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 \( \text{T AUTOLOGY} \) as the languages of boolean formulas that are tautologies. Show that \( \text{T AUTOLOGY} \in \text{co-NP} \).

Question 2 (3 marks)

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

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 \( A = ac - dbe \) 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: \( A = ac - dbe \), \( B = ad - cbe \), 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:** before the end of class on **Tuesday, Nov 14, 2017**. No late assignment will be accepted.