Please answer the following question(s).
If the assessment includes multiple-choice questions, click the "Submit Answers" button when you have completed those questions.

You have 120 minutes to take this assessment.
Please complete this assessment by Thu Dec 20 2007 12:01:35 GMT+0800.

1. [Go to bottom of question.](#)

Debugging Class DNASequence

Prerequisites, Goals, and Outcomes

Prerequisites: Before you begin this exercise, you need mastery of the following:

- *Debugger*:
    - Knowledge of a debugger tool
    - Knowledge of basic techniques of debugging

Goals: Reinforce your ability to debug and fix errors efficiently

Outcomes: You will master the following skills:

- Use a debugger tool to monitor the behavior of a program.
- Apply techniques of debugging to find and fix errors efficiently.

Background

The purpose of this assessment is to practice your debugging skills using a debugger. After you finish this assessment, you should be able to use a debugger to monitor the execution of your code and fix errors more efficiently.

Description

The class DNASequence has methods to examine a DNA sequence. DNA is a polymer composed of four molecules called nucleotides: adenine (A), cytosine (C), guanine (G) and thymine (T). In a computer, a DNA sequence can be represented as a sequence of the characters 'A', 'C', 'G' and 'T':

"ACCCGGTTTGGCAAATGGGACGGGAGGACGGGGAAAATTACTACGGCATTAGC"

The class DNASequence stores the sequence of characters in an object of class String. DNASequence uses the following methods from String:

- *char charAt(int index)*. Obtains the character indicated by the index argument. The first character of a string buffer is at index 0. The index argument must be greater than or equal to 0.

- *int length()*. Obtains the number of characters in the string.

In addition to the constructor and accessor methods, the class DNASequence has the following methods:

- *private void countNucleotides()*. Sets fields numberOfA, numberOfT, numberOfC and numberOfG to the number of occurrences of each nucleotide in the DNA sequence.

  For example, if the DNA sequence is "ATCGAAC", after call the method countNucleotides, field numberOfA will have the value 3, field numberOfT will have the value 1, field numberOfC will have the value 2, and field numberOfG will have the value 1.

- *public boolean twoConsecutive(char input)*. Indicates whether the nucleotide specified by the argument input appears in two consecutive locations in the DNA sequence.

  For example, if the DNA sequence is "ATCGAAC", the result of twoConsecutive('A') will be true and the result of twoConsecutive('C') will be false.

Files

Following is a list of files needed to complete this assessment:

- *DNASequence.java*. This is a source file of class DNASequence that contains errors.
- *DebuggingReport.txt*. This is a template for reporting your

diagnosis of each error and your solutions.

Tasks

The implementation of class DNASequence has four errors. Use a debugger to help you to debug the program and fix the errors. To locate each error, you should follow the process described in page 1.1.8 Debugging.

Maintain a record of your work in the file *DebuggingReport.txt*. Include your diagnosis of each error and your solutions.

Submission

Upon completion, submit **only** the following.

1. *DNASequence.java*. The "fixed" version of *DNASequence.java*
2. *DebuggingReport.txt*. Your debugging report

Go to top of question.

File to submit: Upload File   Forward File   Refresh   Ready for Grading

Go to top of assessment.