

CSCI 538 Computability

Assignment 4 (10 marks)

Question 1 (2 marks)

Let ϕ be a general boolean formula constructed from the boolean variables x_1, x_2, \dots, x_n , \neg, \vee, \wedge and parentheses. ϕ 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 $EQ_{REX} = \{ \langle R, S \rangle \mid R \text{ and } S \text{ are equivalent regular expressions} \}$. 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 $A = ac - db e$ 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: $A = ac - db e$, $B = ad - cbe$, 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.