

## Python 6 Problem Set

1. In the file Python\_06\_nobody.txt find every occurrence of 'Nobody' and print out the position.
2. In the file Python\_06\_nobody.txt substitute every occurrence of 'Nobody' with your favorite person's name and save the file as YourFavoritePersonName.txt (ex. Michael.txt).
3. Find all the lines in a Python\_06.fasta that are the header (>seqName desc) using pattern matching.
4. If a line matches the format of a FASTA header, extract the sequence name and description using sub patterns.
  - Print id:"extracted seq name" desc:"extracted description"
5. Create or modify your FASTA parser to use regular expressions. Also make sure your parser can deal with a sequence that is split over many lines.
6. The enzyme ApoI has a restriction site: R<sup>^</sup>AATTY where R and Y are degenerate nucleotides. See the IUPAC table to identify the nucleotide possibilities for the R and Y. Write a regular expression to find and print all occurrences of the site in the following sequence Python\_06\_ApoI.fasta.

```
1 >seq1
2 GAATTCAAGTTCTTGTGCGCACACAAATCCAATAAAAACTATTGTGCACACAGACGCGAC
3 TTCGCGGTCTCGCTTGTCTTGTGTTGATTTCGTAATTTTCATTTCTCGTTCTGTTTCTACTT
4 AACAATGTGGTGATAATATAAAAAATAAAGCAATTCAAAAGTGATGACTTAATTAATGA
5 GCGATTTTTTTTTTTGAAATCAAATTTTTTGAACATTTTTTTTTTAAATTCAAATTTTGGCGA
6 AAATTCAATATCGGTTCTACTATCCATAATATAATTCATCAGGAATACATCTTCAAAGGC
7 AAACGGTGACAACAAATTCAGGCAATTCAGGCAAATACCGAATGACCAGCTTGGTTATC
8 AATTCTAGAATTTGTTTTTTTGGTTTTTATTTATCATTGTAAATAAGACAAACATTTGTTC
9 CTAGTAAAGAATGTAACACCAGAAGTCACGTAAAATGGTGTCCCCATTGTTTAAACGGTT
10 GTTGGGACCAATGGAGTTCGTGGTAACAGTACATCTTTCCCTTGAATTTGCCATTCAAA
11 ATTTGCGGTGGAATACCTAACAAATCCAGTGAATTTAAGAATTGCGATGGGTAATTGACA
12 TGAATTCGAAGGTCAAAATGCTAAGAGATAGTTTAATTTATGTTTGAGACAATCAATTCCC
13 CAATTTTTCTAAGACTTCAATCAATCTCTTAGAATCCGCCTCTGGAGGTGCACTCAGCCG
14 CACGTCGGGCTCACCAAAATATGTTGGGGTTGTCGGTGAACCTGAATAGAAATTATTGTCG
15 CCTCCATCTTCATGGCCGTGAAATCGGCTCGCTGACGGCTTCTCGCGCTGGATTTTTTC
16 ACTATTTTTGAATACATCATTAACGCAATATATATATATATATATATTTAT
```

7. Determine the site(s) of the physical cut(s) by ApoI in the above sequence. Print out the sequence with "<sup>^</sup>" at the cut site.

Hints:

- Use `sub()`
- Use subpatterns (parentheses and `group()`) to find the cut site within the pattern. - Example: if the pattern is GACGT<sup>^</sup>CT the following sequence

```
1 AAAAAAAGACGTCTTTTTTAAAAAAGACGTCTTTTTT
```

would be cut like this:

```
1 AAAAAAAGACGT^CTTTTTTAAAAAAGACGT^CTTTTTT
```

8. Now that you've done your restriction digest, determine the lengths of your fragments and sort them by length (in the same order they would separate on an electrophoresis gel).

Hint: Convert this string:

```
1 AAAAAAAGACGT^CTTTTTTAAAAAAGACGT^CTTTTTT
```

Into this list:

```
1 ["AAAAAAGACGT", "CTTTTTTAAAAAAGACGT", "CTTTTTT"]
```

9. Download this file of enzymes and their cut sites to fill a dictionary of enzymes paired with their recognition patterns. Be aware of the header lines, and be aware of how the columns are delimited.
10. Write a script which takes two command line arguments: the name of an enzyme and a fasta file with a sequence to be cut. If the provided enzyme is present in the dictionary, and will act successfully on the provided sequence, print out:
  - the provided sequence, annotated with cut sites
  - the number of fragments
  - the fragments in their natural order (unsorted)
  - the fragments in sorted order (largest to smallest)