Question 1 (2 marks)

Let $\phi$ be a general boolean formula constructed from the boolean variables $x_1, x_2, \ldots, x_n$, $\neg, \lor, \land$ and parentheses. $\phi$ is a tautology if it evaluates to 1 for every assignment of 1 and 0 to the input variables. Define TAUTOLOGY as the languages of boolean formulas that are tautologies. Show that TAUTOLOGY $\in$ co-NP.

Question 2 (3 marks)

Let $EQ_{REX} = \{< R, S > | R$ and $S$ are equivalent regular expressions$\}$. Show that $EQ_{REX} \in$ PSPACE.

Question 3 (2 marks)

Given a graph $G$, the MINIMUM COLORING problem asks one to color the vertices of $G$ with the minimum number of colors (such that no two nodes connecting an edge have the same color). So this is a (minimization) optimization problem. Prove that there is no approximation algorithm for MINIMUM COLORING with factor less than $4/3$, unless P=NP. (Hint: In assignment 3 we showed that even deciding whether the optimal color number is 3 is NP-complete.)

Question 4 (3 marks)

In class we showed that the Zero Exemplar Breakpoint Distance problem is NP-complete, if each gene is allowed to repeat at most 3 times. In this problem, you are to study the approximability of the Exemplar Breakpoint Distance problem on signed genomes (defined below).

Given a set of distinct genes $G$, an exemplar signed genome is a signed permutation of the genes (i.e., without gene repetition but each gene could have a positive or negative sign). Example: $G = \{a, b, c, d, e\}$, then $A = ac \cdot dbe$ is an exemplar signed genome over $G$. Given two exemplar signed genomes $A, B$, if two consecutive genes $xy$ appears in $A$ but neither $xy$ nor $-y - x$ appears in $B$ then $xy$ is a breakpoint in $A$. (Note that $-(xy) = -y - x$ and $-(-x) = x$.) The breakpoint distance between $A$ and $B$ is the number of breakpoints in $A$ (symmetrically in $B$). Example: $A = ac \cdot dbe, B = ad - cbe$, the breakpoint distance $bd(A, B) = 2$.

Now, given two signed genomes $A', B'$ with gene repetitions, the exemplar breakpoint distance between $A', B'$ is the minimum breakpoint distance between two exemplar genomes $A, B$ obtained from $A', B'$ by deleting redundant genes.
Show that if each gene appears in $A'$ ($B'$) at most twice, then the problem does not admit a factor 1.36 approximation via a reduction from Vertex Cover. (Vertex Cover is known to have no approximation with a factor 1.36 unless $P=NP$.)

**Date Due:** 11:30pm, **Friday, Nov 15, 2019.** You should upload your assignment in pdf format on D2L, under the “Assignment 4” directory.