1. Boyer-Moore: How many alignments are *skipped* by the bad character rule for this alignment? Note: the number of skips is one less than the number of positions P shifts by. That is, if the pattern shifts by 2 positions, that's 1 alignment skipped. Also note: the question is asking only about the alignment shown. Do not consider any other alignments of P to T in your answer.

   ```
   T:  GGCTATAATGCGTA
   ```

   ```
   P:  -TAATAAA
   ```

   Shift over 1 position, so **0** skips.

2. Boyer-Moore: How many alignments are skipped by the good suffix rule in this scenario?

   ```
   T:  GGCTATAATGCGTA
   ```

   ```
   P:   TAATAAA
   ```

   3

3. Boyer-Moore: True or false, for given P and T, it's possible that some characters from T will never be examined, i.e., won't be involved in any character comparisons.

   False

   True

4. Consider a version of Boyer-Moore that uses only the bad character rule (no good suffix rule), and say our pattern P is a random string of 50% As and 50% Ts. In which scenario would you expect Boyer-Moore to skip the most alignments?

   The text T consists of 25% As, 25% Ts, 25% Cs and 25%Gs

   The text T consists of 40% As, 40% Ts, 10% Cs and 10%Gs

   The text T consists of 10% As, 10% Ts, 40% Cs and 40%Gs

5. The naive exact matching algorithm preprocesses:

   Neither

   The text T

   Both

   The pattern P

6. The Boyer-Moore algorithm preprocesses:

    Both

    The pattern P

    Neither

    The text T

7. In which of the these scenarios is an offline matching algorithm not appropriate?

    A tool that evaluates a password by comparing it against a large database of bad (easy-to-guess) passwords

    A tool that searches for words in an archive of every speech made in the U.S. Congress

    Your web browser's "find" function that allows you to find a particular word on the web page you are currently viewing

8. Say we have a k-mer index containing all 5-mers from T. We query the index using the first 5-mer from P and the index returns a single index hit. What can we say about whether P occurs in T? Assume T is longer than P and that P is at least 6 bases long.

    It definitely does

    It definitely does not

    We don't know; not enough information

9. Say we have a k-mer index containing all k-mers from T and we query it with 3 different k-mers from the pattern P. The first query returns 0 hits, the second returns 1 hit, and the third returns 3 hits. What can we say about whether P occurs in T?

    It definitely does

    It definitely does not

    We don't know; not enough information

10. Which of the following is not an "edit" allowed in edit distance:

    Transposition

    Deletion

    Insertion

    Substitution