

It1007 Midterm Quiz Name: _____

Question 1 [40 marks]

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

Code	Output
<pre>def foo(): if False: return 1 elif False: return 2 elif 0: return 3 if True: return 4 else: return 5 print(foo())</pre>	4
<pre>d = { 1:3, 3:5, 5:7, 7:9, 9:1 } x = 1 for i in range(7): x = d[x] print(x)</pre>	5
<pre>import numpy as np m = np.zeros((20,20)) for i in range(1,20): for j in range(1,20): m[i,j] = m[i-1,j]+m[i,j-1]+ 1 print(int(m[3,4]))</pre>	34
<pre>s = '9' for i in range(0,9): n = str(int(s[0])-1) s = n + s + n print(int(s))</pre>	123456789876543210
<pre>def wt(x): n = 0 for i in range(x): n+=x print(wt(100))</pre>	None
<pre>l = [i*i for i in range(1,20,2)] print(l[3])</pre>	49

Question 2 Part a [20 marks]

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, seq):
    return seq in dna
```

Question 2 Part b [40 marks]

Two sequences of DNA are said to be *similar* if they are only differed by exactly one character. Write a function `isSimilarDNA(s1,s2)` to return True if `s1` and `s2` are similar, and return False otherwise. You can assume the length of the two input strings are the same. For example, if `dna1 = 'ACTGAT'`, `dna2 = 'ACAGAT'` and `dna3 = 'ACAGAG'`.

Calls	Returns
<code>similarDNA(dna1,dna2)</code>	True
<code>similarDNA(dna2,dna3)</code>	True
<code>similarDNA(dna1,dna3)</code>	False
<code>similarDNA(dna1,dna1)</code>	False

```
def similarDNA(d1,d2):
    l = len(s1)
    ndiff = 0
    for i in range(l):
        if s1[i]!=s2[i]:
            ndiff+=1
    return ndiff == 1
```

Warning: Marks will be deducted if your code is unnecessary lengthy. And **zero mark** if it exceeds 10 lines. Each vertical line is the position for indentations for you to follow.