

This exercise is designed to help you understand and update someone else's code. A number of steps will be required to complete the exercise. There are also a set of questions to be answered at the end.

The findAll method should find all occurrences of a search term (findme) in a Sequence object. It should also calculate what percentage of findme is in the sequence and replace occurrences of findme with N if the percentage is greater than 20.

- Find the findAll.py file on Blackboard
- Add the code to guide.py as a class method for Sequence
- Create a new variable mySeq and instantiate it with the following sequence using a DNA alphabet
 - "ACTGGCTGAATGCTGAGATCGATGGCTAGCTTGGC"
- Use the new findAll () method to find the subsequence "TGGC"
- The output should look exactly as follows if the code is working properly. However, it is unlikely that it will work immediately as the code contains a number of bugs. It is your job to fix all the bugs so your output will look as it does in the two example outputs below

```
>>> mySeq.findAll("TGGC")
ACTG
CTGG
TGGC Match at position  2
GGCT
GCTG
CTGA
TGAA
GAAT
AATG
ATGC
TGCT
GCTG
CTGA
TGAG
GAGA
AGAT
GATC
ATCG
TCGA
CGAT
GATG
ATGG
TGGC Match at position  22
GGCT
GCTA
CTAG
TAGC
AGCT
GCTT
CTTG
TTGG
TGGC Match at position  31
-----
Percentage of findme in sequence:  34.2857142857
Removing contamination
([2, 22, 31], 34.285714285714285, 'ACNNNNTGAATGCTGAGATCGANNNNNTAGCTNNNN')
```

```

>>> mySeq.findAll("A")
A Match at position 0
C
T
G
G
C
T
G
A Match at position 8
A Match at position 9
T
G
C
T
G
A Match at position 15
G
A Match at position 17
T
C
G
A Match at position 21
T
G
G
C
T
A Match at position 27
G
C
T
T
G
G
C
-----
Percentage of findme in sequence: 20.0
([0, 8, 9, 15, 17, 21, 27], 20.0)
>>>

```

Questions

1. How does a sliding window work? Why is it useful? What can you find using this approach?
2. Describe the two types of "bugs" encountered in this exercise and steps you might take to address them. One bug would be a traceback output from python