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 $\beta$. (Use the existence of a linear-time exact matching algorithm to solve this problem.)

3. (Gusfield, Ex. 1.3) Suffix-prefix matching. Give an algorithm that takes in 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.

4. 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.

5. The $Z$ algorithm works in linear time. This would seem to suggest that the algorithm examines any character at most a fixed number of times. Does this conjecture hold? Either justify a fixed upper bound to the number of times that any character is examined by the algorithm, or give a counter-example showing that some characters may be examined by the algorithm an unlimited number of times.