Programming For Bioinformatics

BNFO 135

Midterm Exam

Fall 2015

October 27, 2015

Do not open this exam until instructed to do so. The exam consists of 20 problems. Please check that you have all the pages.

The answers to the exam problems should be written in the space provided with the question. Read each question carefully before answering. Make sure you print your answer neatly!

During the exam it is prohibited to:
1. Use any books or notes.
2. Use any electronic aid, including calculators.
3. Exchange information with any person other than the exam proctor.
4. Leave the exam room before you turn in your exam.

It is strongly suggested that you use all the time available. If you finish early, double check your work. By signing below you acknowledge that you have read and understood all of the instructions above.

Good luck!

NJIT Academic Honor Code Agreement

On my honor, I pledge that I have not violated the provisions of the NJIT Academic Honor Code.

Name: ___________________________ SID: ___________________________

Signature: ___________________________ Section: ___________________________
Enter the answers to problems 1-18 here. Any syntax errors you might think are in the following questions are typographical errors. Circle the correct answer.

1. T F
2. T F
3. T F
4. T F
5. T F
6. T F
7. T F
8. T F
9. T F
10. T F
11. A B C D
12. A B C D
13. A B C D
14. A B C D
15. A B C D
16. A B C D
17. A B C D
18. A B C D
Problem 1.
  Python is a programming language.

Problem 2.
  AUCG are the four bases of DNA.

Problem 3.
  An string index must have a ‘from’ and a ‘to’ value.

Problem 4.
  A syntax error is something to avoid.

Problem 5.
  The ‘repeat’ statement is used to repeatedly execute some code.

Problem 6.
  The assignment operator, ‘=’, tests for equality.

Problem 7.
  The ‘print’ function can be used to display messages.

Problem 8.
  Guanine is represented by the ‘U’ symbol.

Problem 9.
  A for statement is a kind of loop.

Problem 10.
  An if statement is used to open a file.
Problem 11.

What is the output of the following lines of code?

dna = 'GATGATACTA'
if 'ATG' in dna:
    print('found')
else:
    print('not found')

A. found
B. not found
C. found not found
D. not found found

Problem 12.

What is the output of the following lines of code?

for i in range(2):
    print(i, end=' ')
print()

A. i
B. i i
C. 0 1
D. 1 2
Problem 13.

What is the output of the following lines of code?

dna = 'ATGA'
rna = str()
for ch in dna:
    if ch == 'T':
        rna += 'U'
    else:
        rna += ch
print(rna)

A. AUGA
B. ATGA
C. TUGT
D. UACU

Problem 14.

What is the output of the following lines of code?

i = 0
seq = 'GCAGTATTAGCCAT'
while i < len(seq):
    print(seq[i], end='')
    i += 2
print()

A. ATTACA
B. ATTACAT
C. GATTACA
D. GATTACAT
Problem 15.

What is the output of the following lines of code?

```python
for base in 'ACXTA':
    if base in 'ACGTacgt':
        print('T', end='')
    else:
        print('F', end=')
```

A. TTTTT
B. TTTFT
C. TTFTT
D. TFTTT

Problem 16.

What is the output of the following lines of code?

```python
dna = 'TAGTACTA'
gccount = 0
for ch in dna:
    if ch == 'C' or ch == 'G':
        gccount += 1
print(gccount / len(dna) * 100, '%')
```

A. 15.0 %
B. 20.0 %
C. 25.0 %
D. 30.0 %
Problem 17.

Given the following lines of code:

```python
i = 0
while i < 5:
    print(i)
    i = i + 1
```

Which of the following is true?

A. The interpreter will warn of an infinite loop
B. The while loop will execute forever (infinite loop)
C. The while loop will execute 5 times
D. The while loop will execute 6 times

Problem 18.

Which of the following statements evaluates to **True**?

i. `len('TAGTA') == 4`
ii. `len('TACTA') <= len('TAGTA')`
iii. `len('CATGAT') < len('TACTA')`
iv. `len('TACTAC') == 6`

A. i and ii
B. i and iii
C. ii and iv
D. iii and iv
Problem 19.

Write a Python program that prompts the user to enter a DNA sequence and determines whether it has more ‘G’ nucleotides than ‘A’ nucleotides. If the number of ‘G’ nucleotides is larger than the number of ‘A’ nucleotides print “G > A”. If the number of ‘G’ nucleotides is less than the number of ‘A’ nucleotides then print “G < A”. Otherwise print “G == A”.
Problem 20.

Write a Python program that opens a file called “dna.txt”, a file in fasta format that contains one sequence, and prints the reverse complement of the dna sequence. For example, if the file contains:

>bonobo
tactagat

then the program should print atctagta. Your program should work for any DNA sequence and not just the one in the example.