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: GGCTAT**AA**TGCGTA

P: -TAATA**AA**

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

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

T: GGCTAT**AA**TGCGTA

P:  TAATA**AA**

**3**

1. 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**

1. 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**

1. The naive exact matching algorithm preprocesses:

**Neither**

The text T

Both

The pattern P

1. The Boyer-Moore algorithm preprocesses:

Both

**The pattern P**

Neither

The text T

1. 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**

1. 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**

1. 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

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

**Transposition**

Deletion

Insertion

Substitution