'infinite loop' respectively.

Code	Output
a = 1 ++a print(a)	1
<pre>b = 128 def half(x): return x / 2</pre>	16.0
<pre>print(half(half(b))))</pre>	
a,b,c = 1,2,3 a,b,c = b,a,a a,b,c = c,a,b print(str(a)+str(b)+str(c))	121

Question 3

The DNA of any creature can be represented by a string of characters with 'A', 'C', 'G' and 'T', for example, DNA = 'AGCTAGTACGTACTGACACGTCA'. (In real life, the length of a DNA could be a few thousands to millions.) Sometimes we can nail down some special subsequence for a certain inheritance or characteristic. In this problem, you will write a function to check if a certain DNA contains a subsequence of any length. Here is some sample output:

```
>>> DNA =
'AGCTAGTCATACCTATGTACTGACACGTCA'
>>> print(sub_sequence(DNA,'ACA'))
True
>>> print(sub_sequence(DNA,'ACCTAA'))
False
```

```
def sub_sequence(DNA, subseq):
    return subseq in DNA
```