1. Using asymptotic notation, derive upper and lower bounds for the number of different
   (a) prefixes and suffixes
   (b) substrings, and
   (c) subsequences
   of a string $S = s_1 \ldots s_n$.

2. (Gusfield, Ex. 1.2) A circular string of length $n$ is a string in which character $n$ is considered to precede character 1. (Bacterial and mitochondrial DNA is typically circular.) Design a linear-time algorithm to determine whether a linear string $\alpha$ is a substring of a circular string $\beta$. (Notice that the length of the substring can be larger than the length of $\beta$. For example, the linear string CATCATCA is a substring of the circular string ATC. Use the existence of a linear-time exact matching algorithm to solve this problem.)

3. Show the character comparisons performed by
   (a) the naive method and
   (b) the Z algorithm
   to search for occurrences of the pattern “AATAAT” in the target
   
   ACAATAATAAT
   
4. (Gusfield, Ex. 1.5) If the Z algorithm finds that $Z_2 = q > 0$, all the values $Z_3, \ldots, Z_{q+1}, Z_{q+2}$ can then be obtained immediately without additional character comparisons and without executing the main body of Algorithm Z. Elaborate and justify the details of this claim.

5. (Gusfield, Ex. 1.3) **Suffix-prefix matching.** Give an algorithm that takes two strings $\alpha$ and $\beta$, of lengths $n$ and $m$, and finds the longest suffix of $\alpha$ that exactly matches a prefix of $\beta$. The algorithm should run in $O(n + m)$ time.
   (Hint: Z algorithm.)